

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
19 September 2002 (19.09.2002)

PCT

(10) International Publication Number  
**WO 02/071928 A2**

(51) International Patent Classification<sup>7</sup>: **A61B**  
(21) International Application Number: PCT/US02/07826  
(22) International Filing Date: 14 March 2002 (14.03.2002)  
(25) Filing Language: English  
(26) Publication Language: English

(30) Priority Data:  
60/276,025 14 March 2001 (14.03.2001) US  
60/276,026 14 March 2001 (14.03.2001) US  
60/311,732 10 August 2001 (10.08.2001) US  
60/323,580 19 September 2001 (19.09.2001) US  
60/325,149 26 September 2001 (26.09.2001) US  
60/324,967 26 September 2001 (26.09.2001) US  
60/325,102 26 September 2001 (26.09.2001) US

(71) Applicant (for all designated States except US): **MILLENNIUM PHARMACEUTICALS, INC.** [US/US]; 75 Sidney Street, Cambridge, MA 02139 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **MONAHAN, John, E.** [US/US]; 942 West Street, Walpole, MA 02081 (US). **GANNAVARAPU, Manjula** [IN/US]; 10 Windemere Drive, Acton, MA 01720 (US). **HOERSCH, Sebastian** [US/US]; 127 Brattle Street, Arlington, MA 02474 (US). **KAMATKAR, Shubhangi** [US/US]; 655 Saw Mill Brook Parkway, Apt. 1, Newton, MA 02459 (US). **KOVATIS, Steven, G.** [US/US]; 94 Aldrich Road, Wilmington, MA 01887 (US). **MEYERS, Rachel, E.** [US/US]; 115 Devonshire Road, Newton, MA 02468 (US). **MORRISEY, Michael, P.** [US/US]; 140 Kenrick Street, Apt. 32, Brighton, MA 02135 (US). **OLANDT, Peter, J.** [US/US]; 29 Florence Street, Newton, MA 02459 (US). **SEN, Ami** [US/US]; 66 Dinsmore Avenue, Apt. 507, Framingham,

MA 01702 (US). **VIEBY, Petter, Ole** [US/US]; 16 Nipmuck Drive, Westborough, MA 01581 (US). **MILLS, Gordon, B.** [CA/US]; 4124 Amherst Street, Houston, TX 77005 (US). **BAST, Robert, C., Jr.** [US/US]; 14 Memorial Point Lane, Houston, TX 77024 (US). **LU, Karen** [US/US]; 4127 Amherst Street, Houston, TX 77005 (US). **SCHMANDT, Rosemarie, E.** [CA/US]; 7300 Brompton Road, Apt. 5512, Houston, TX 77025 (US). **ZHAO, Xumei** [US/US]; 6 Wildwood Lane, Burlington, MA 01803 (US). **GLATT, Karen** [US/US]; 17 Beacon Street, Natick, MA 01760 (US).

(74) Agents: **SMITH, DeAnn, F. et al.**; Lahive & Cockfield, LLP, 28 State Street, Boston, MA 02109 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

**Published:**

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: NUCLEIC ACID MOLECULES AND PROTEINS FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF OVARIAN CANCER

(57) Abstract: The invention relates to newly discovered nucleic acid molecules and proteins associated with ovarian cancer. Compositions, kits, and methods for detecting, characterizing, preventing, and treating human ovarian cancers are provided.

- 1 -

NUCLEIC ACID MOLECULES AND PROTEINS FOR THE IDENTIFICATION,  
ASSESSMENT, PREVENTION, AND THERAPY OF  
OVARIAN CANCER

5

## RELATED APPLICATIONS

The present application claims priority from U.S. provisional patent application serial no. 60/276,025, filed on March 14, 2001, which was abandoned on September 25, 2001, and from U.S. provisional patent application serial no. 60/325,149, filed on September 26, 2001. The present application also claims priority from U.S. provisional  
10 patent application serial no. 60/276,026, filed on March 14, 2001, which was abandoned on September 25, 2001, and from U.S. provisional patent application serial no. 60/324,967, filed September 26, 2001. The present application additionally claims priority from U.S. provisional patent application serial no. 60/311,732, filed August 10, 2001, which was abandoned on September 25, 2001, and from U.S. provisional patent  
15 application serial no. 60/325,102, filed September 26, 2001. The present application also claims priority from U.S. provisional patent application serial no. 60/323,580, filed September 19, 2001. All of the above applications are expressly incorporated by reference.

20

## FIELD OF THE INVENTION

The field of the invention is ovarian cancer, including diagnosis, characterization, management, and therapy of ovarian cancer.

## BACKGROUND OF THE INVENTION

25

Ovarian cancer is responsible for significant morbidity and mortality in populations around the world. Ovarian cancer is classified, on the basis of clinical and pathological features, in three groups, namely epithelial ovarian cancer (EOC; >90% of ovarian cancer in Western countries), germ cell tumors (*circa* 2-3% of ovarian cancer), and stromal ovarian cancer (*circa* 5% of ovarian cancer; Ozols *et al.*, 1997, *Cancer Principles and Practice of Oncology*, 5th ed., DeVita *et al.*, Eds. pp. 1502). Relative to  
30 EOC, germ cell tumors and stromal ovarian cancers are more easily detected and treated

- 2 -

at an early stage, translating into higher/better survival rates for patients afflicted with these two types of ovarian cancer.

There are numerous types of ovarian tumors, some of which are benign, and others of which are malignant. Treatment (including non-treatment) options and predictions of patient outcome depend on accurate classification of the ovarian cancer. Ovarian cancers are named according to the type of cells from which the cancer is derived and whether the ovarian cancer is benign or malignant. Recognized histological tumor types include, for example, serous, mucinous, endometrioid, and clear cell tumors. In addition, ovarian cancers are classified according to recognized grade and stage scales.

In grade I, the tumor tissue is well differentiated. In grade II, tumor tissue is moderately well differentiated. In grade III, the tumor tissue is poorly differentiated. This grade correlates with a less favorable prognosis than grades I and II. Stage I is generally confined within the capsule surrounding one (stage IA) or both (stage IB) ovaries, although in some stage I (*i.e.* stage IC) cancers, malignant cells may be detected in ascites, in peritoneal rinse fluid, or on the surface of the ovaries. Stage II involves extension or metastasis of the tumor from one or both ovaries to other pelvic structures. In stage IIA, the tumor extends or has metastasized to the uterus, the fallopian tubes, or both. Stage IIB involves extension of the tumor to the pelvis. Stage IIC is stage IIA or IIB in which malignant cells may be detected in ascites, in peritoneal rinse fluid, or on the surface of the ovaries. In stage III, the tumor comprises at least one malignant extension to the small bowel or the omentum, has formed extrapelvic peritoneal implants of microscopic (stage IIIA) or macroscopic (< 2 centimeter diameter, stage IIIB; > 2 centimeter diameter, stage IIIC) size, or has metastasized to a retroperitoneal or inguinal lymph node (an alternate indicator of stage IIIC). In stage IV, distant (*i.e.* non-peritoneal) metastases of the tumor can be detected.

The durations of the various stages of ovarian cancer are not presently known, but are believed to be at least about a year each (Richart *et al.*, 1969, *Am. J. Obstet. Gynecol.* 105:386). Prognosis declines with increasing stage designation. For example, 5-year survival rates for patients diagnosed with stage I, II, III, and IV ovarian cancer are 80%, 57%, 25%, and 8%, respectively.

- 3 -

Despite being the third most prevalent gynecological cancer, ovarian cancer is the leading cause of death among those afflicted with gynecological cancers. The disproportionate mortality of ovarian cancer is attributable to a substantial absence of symptoms among those afflicted with early-stage ovarian cancer and to difficulty  
5 diagnosing ovarian cancer at an early stage. Patients afflicted with ovarian cancer most often present with non-specific complaints, such as abnormal vaginal bleeding, gastrointestinal symptoms, urinary tract symptoms, lower abdominal pain, and generalized abdominal distension. These patients rarely present with paraneoplastic symptoms or with symptoms which clearly indicate their affliction. Presently, less than  
10 about 40% of patients afflicted with ovarian cancer present with stage I or stage II. Management of ovarian cancer would be significantly enhanced if the disease could be detected at an earlier stage, when treatments are much more generally efficacious.

Ovarian cancer may be diagnosed, in part, by collecting a routine medical history from a patient and by performing physical examination, x-ray examination, and  
15 chemical and hematological studies on the patient. Hematological tests which may be indicative of ovarian cancer in a patient include analyses of serum levels of proteins designated CA125 and DF3 and plasma levels of lysophosphatidic acid (LPA). Palpation of the ovaries and ultrasound techniques (particularly including endovaginal ultrasound and color Doppler flow ultrasound techniques) can aid detection of ovarian  
20 tumors and differentiation of ovarian cancer from benign ovarian cysts. However, a definitive diagnosis of ovarian cancer typically requires performing exploratory laparotomy of the patient.

Potential tests for the detection of ovarian cancer (*e.g.*, screening, reflex or monitoring) may be characterized by a number of factors. The "sensitivity" of an  
25 assay refers to the probability that the test will yield a positive result in an individual afflicted with ovarian cancer. The "specificity" of an assay refers to the probability that the test will yield a negative result in an individual not afflicted with ovarian cancer. The "positive predictive value" (PPV) of an assay is the ratio of true positive results (*i.e.* positive assay results for patients afflicted with ovarian cancer) to all positive results  
30 (*i.e.* positive assay results for patients afflicted with ovarian cancer + positive assay results for patients not afflicted with ovarian cancer). It has been estimated that in order for an assay to be an appropriate population-wide screening tool for ovarian cancer the



assay must have a PPV of at least about 10% (Rosenthal *et al.*, 1998, *Sem. Oncol.* 25:315-325). It would thus be desirable for a screening assay for detecting ovarian cancer in patients to have a high sensitivity and a high PPV. Monitoring and reflex tests would also require appropriate specifications.

5           Owing to the cost, limited sensitivity, and limited specificity of known methods of detecting ovarian cancer, screening is not presently performed for the general population. In addition, the need to perform laparotomy in order to diagnose ovarian cancer in patients who screen positive for indications of ovarian cancer limits the desirability of population-wide screening, such that a PPV even greater than 10%  
10   would be desirable.

          Prior use of serum CA125 level as a diagnostic marker for ovarian cancer indicated that this method exhibited insufficient specificity for use as a general screening method. Use of a refined algorithm for interpreting CA125 levels in serial retrospective samples obtained from patients improved the specificity of the method  
15   without shifting detection of ovarian cancer to an earlier stage (Skakes, 1995, *Cancer* 76:2004). Screening for LPA to detect gynecological cancers including ovarian cancer exhibited a sensitivity of about 96% and a specificity of about 89%. However, CA125-based screening methods and LPA-based screening methods are hampered by the presence of CA125 and LPA, respectively, in the serum of patients afflicted with  
20   conditions other than ovarian cancer. For example, serum CA125 levels are known to be associated with menstruation, pregnancy, gastrointestinal and hepatic conditions such as colitis and cirrhosis, pericarditis, renal disease, and various non-ovarian malignancies. Serum LPA is known, for example, to be affected by the presence of non-ovarian gynecological malignancies. A screening method having a greater specificity for  
25   ovarian cancer than the current screening methods for CA125 and LPA could provide a population-wide screening for early stage ovarian cancer.

          Presently greater than about 60% of ovarian cancers diagnosed in patients are stage III or stage IV cancers. Treatment at these stages is largely limited to cytoreductive surgery (when feasible) and chemotherapy, both of which aim to slow the  
30   spread and development of metastasized tumor. Substantially all late stage ovarian cancer patients currently undergo combination chemotherapy as primary treatment, usually a combination of a platinum compound and a taxane. Median survival for

- 5 -

responding patients is about one year. Combination chemotherapy involving agents such as doxorubicin, cyclophosphamide, cisplatin, hexamethylmelamine, paclitaxel, and methotrexate may improve survival rates in these groups, relative to single-agent therapies. Various recently-developed chemotherapeutic agents and treatment regimens have also demonstrated usefulness for treatment of advanced ovarian cancer. For example, use of the topoisomerase I inhibitor topectan, use of amifostine to minimize chemotherapeutic side effects, and use of intraperitoneal chemotherapy for patients having peritoneally implanted tumors have demonstrated at least limited utility. Presently, however, the 5-year survival rate for patients afflicted with stage III ovarian cancer is 25%, and the survival rate for patients afflicted with stage IV ovarian cancer is 8%.

In summary, the earlier ovarian cancer is detected, the aggressiveness of therapeutic intervention and the side effects associated with therapeutic intervention are minimized. More importantly, the earlier the cancer is detected, the survival rate and quality of life of ovarian cancer patients is enhanced. Thus, a pressing need exists for methods of detecting ovarian cancer as early as possible. There also exists a need for methods of detecting recurrence of ovarian cancer as well as methods for predicting and monitoring the efficacy of treatment. There further exists a need for new therapeutic methods for treating ovarian cancer. The present invention satisfies these needs.

20

#### SUMMARY OF THE INVENTION

The invention relates to cancer markers (hereinafter "markers" or "markers of the inventions"), which are listed in Tables 1-3. The invention provides nucleic acids and proteins that are encoded by or correspond to the markers (hereinafter "marker nucleic acids" and "marker proteins," respectively). The invention further provides antibodies, antibody derivatives and antibody fragments which bind specifically with such proteins and/or fragments of the proteins.

In one aspect, the invention relates to various diagnostic, monitoring, test and other methods related to ovarian cancer detection and therapy. In one embodiment, the invention provides a diagnostic method of assessing whether a patient has ovarian cancer or has higher than normal risk for developing ovarian cancer, comprising the steps of comparing the level of expression of a marker of the invention in a patient

30

sample and the normal level of expression of the marker in a control, *e.g.*, a sample from a patient without ovarian cancer. A significantly higher level of expression of the marker in the patient sample as compared to the normal level is an indication that the patient is afflicted with ovarian cancer or has higher than normal risk for developing  
5 ovarian cancer.

In a preferred embodiment of the diagnostic method, the marker is over-expressed by at least two-fold in at least about 20% of stage I ovarian cancer patients, stage II ovarian cancer patients, stage III ovarian cancer patients, stage IV ovarian cancer patients, grade I ovarian cancer patients, grade II ovarian cancer patients, grade  
10 III ovarian cancer patients, epithelial ovarian cancer patients, stromal ovarian cancer patients, germ cell ovarian cancer patients, malignant ovarian cancer patients, benign ovarian cancer patients, serous neoplasm ovarian cancer patients, mucinous neoplasm ovarian cancer patients, endometrioid neoplasm ovarian cancer patients and/or clear cell neoplasm ovarian cancer patients.

The diagnostic methods of the present invention are particularly useful for patients with an identified pelvic mass or symptoms associated with ovarian cancer. The methods of the present invention can also be of particular use with patients having an enhanced risk of developing ovarian cancer (*e.g.*, patients having a familial history of ovarian cancer, patients identified as having a mutant oncogene, and patients at least  
15 about 50 years of age).

In a preferred diagnostic method of assessing whether a patient is afflicted with ovarian cancer (*e.g.*, new detection ("screening"), detection of recurrence, reflex testing), the method comprises comparing:

- a) the level of expression of a marker of the invention in a patient sample,  
25 and
- b) the normal level of expression of the marker in a control non-ovarian cancer sample.

A significantly higher level of expression of the marker in the patient sample as compared to the normal level is an indication that the patient is afflicted with ovarian  
30 cancer.

- 7 -

The invention also provides diagnostic methods for assessing the efficacy of a therapy for inhibiting ovarian cancer in a patient. Such methods comprise comparing:

- 5 a) expression of a marker of the invention in a first sample obtained from the patient prior to providing at least a portion of the therapy to the patient, and
- b) expression of the marker in a second sample obtained from the patient following provision of the portion of the therapy.

10 A significantly lower level of expression of the marker in the second sample relative to that in the first sample is an indication that the therapy is efficacious for inhibiting ovarian cancer in the patient.

It will be appreciated that in these methods the "therapy" may be any therapy for treating ovarian cancer including, but not limited to, chemotherapy, radiation therapy, surgical removal of tumor tissue, gene therapy and biologic therapy such as the  
15 administering of antibodies and chemokines. Thus, the methods of the invention may be used to evaluate a patient before, during and after therapy, for example, to evaluate the reduction in tumor burden.

In a preferred embodiment, the diagnostic methods of the present invention are directed to therapy using a chemical or biologic agent. These methods  
20 comprise comparing:

- a) expression of a marker of the invention in a first sample obtained from the patient and maintained in the presence of the chemical or biologic agent, and
- 25 b) expression of the marker in a second sample obtained from the patient and maintained in the absence of the agent.

A significantly lower level of expression of the marker in the first sample relative to that in the second sample is an indication that the agent is efficacious for inhibiting ovarian cancer in the patient. In one embodiment, the first and second samples can be portions of a single sample obtained from the patient or portions of pooled samples obtained  
30 from the patient.

The invention additionally provides a monitoring method for assessing the progression of ovarian cancer in a patient, the method comprising:

- a) detecting in a patient sample at a first time point, the expression of a marker of the invention;
- 5       b) repeating step a) at a subsequent time point in time; and
- c) comparing the level of expression detected in steps a) and b), and therefrom monitoring the progression of ovarian cancer in the patient.

A significantly higher level of expression of the marker in the sample at the subsequent time point from that of the sample at the first time point is an indication that the ovarian cancer has progressed, whereas a significantly lower level of expression is an indication  
10       that the ovarian cancer has regressed.

The invention further provides a diagnostic method for determining whether ovarian cancer has metastasized or is likely to metastasize in the future, the method comprising comparing:

- 15       a) the level of expression of a marker of the invention in a patient sample, and
- b) the normal level (or non-metastatic level) of expression of the marker in a control sample.

A significantly higher level of expression in the patient sample as compared to the  
20       normal level (or non-metastatic level) is an indication that the ovarian cancer has metastasized or is likely to metastasize in the future.

The invention moreover provides a test method for selecting a composition for inhibiting ovarian cancer in a patient. This method comprises the steps of:

- 25       a) obtaining a sample comprising cancer cells from the patient;
- b) separately maintaining aliquots of the sample in the presence of a plurality of test compositions;
- c) comparing expression of a marker of the invention in each of the aliquots; and
- 30       d) selecting one of the test compositions which significantly reduces the level of expression of the marker in the aliquot containing that test

composition, relative to the levels of expression of the marker in the presence of the other test compositions.

The invention additionally provides a test method of assessing the ovarian carcinogenic potential of a compound. This method comprises the steps of:

- 5           a) maintaining separate aliquots of ovarian cells in the presence and absence of the compound; and
- b) comparing expression of a marker of the invention in each of the aliquots.

10           A significantly higher level of expression of the marker in the aliquot maintained in the presence of the compound, relative to that of the aliquot maintained in the absence of the compound, is an indication that the compound possesses ovarian carcinogenic potential.

In addition, the invention further provides a method of inhibiting ovarian cancer in a patient. This method comprises the steps of:

- 15           a) obtaining a sample comprising cancer cells from the patient;
- b) separately maintaining aliquots of the sample in the presence of a plurality of compositions;
- c) comparing expression of a marker of the invention in each of the aliquots; and
- 20           d) administering to the patient at least one of the compositions which significantly lowers the level of expression of the marker in the aliquot containing that composition, relative to the levels of expression of the marker in the presence of the other compositions.

In the aforementioned methods, the samples or patient samples comprise cells obtained from the patient. The cells may be found in an ovarian tissue sample

25   collected, for example, by an ovarian tissue biopsy or histology section. In one embodiment, the patient sample is an ovary-associated body fluid. Such fluids include, for example, blood fluids, lymph, ascites fluids, gynecological fluids, cystic fluids, urine, and fluids collected by peritoneal rinsing. In another embodiment, the sample comprises cells obtained from the patient. In this embodiment, the cells may be found in

30   a fluid selected from the group consisting of a fluid collected by peritoneal rinsing, a fluid collected by uterine rinsing, a uterine fluid, a uterine exudate, a pleural fluid, and an ovarian exudate. In a further embodiment, the patient sample is *in vivo*.

According to the invention, the level of expression of a marker of the invention in a sample can be assessed, for example, by detecting the presence in the sample of:

- 5       • the corresponding marker protein or a fragment of the protein (*e.g.* by using a reagent, such as an antibody, an antibody derivative, an antibody fragment or single-chain antibody, which binds specifically with the protein or protein fragment).
- 10       • the corresponding marker nucleic acid or a fragment of the nucleic acid (*e.g.* by contacting transcribed polynucleotides obtained from the sample with a substrate having affixed thereto one or more nucleic acids having the entire or a segment of the sequence or a complement thereof)
- a metabolite which is produced directly (*i.e.*, catalyzed) or indirectly by the corresponding marker protein.

According to the invention, any of the aforementioned methods may be performed using a plurality (*e.g.* 2, 3, 5, or 10 or more) of ovarian cancer markers, including ovarian cancer markers known in the art. In such methods, the level of expression in the sample of each of a plurality of markers, at least one of which is a marker of the invention, is compared with the normal level of expression of each of the plurality of markers in samples of the same type obtained from control humans not afflicted with ovarian cancer. A significantly altered (*i.e.*, increased or decreased as specified in the above-described methods using a single marker) level of expression in the sample of one or more markers of the invention, or some combination thereof, relative to that marker's corresponding normal levels, is an indication that the patient is afflicted with ovarian cancer. For all of the aforementioned methods, the marker(s) are preferably selected such that the positive predictive value of the method is at least about 10%.

In a further aspect, the invention provides an antibody, an antibody derivative, or an antibody fragment, which binds specifically with a marker protein or a fragment of the protein. The invention also provides methods for making such antibody, antibody derivative, and antibody fragment. Such methods may comprise immunizing a mammal with a protein or peptide comprising the entirety, or a segment of 10 amino acids or more, of a marker protein, wherein the protein or peptide may be obtained from

- 11 -

a cell or by chemical synthesis. The methods of the invention also encompass producing monoclonal and single-chain antibodies, which would further comprise isolating splenocytes from the immunized mammal, fusing the isolated splenocytes with an immortalized cell line to form hybridomas, and screening individual hybridomas for those that produce an antibody that binds specifically with a marker protein or a fragment of the protein.

In another aspect, the invention relates to various diagnostic and test kits. In one embodiment, the invention provides a kit for assessing whether a patient is afflicted with ovarian cancer. The kit comprises a reagent for assessing expression of a marker of the invention. In another embodiment, the invention provides a kit for assessing the suitability of a chemical or biologic agent for inhibiting an ovarian cancer in a patient. Such kit comprises a reagent for assessing expression of a marker of the invention, and may also comprise one or more of such agents. In a further embodiment, the invention provides kits for assessing the presence of ovarian cancer cells or treating ovarian cancers. Such kits comprise an antibody, an antibody derivative, or an antibody fragment, which binds specifically with a marker protein, or a fragment of the protein. Such kits may also comprise a plurality of antibodies, antibody derivatives, or antibody fragments wherein the plurality of such antibody agents binds specifically with a marker protein, or a fragment of the protein.

In an additional embodiment, the invention also provides a kit for assessing the presence of ovarian cancer cells, wherein the kit comprises a nucleic acid probe that binds specifically with a marker nucleic acid or a fragment of the nucleic acid. The kit may also comprise a plurality of probes, wherein each of the probes binds specifically with a marker nucleic acid, or a fragment of the nucleic acid.

In a further aspect, the invention relates to methods for treating a patient afflicted with ovarian cancer or at risk of developing ovarian cancer. Such methods may comprise reducing the expression and/or interfering with the biological function of a marker of the invention. In one embodiment, the method comprises providing to the patient an antisense oligonucleotide or polynucleotide complementary to a marker nucleic acid, or a segment thereof. For example, an antisense polynucleotide may be provided to the patient through the delivery of a vector that expresses an antisense polynucleotide of a marker nucleic acid or a fragment thereof. In another embodiment,



the method comprises providing to the patient an antibody, an antibody derivative, or antibody fragment, which binds specifically with a marker protein or a fragment of the protein. In a preferred embodiment, the antibody, antibody derivative or antibody fragment binds specifically with a protein having the sequence of any of the markers  
5 listed in Table 1, or a fragment of such a protein.

It will be appreciated that the methods and kits of the present invention may also include known cancer markers including known ovarian cancer markers. It will further be appreciated that the methods and kits may be used to identify cancers other than ovarian cancer.

10

### BRIEF DESCRIPTION OF THE DRAWINGS

*Figure 1* depicts a graph which represents the results of the TaqMan® expression study.

15

### DETAILED DESCRIPTION OF THE INVENTION

The invention relates to newly discovered markers, identified in Tables 1-3, that are associated with the cancerous state of ovarian cells. It has been discovered that the higher than normal level of expression of any of these markers or combination of these markers correlates with the presence of ovarian cancer in a patient. Methods  
20 are provided for detecting the presence of ovarian cancer in a sample, the absence of ovarian cancer in a sample, the stage of an ovarian cancer, and with other characteristics of ovarian cancer that are relevant to prevention, diagnosis, characterization, and therapy of ovarian cancer in a patient. Methods of treating ovarian cancer are also provided.

Tables 1-3 list the markers of the present invention. In the Tables the  
25 markers are identified with a name ("Marker"), the name the gene is commonly known by, if applicable ("Gene Name"), the Sequence Listing identifier of the cDNA sequence of a nucleotide transcript encoded by or corresponding to the marker ("SEQ ID NO (nts)"), the Sequence Listing identifier of the amino acid sequence of a protein encoded by the nucleotide transcript ("SEQ ID NO (AAs)"), and the location of the protein  
30 coding sequence within the cDNA sequence ("CDS").

Table 1 lists all of the markers of the invention, which are over-expressed in ovarian cancer cells compared to normal (*i.e.*, non-cancerous) ovarian cells and comprises markers listed in Tables 2 and 3. Table 2 lists newly-identified nucleotide

and amino acid sequences useful as ovarian cancer markers. Table 3 lists newly-identified nucleotide sequences useful as ovarian cancer markers.

In addition to their use in ovarian cancer, it has been found that the markers of the present invention may be used in the diagnosis, characterization, management, and therapy of additional diseases. For example, OV65 (SEQ ID NOS: 305 and 306), M593 (SEQ ID NOS: 307 and 308) and M594 (SEQ ID NOS: 309 and 310), are spondin molecules, and have one or more of the following activities: (1) neural cell adhesion and (2) neurite extension and can thus be used in, for example, the diagnosis and treatment of brain and CNS related disorders. Such brain and CNS related disorders include, but are not limited to, bacterial and viral meningitis, Alzheimers Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers (e.g., metastatic carcinoma of the brain, glioblastoma, lymphoma, astrocytoma, acoustic neuroma), hydrocephalus, and encephalitis. In another example, OV65, M593 and M594 polypeptides, nucleic acids, and modulators thereof can be used to treat disorders of the brain, such as cerebral edema, hydrocephalus, brain herniations, iatrogenic disease (due to, e.g., infection, toxins, or drugs), inflammations (e.g., bacterial and viral meningitis, encephalitis, and cerebral toxoplasmosis), cerebrovascular diseases (e.g., hypoxia, ischemia, infarction, intracranial hemorrhage, vascular malformations, and hypertensive encephalopathy), and tumors (e.g., neuroglial tumors, neuronal tumors, tumors of pineal cells, meningeal tumors, primary and secondary lymphomas, intracranial tumors, and medulloblastoma), and to treat injury or trauma to the brain.

OV25 (SEQ ID NOS: 360 and 361), an HE4 protein, has one or more of the following activities: (1) sperm maturation and (2) inhibition of extracellular proteases and can thus be used in, for example, the treatment and diagnosis of diseases and disorders relating to spermatogenesis. For example, OV25 polypeptides, nucleic acids, and modulators thereof can be used to treat testicular disorders, such as unilateral testicular enlargement (e.g., nontuberculous, granulomatous orchitis); inflammatory diseases resulting in testicular dysfunction (e.g., gonorrhea and mumps); cryptorchidism; sperm cell disorders (e.g., immotile cilia syndrome and germinal cell aplasia); acquired testicular defects (e.g., viral orchitis); and tumors (e.g., germ cell tumors, interstitial cell tumors, androblastoma, testicular lymphoma and adenomatoid tumors).

OV52 (SEQ ID NOS: 190 and 191), a Pump-1 proteinase, has been found to have one or more of the following activities: (1) breakdown of extracellular matrix in normal physiological processes, such as embryonic development, reproduction, and remodeling, as well as in (2) disease processes, such as arthritis, and metastasis. Hence, 5 OV52 nucleic acids, proteins, and modulators thereof can be used to modulate disorders associated with adhesion and migration of cells, *e.g.*, platelet aggregation disorders (*e.g.*, Glanzmann's thromboasthenia, which is a bleeding disorder characterized by failure of platelet aggregation in response to cell stimuli), inflammatory disorders (*e.g.*, leukocyte adhesion deficiency, which is a disorder associated with impaired migration of 10 neutrophils to sites of extravascular inflammation), connective tissue disorders, arthritis, disorders associated with abnormal tissue migration during embryo development, and tumor metastasis.

M604 (SEQ ID NOS: 48 and 49), OV10 (SEQ ID NOS: 50 and 51), and M360 (SEQ ID NOS: 52 and 53), are Claudin molecules which have one or more of the 15 following activities: (1) it elicits fluid accumulation in the intestinal tract by altering the membrane permeability of intestinal epithelial cells and (2) thus acts as the causative agent of diarrhea. The polypeptides, nucleic acids, and modulators thereof can be used to treat colonic disorders, such as congenital anomalies (*e.g.*, megacolon and imperforate anus), idiopathic disorders (*e.g.*, diverticular disease and melanosis coli), vascular 20 lesions (*e.g.*, ischemic colitis, hemorrhoids, angiodysplasia), inflammatory diseases (*e.g.*, colitis (*e.g.*, idiopathic ulcerative colitis, pseudomembranous colitis), and lymphopathia venereum), Crohn's disease, and tumors (*e.g.*, hyperplastic polyps, adenomatous polyps, bronchogenic cancer, colonic carcinoma, squamous cell carcinoma, adenoacanthomas, sarcomas, lymphomas, argentaffinomas, carcinoids, and 25 melanocarcinomas).

OV48 (SEQ ID NOS: 226 and 227), OV49 (SEQ ID NOS: 228 and 229) and OV50 (SEQ ID NOS: 230 and 231), markers for an osteopontin protein, have one or more of the following activities: (1) they act as a vessel extracellular matrix protein involved in calcification and (2) atherosclerosis. Hence, OV48, OV49 and OV50 30 nucleic acids, proteins, and modulators thereof can be used to treat heart disorders, *e.g.*, ischemic heart disease, atherosclerosis, hypertension, angina pectoris, Hypertrophic Cardiomyopathy, and congenital heart disease. They can also be used to treat

cardiovascular disorders, such as ischemic heart disease (*e.g.*, angina pectoris, myocardial infarction, and chronic ischemic heart disease), hypertensive heart disease, pulmonary heart disease, valvular heart disease (*e.g.*, rheumatic fever and rheumatic heart disease, endocarditis, mitral valve prolapse, and aortic valve stenosis), congenital heart disease (*e.g.*, valvular and vascular obstructive lesions, atrial or ventricular septal defect, and patent ductus arteriosus), or myocardial disease (*e.g.*, myocarditis, congestive cardiomyopathy, and hypertrophic cardiomyopathy).

OV37 (SEQ ID NOS: 176 and 177), a lipocalin marker, is known to be a component of the neutrophil gelatinase complex. OV37 nucleic acids, proteins, and modulators thereof can be used to modulate the proliferation, differentiation, and/or function of leukocytes. Thus, OV37 nucleic acids, proteins, and modulators thereof can be used to treat bone marrow, blood, and hematopoietic associated diseases and disorders, *e.g.*, acute myeloid leukemia, hemophilia, leukemia, anemia (*e.g.*, sickle cell anemia), and thalassemia. OV37 polypeptides, nucleic acids, and modulators thereof can be used to treat leukocytic disorders, such as leukopenias (*e.g.*, neutropenia, monocytopenia, lymphopenia, and granulocytopenia), leukocytosis (*e.g.*, granulocytosis, lymphocytosis, eosinophilia, monocytosis, acute and chronic lymphadenitis), malignant lymphomas (*e.g.*, Non-Hodgkin's lymphomas, Hodgkin's lymphomas, leukemias, agnogenic myeloid metaplasia, multiple myeloma, plasmacytoma, Waldenstrom's macroglobulinemia, heavy-chain disease, monoclonal gammopathy, histiocytoses, eosinophilic granuloma, and angioimmunoblastic lymphadenopathy).

OV2 (SEQ ID NOS: 285 and 286), is known to be a protease inhibitor, which is associated with emphysema and liver disease. Hence OV2 polypeptides, nucleic acids, and modulators thereof can be used to diagnose and treat pulmonary (lung) disorders, such as atelectasis, cystic fibrosis, rheumatoid lung disease, pulmonary congestion or edema, chronic obstructive airway disease (*e.g.*, emphysema, chronic bronchitis, bronchial asthma, and bronchiectasis), diffuse interstitial diseases (*e.g.*, sarcoidosis, pneumoconiosis, hypersensitivity pneumonitis, bronchiolitis, Goodpasture's syndrome, idiopathic pulmonary fibrosis, idiopathic pulmonary hemosiderosis, pulmonary alveolar proteinosis, desquamative interstitial pneumonitis, chronic interstitial pneumonia, fibrosing alveolitis, hamman-rich syndrome, pulmonary eosinophilia, diffuse interstitial fibrosis, Wegener's granulomatosis, lymphomatoid

granulomatosis, and lipid pneumonia), or tumors (*e.g.*, bronchogenic carcinoma, bronchioloalveolar carcinoma, bronchial carcinoid, hamartoma, and mesenchymal tumors). In another example, OV2 polypeptides, nucleic acids, and modulators thereof can be used to diagnose and treat hepatic (liver) disorders, such as jaundice, hepatic failure, hereditary hyperbilirubinemias (*e.g.*, Gilbert's syndrome, Crigler-Najjar syndromes and Dubin-Johnson and Rotor's syndromes), hepatic circulatory disorders (*e.g.*, hepatic vein thrombosis and portal vein obstruction and thrombosis), hepatitis (*e.g.*, chronic active hepatitis, acute viral hepatitis, and toxic and drug-induced hepatitis), cirrhosis (*e.g.*, alcoholic cirrhosis, biliary cirrhosis, and hemochromatosis), or malignant tumors (*e.g.*, primary carcinoma, hepatoma, hepatoblastoma, liver cysts, and angiosarcoma).

OV32 (SEQ ID NOS: 166 and 167) and OV33 (SEQ ID NOS: 168 and 169), kallikrein markers, are useful in detection of primary mammary carcinomas, as well as primary ovarian cancers. Hence, OV32 and OV33 polypeptides, nucleic acids, and modulators thereof can be used to diagnose and treat ovarian disorders, such as ovarian endometriosis, non-neoplastic cysts (*e.g.*, follicular and luteal cysts and polycystic ovaries) and tumors (*e.g.*, carcinomas, tumors of surface epithelium, germ cell tumors, ovarian fibroma, sex cord-stromal tumors, and ovarian cancers (*e.g.*, metastatic carcinomas, and ovarian teratoma)).

OV68 (SEQ ID NOS: 192 and 193), OV69 (SEQ ID NOS: 194 and 195), OV70 (SEQ ID NOS: 196 and 197), OV71 (SEQ ID NOS: 198 and 199), OV72 (SEQ ID NOS: 200 and 201), OV41 (SEQ ID NOS: 202 and 203), OV42 (SEQ ID NOS: 204 and 205), OV43 (SEQ ID NOS: 206 and 205), OV44 (SEQ ID NOS: 207 and 208) and OV83 (SEQ ID NOS: 209 and 210), are all mesothelin markers, and have been found to play a role in cellular adhesion. The nucleic acids, proteins, and modulators thereof can be used to diagnose, treat and modulate disorders associated with adhesion and migration of cells, *e.g.*, platelet aggregation disorders (*e.g.*, Glanzmann's thrombasthenia, which is a bleeding disorder characterized by failure of platelet aggregation in response to cell stimuli), inflammatory disorders (*e.g.*, leukocyte adhesion deficiency, which is a disorder associated with impaired migration of neutrophils to sites of extravascular inflammation), disorders associated with abnormal tissue migration during embryo development, and tumor metastasis.

- 17 -

OV17 (SEQ ID NOS: 110 and 111), OV18 (SEQ ID NOS: 112 and 111), OV19 (SEQ ID NOS: 113 and 111), OV20 (SEQ ID NOS: 114 and 111), OV21 (SEQ ID NOS: 115 and 111) and OV22 (SEQ ID NOS: 116 and 117) are folate receptors, which are known to be markers of ovarian cancer. The nucleic acids, proteins, and modulators thereof can be used to diagnose, treat and modulate ovarian disorders (*e.g.*, ovarian cyst, ovarian fibroma, ovarian endometriosis, ovarian teratoma). Although these markers have been previously associated with ovarian cancer, the expression of such markers has not yet been identified in combination with the expression of other markers including those of the present invention. Such combination of markers will provide improved methods of diagnosing, characterizing, managing and treating ovarian cancer.

OV66 (SEQ ID NOS: 54 and 55), OV7 (SEQ ID NOS: 56 and 57), OV8 (SEQ ID NOS: 58 and 59) and OV81 (SEQ ID NOS: 60 and 61) are ceruloplasmin markers, known to encode a plasma metalloprotein that binds copper in the plasma. The nucleic acids, proteins, and modulators thereof can be used to diagnose, treat and modulate disorders in blood haemostasis and diseases caused by such an imbalance *e.g.*, (1) cardiovascular diseases or disorders, such as ischemic heart disease (*e.g.*, angina pectoris, myocardial infarction, and chronic ischemic heart disease), hypertensive heart disease, pulmonary heart disease, valvular heart disease (*e.g.*, rheumatic fever and rheumatic heart disease, endocarditis, mitral valve prolapse, and aortic valve stenosis), congenital heart disease (*e.g.*, valvular and vascular obstructive lesions, atrial or ventricular septal defect, and patent ductus arteriosus), or myocardial disease (*e.g.*, myocarditis, congestive cardiomyopathy, and hypertrophic cardiomyopathy); (2) neuronal diseases such as Alzheimers Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis, brain cancers (*e.g.*, metastatic carcinoma of the brain, glioblastoma, lymphoma, astrocytoma, acoustic neuroma), hydrocephalus, and encephalitis; and (3) Wilson's Disease.

- 18 -

**TABLE 1**

Marker	Gene Name	SEQ ID NO (nts)	SEQ ID NO (AAs)	CDS
OV1	ABCB1: ATP-binding cassette, sub-family B (MDR/TAP), member 1	1	2	425..4264
M430	ADPRT: ADP-ribosyltransferase	3	4	160..3204
M571	ANXA2: annexin A2, variant 1	5	6	134..1153
M572	ANXA2: annexin A2, variant 2	7	8	50..1069
M573	ANXA4: annexin A4	9	10	74..1039
OV3	AQP5: aquaporin 5	11	12	519..1316
M352	ARHGAP8: Rho GTPase activating protein 8, variant 1	13	14	142..1536
M353	ARHGAP8: Rho GTPase activating protein 8, variant 2	15	16	1..2043
M354	ARHGAP8: Rho GTPase activating protein 8, variant 3	17	18	1..2256
M608	ARHGAP8: Rho GTPase activating protein 8, variant 4	17	19	1..2157
M355	ARHGAP8: Rho GTPase activating protein 8, variant 5	20	21	<1..1314
M356	ARHGAP8: Rho GTPase activating protein 8, variant 6	22	23	1..1902
M357	ARHGAP8: Rho GTPase activating protein 8, variant 7	24	25	<1..1281
M358	ARHGAP8: Rho GTPase activating protein 8, variant 8	26	27	1..1386
M359	ARHGAP8: Rho GTPase activating protein 8, variant 9	28	29	<1..1059
OV5	BICD1: Bicaudal D homolog 1 (Drosophila)	30	31	82..3009
M431	BTG2: BTG family, member 2	32	33	72..548
M432	CADPS: Ca <sup>2+</sup> -dependent activator protein for secretion	34	35	240..4412
M609	CDH1: cadherin 1, type 1, E-cadherin (epithelial)	36	37	125..2773
M433	CDH6: cadherin 6, type 2, K-cadherin	38	39	327..2699
M434	CDKN2A: cyclin-dependent kinase inhibitor 2A	40	41	41..511
OV9	CGN: cingulin	42	43	152..3763
OV6	CHI3L1: cartilage glycoprotein-39	44	45	127..1278
M435	CKMT1: creatine kinase, mitochondrial 1 (ubiquitous)	46	47	164..1417
M604	CLDN10: claudin 10	48	49	36..772
OV10	CLDN16: claudin 16	50	51	69..986
M360	CLDN4: claudin 4	52	53	183..812
OV66	CP: ceruloplasmin (ferroxidase), variant 1	54	55	1..3210
OV7	CP: ceruloplasmin (ferroxidase), variant 2	56	57	<1..2561
OV8	CP: ceruloplasmin (ferroxidase), variant 3	58	59	1..3198
OV81	CP: ceruloplasmin (ferroxidase), variant 4	60	61	76..3348
M103	CRABP2: cellular retinoic acid-binding protein 2	62	63	138..554

OV40	DD96: Epithelial protein up-regulated in carcinoma, membrane associated protein 17	64	65	202..546
OV4	DEC2: basic helix-loop-helix protein	66	67	135..1583
M575	dehydrogenase	68	69	339..1364
M436	DLX5: distal-less homeo box 5	70	71	204..1073
OV12	EAB1: Eab1 protein	72	73	<1..1305
OV13	ESX protein	74	75	96..1211
OV67	EVI-1: Evi-1 protein, variant 1	76	77	250..2406
OV14	EVI-1: Evi-1 protein, variant 2	78	79	250..3405
OV15	EVI-1: Evi-1 protein, variant 3	80	81	250..2433
OV16	EVI-1: Evi-1 protein, variant 4	82	83	250..3378
M437	FLJ10546: hypothetical protein FLJ10546	84	85	28..1815
OV28	FLJ12799: hypothetical protein FLJ12799	86	87	39..797
M576	FLJ13710: hypothetical protein FLJ13710	88	89	96..1712
M438	FLJ13782: hypothetical protein FLJ13782	90	91	13..1890
OV29	FLJ20150: hypothetical protein FLJ20150	92	93	78..983
M439	FLJ20327: hypothetical protein FLJ20327	94	95	306..2186
M440	FLJ20758: hypothetical protein FLJ20758, variant 1	96	97	<2..1270
M441	FLJ20758: hypothetical protein FLJ20758, variant 2	98	99	<2..2095
M442	FLJ20758: hypothetical protein FLJ20758, variant 3	100	101	465..1307
M443	FLJ22252: likely ortholog of mouse SRY-box containing gene 17	102	103	205..1449
M444	FLJ22316: hypothetical protein FLJ22316	104	105	508..1206
M400	FLJ22418: hypothetical protein FLJ22418	106	107	71..919
M445	FLJ23499: hypothetical protein FLJ23499	108	109	21..473
OV17	FOLR1: folate receptor 1 (alpha), variant 1	110	111	139..912
OV18	FOLR1: folate receptor 1 (alpha), variant 2	112	111	211..984
OV19	FOLR1: folate receptor 1 (alpha), variant 3	113	111	46..819
OV20	FOLR1: folate receptor 1 (alpha), variant 4	114	111	437..1210
OV21	FOLR1: folate receptor 1 (alpha), variant 5	115	111	11..784
OV22	FOLR3: folate receptor 3 (gamma)	116	117	57..788
OV23	GPR39: G protein-coupled receptor 39	118	119	1..1362
M446	GPRC5B: G protein-coupled receptor, family C, group 5, member B	120	121	109..1320
OV24	G-protein coupled receptor	122	123	274..1236
M447	GRB7: growth factor receptor-bound protein 7	124	125	220..1818
OV11	HAIK1: type I intermediate filament cyto keratin	126	127	61..1329
M448	HOXB7: homeo box B7	128	129	100..753
M138	HSECP1: secretory protein, variant 1	130	131	27..863
M449	HSECP1: secretory protein, variant 2	132	133	136..768
M450	HSECP1: secretory protein, variant 3	134	135	202..933
M451	HSNFRK: HSNFRK protein	136	137	642..2939
OV26	hypothetical protein (1)	138	139	<1..1140
OV27	hypothetical protein (2)	140	141	242..1483
OV31	IFI30: interferon, gamma-inducible protein 30	142	143	41..952
OV58	IGF2: somatomedin A	144	145	553..1095



M452	IMP-2: IGF-II mRNA-binding protein 2	146	147	436..2106
M453	INDO: indoleamine-pyrrole 2, 3 dioxygenase	148	149	23..1234
OV73	IPT: tRNA isopentenylpyrophosphate transferase, variant 1	150	151	15..1418
M610	IPT: tRNA isopentenylpyrophosphate transferase, variant 2	152	153	15..1418
M454	ITGA3: integrin, alpha 3	154	155	74..3274
OV30	ITGB8: integrin, beta 8	156	157	681..2990
OV34	KIAA0762: KIAA0762 protein	158	159	<1..1875
M455	KIAA0869: KIAA0869 protein	160	161	<1..2668
OV35	KIAA1154: KIAA1154 protein	162	163	<1..677
OV36	KIAA1456: KIAA1456 protein	164	165	<366..1631
OV32	KLK10: kallikrein 10	166	167	82..912
OV33	KLK6: kallikrein 6	168	169	246..980
M456	KRT7: keratin 7, variant 1	170	171	57..1466
M611	KRT7: keratin 7, variant 2	172	173	54..1463
OV53	LC27: Putative integral membrane transporter	174	175	204..1055
OV37	LCN2: Lipocalin 2 (oncogene 24p3)	176	177	1..597
M457	LEFTB: left-right determination, factor B	178	179	71..1171
M559	LPHB: lipophilin B (uteroglobin family member), prostatein-like	180	181	64..336
OV38	LYST-interacting protein LIP6	182	183	11..586
OV39	MEIS1: MEIS1 protein	184	185	66..1238
M458	MGB2: mammaglobin 2	186	187	65..352
M459	MGC3184: similar to sialyltransferase 7 ((alpha-N-acetylneuraminyl 2, 3-betagalactosyl-1, 3)-N-acetyl galactosaminide alpha-2, 6-sialyltransferase) E	188	189	176..1186
OV52	MMP7: Matrix metalloproteinase 7 (matrilysin, uterine)	190	191	28..831
OV68	MSLN: mesothelin, variant 1	192	193	88..2196
OV69	MSLN: mesothelin, variant 2	194	195	88..1980
OV70	MSLN: mesothelin, variant 3	196	197	88..1950
OV71	MSLN: mesothelin, variant 4	198	199	88..2172
OV72	MSLN: mesothelin, variant 5	200	201	88..1926
OV41	MSLN: mesothelin, variant 6	202	203	<1..>1195
OV42	MSLN: mesothelin, variant 7	204	205	85..1953
OV43	MSLN: mesothelin, variant 8	206	205	88..1956
OV44	MSLN: mesothelin, variant 9	207	208	89..1975
OV83	MSLN: mesothelin, variant 10	209	210	295..2187
OV45	MUC1: mucin 1	211	212	58..1605
M460	MUC16: mucin 16, variant 1	213	214	<1..5352
M461	MUC16: mucin 16, variant 2	215	216	25..3471
M612	MUC16: mucin 16, variant 3	215	217	<1..5673
M462	MYOM2: myomesin (M-protein)	218	219	49..4446
M463	NaPi-1ib: sodium dependent phosphate transporter isoform	220	221	36..2105
M464	NME5: protein expressed in non-metastatic cells 5	222	223	15..653

OV47	NUFIP1: nuclear fragile X mental retardation protein interacting protein 1	224	225	1..1488
OV48	OPN-a: Secreted phosphoprotein-1 (osteopontin, bone sialoprotein)	226	227	1..942
OV49	OPN-b: Secreted phosphoprotein-1 (osteopontin, bone sialoprotein)	228	229	88..990
OV50	OPN-c: Secreted phosphoprotein-1 (osteopontin, bone sialoprotein)	230	231	1..861
M578	PAEP: progesterone-associated endometrial protein, variant 1	232	233	36..578
M579	PAEP: progesterone-associated endometrial protein, variant 2	234	233	36..578
M580	PAEP: progesterone-associated endometrial protein, variant 3	235	233	36..578
M581	PAEP: progesterone-associated endometrial protein, variant 4	236	233	36..578
M583	PAEP: progesterone-associated endometrial protein, variant 5	237	238	45..305
M582	PAEP: progesterone-associated endometrial protein, variant 6	239	240	45..521
M613	PAEP: progesterone-associated endometrial protein, variant 7	239	241	45..521
M465	PAX8: paired box gene 8, isoform 8A	242	243	11..1363
M466	PAX8: paired box gene 8, isoform 8B, variant 1	244	245	11..1174
M614	PAX8: paired box gene 8, isoform 8B, variant 2	244	246	11..1174
M467	PAX8: paired box gene 8, isoform 8C	247	248	161..1357
M468	PAX8: paired box gene 8, isoform 8D	249	250	161..1126
M469	PAX8: paired box gene 8, isoform 8E	251	252	161..1024
M470	PRAME: preferentially expressed antigen in melanoma	253	254	236..1765
M615	PRKCI: protein kinase C, iota	255	256	205..1968
M605	PRP4: serine/threonine-protein kinase PRP4 homolog, variant 1	257	258	<1..3133
M606	PRP4: serine/threonine-protein kinase PRP4 homolog, variant 2	259	258	<1..3133
M607	PRP4: serine/threonine-protein kinase PRP4 homolog, variant 3	260	258	<1..3133
OV80	PRSS8: prostatic	261	262	229..1260
OV51	PTGS1: prostaglandin-endoperoxide synthase 1	263	264	6..1805
M312	PTK9: protein tyrosine kinase 9	265	266	61..1113
OV54	pyruvate dehydrogenase complex component E2	267	268	49..>358
OV55	S100A1: S100 calcium-binding protein A1	269	270	114..398
M471	S100A11: S100 calcium-binding protein A11 (calgizzarin)	271	272	121..438
M68	S100A2: S100 calcium-binding protein A2	273	274	41..334
M585	S100A6: S100 calcium-binding protein A6 (calcyclin)	275	276	103..375

OV57	SCNN1A: sodium channel, nonvoltage-gated 1 alpha, variant 1	277	278	100..2109
OV85	SCNN1A: sodium channel, nonvoltage-gated 1 alpha, variant 2	279	280	96..2105
M472	secreted protein (HETKL27)	281	282	88..618
M473	SEMA3A: sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	283	284	16..2331
OV2	SERPINA1: alpha-1 antitrypsin	285	286	35..1291
M474	Similar to hypothetical protein, MGC: 7199	287	288	173..1053
M586	Similar to proteasome (prosome, macropain) subunit, alpha type, 3	289	290	45..791
M587	Similar to zinc finger protein 136	291	292	139..1524
M475	SLPI: secretory leukocyte protease inhibitor (antileukoproteinase), variant 1	293	294	271..447
M185	SLPI: secretory leukocyte protease inhibitor (antileukoproteinase), variant 2	295	296	19..417
OV60	SNCG: synuclein, gamma	297	298	49..432
OV59	SORL1: sortilin-related receptor	299	300	198..6842
OV56	SPINT2: serine protease inhibitor, Kunitz type, 2, variant 1	301	302	301..1059
OV84	SPINT2: serine protease inhibitor, Kunitz type, 2, variant 2	303	304	332..919
OV65	SPON1: VSGP/F-spondin, variant 1	305	306	25..2448
M593	SPON1: VSGP/F-spondin, variant 2	307	308	180..2984
M594	SPON1: VSGP/F-spondin, variant 3	309	310	180..2687
OV82	ST14: matriptase	311	312	209..2557
M476	TACSTD2: tumor-associated calcium signal transducer 2	313	314	616..1587
M588	TFPI2: tissue factor pathway inhibitor 2	315	316	57..764
OV86	TMPRSS4: transmembrane protease, serine 4	317	318	310..1623
OV74	TPH: tryptophan hydroxylase, variant 1	319	320	1..1335
OV75	TPH: tryptophan hydroxylase, variant 2	321	322	1..1401
M327	TSPAN-1: Tetraspan NET-1 protein, variant 1	323	324	124..900
M328	TSPAN-1: Tetraspan NET-1 protein, variant 2	325	326	1..726
OV46	TTID: myotilin	327	328	281..1777
M589	UCH2: Ubiquitin carboxyl-terminal hydrolases family 2	329	330	551..2940
OV63	unnamed gene (1)	331	332	71..919
OV64	unnamed gene (2)	333	334	28..804
OV76	unnamed gene (3)	335	336	69..773
OV77	unnamed gene (4)	337	338	223..1284
OV78	unnamed gene (5), variant 1	339	340	84..2450
M616	unnamed gene (5), variant 2	341	342	84..2450
OV79	unnamed gene (6)	343	344	69..392
OV87	unnamed gene (7)	345	346	509..2428
OV88	unnamed gene (8)	347	348	71..919
M477	unnamed gene (9), variant 1	349	350	246..992
M617	unnamed gene (9), variant 2	349	351	246..992
M478	unnamed gene (9), variant 3	352	353	246..1004

M479	unnamed gene (9), variant 4	354	355	246..1049
M590	unnamed gene (10), variant 1	356	357	21..404
M591	unnamed gene (10), variant 2	358	357	21..404
M592	unnamed gene (10), variant 3	359	357	21..404
OV25	WFDC2: Epididymis-specific, whey-acidic protein type, four-disulfide core; putative ovarian carcinoma marker	360	361	28..405
M480	XRCC5, KU80: ATP-dependant DNA helicase II	362	363	34..2232

**TABLE 2**

Marker	Gene Name	SEQ ID NO (nts)	SEQ ID NO (AAs)	CDS
M354	ARHGAP8: Rho GTPase activating protein 8, variant 3	17	18	1..2256
M608	ARHGAP8: Rho GTPase activating protein 8, variant 4	17	19	1..2157
M355	ARHGAP8: Rho GTPase activating protein 8, variant 5	20	21	<1..1314
M356	ARHGAP8: Rho GTPase activating protein 8, variant 6	22	23	1..1902
M357	ARHGAP8: Rho GTPase activating protein 8, variant 7	24	25	<1..1281
M358	ARHGAP8: Rho GTPase activating protein 8, variant 8	26	27	1..1386
M359	ARHGAP8: Rho GTPase activating protein 8, variant 9	28	29	<1..1059
OV66	CP: ceruloplasmin (ferroxidase), variant 1	54	55	1..3210
OV81	CP: ceruloplasmin (ferroxidase), variant 4	60	61	76..3348
M575	dehydrogenase	68	69	339..1364
OV67	EVI-1: Evi-1 protein, variant 1	76	77	250..2406
M440	FLJ20758: hypothetical protein FLJ20758, variant 1	96	97	<2..1270
M441	FLJ20758: hypothetical protein FLJ20758, variant 2	98	99	<2..2095
M449	HSECP1: secretory protein, variant 2	132	133	136..768
M450	HSECP1: secretory protein, variant 3	134	135	202..933
OV73	IPT: tRNA isopentenylpyrophosphate transferase, variant 1	150	151	15..1418
M610	IPT: tRNA isopentenylpyrophosphate transferase, variant 2	152	153	15..1418
M611	KRT7: keratin 7, variant 2	172	173	54..1463
OV68	MSLN: mesothelin, variant 1	192	193	88..2196
OV69	MSLN: mesothelin, variant 2	194	195	88..1980
OV70	MSLN: mesothelin, variant 3	196	197	88..1950
OV71	MSLN: mesothelin, variant 4	198	199	88..2172
OV72	MSLN: mesothelin, variant 5	200	201	88..1926
OV83	MSLN: mesothelin, variant 10	209	210	295..2187
M460	MUC16: mucin 16, variant 1	213	214	<1..5352
M583	PAEP: progesterone-associated endometrial protein, variant 5	237	238	45..305

- 24 -

M613	PAEP: progesterone-associated endometrial protein, variant 7	239	241	45..521
M614	PAX8: paired box gene 8, isoform 8B, variant 2	244	246	11..1174
M605	PRP4: serine/threonine-protein kinase PRP4 homolog, variant 1	257	258	<1..3133
M606	PRP4: serine/threonine-protein kinase PRP4 homolog, variant 2	259	258	<1..3133
M607	PRP4: serine/threonine-protein kinase PRP4 homolog, variant 3	260	258	<1..3133
OV85	SCNN1A: sodium channel, nonvoltage-gated 1 alpha, variant 2	279	280	96..2105
M475	SLPI: secretory leukocyte protease inhibitor (antileukoprotease), variant 1	293	294	271..447
OV84	SPINT2: serine protease inhibitor, Kunitz type, 2, variant 2	303	304	332..919
M593	SPON1: VSGP/F-spondin, variant 2	307	308	180..2984
M594	SPON1: VSGP/F-spondin, variant 3	309	310	180..2687
OV82	ST14: matrilysin	311	312	209..2557
OV86	TMPRSS4: transmembrane protease, serine 4	317	318	310..1623
OV74	TPH: tryptophan hydroxylase, variant 1	319	320	1..1335
OV75	TPH: tryptophan hydroxylase, variant 2	321	322	1..1401
M327	TSPAN-1: Tetraspan NET-1 protein, variant 1	323	324	124..900
M589	UCH2: Ubiquitin carboxyl-terminal hydrolases family 2	329	330	551..2940
OV76	unnamed gene (3)	335	336	69..773
OV77	unnamed gene (4)	337	338	223..1284
OV78	unnamed gene (5), variant 1	339	340	84..2450
M616	unnamed gene (5), variant 2	341	342	84..2450
OV79	unnamed gene (6)	343	344	69..392
OV87	unnamed gene (7)	345	346	509..2428
OV88	unnamed gene (8)	347	348	71..919
M477	unnamed gene (9), variant 1	349	350	246..992
M617	unnamed gene (9), variant 2	349	351	246..992
M478	unnamed gene (9), variant 3	352	353	246..1004
M479	unnamed gene (9), variant 4	354	355	246..1049

TABLE 3

Marker	Gene Name	SEQ ID NO (nts)	SEQ ID NO (AAs)	CDS
M604	CLDN10: claudin 10	48	49	36..772
OV14	EVI-1: Evi-1 protein, variant 2	78	79	250..3405
OV15	EVI-1: Evi-1 protein, variant 3	80	81	250..2433
OV16	EVI-1: Evi-1 protein, variant 4	82	83	250..3378
M576	FLJ13710: hypothetical protein FLJ13710	88	89	96..1712
M444	FLJ22316: hypothetical protein FLJ22316	104	105	508..1206
OV30	ITGB8: integrin, beta 8	156	157	681..2990
OV43	MSLN: mesothelin, variant 8	206	205	88..1956

- 25 -

<b>M581</b>	PAEP: progestagen-associated endometrial protein, variant 4	236	233	36..578
<b>M582</b>	PAEP: progestagen-associated endometrial protein, variant 6	239	240	45..521
<b>M466</b>	PAX8: paired box gene 8, isoform 8B, variant 1	244	245	11..1174
<b>M467</b>	PAX8: paired box gene 8, isoform 8C	247	248	161..1357
<b>M468</b>	PAX8: paired box gene 8, isoform 8D	249	250	161..1126
<b>M469</b>	PAX8: paired box gene 8, isoform 8E	251	252	161..1024
<b>OV2</b>	SERPINA1: alpha-1 antitrypsin	285	286	35..1291
<b>M474</b>	Similar to hypothetical protein, MGC: 7199	287	288	173..1053
<b>M590</b>	unnamed gene (10), variant 1	356	357	21..404
<b>M591</b>	unnamed gene (10), variant 2	358	357	21..404
<b>M592</b>	unnamed gene (10), variant 3	359	357	21..404

### Definitions

As used herein, each of the following terms has the meaning associated with it in this section.

The articles "a" and "an" are used herein to refer to one or to more than one (*i.e.* to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

A "marker" is a gene whose altered level of expression in a tissue or cell from its expression level in normal or healthy tissue or cell is associated with a disease state, such as cancer. A "marker nucleic acid" is a nucleic acid (*e.g.*, mRNA, cDNA) encoded by or corresponding to a marker of the invention. Such marker nucleic acids can be DNA (*e.g.*, cDNA) comprising the sequences listed in Table 1 or the complement of such sequences. The marker nucleic acids also can be RNA comprising the sequences listed in Table 1 or the complement of such sequence, wherein all thymidine residues are replaced with uridine residues. A "marker protein" is a protein encoded by or corresponding to a marker of the invention. A marker protein comprises the sequence of any of the sequences listed in Table 1. The terms "protein" and "polypeptide" are used interchangeably.

The term "probe" refers to any molecule which is capable of selectively binding to a specifically intended target molecule, for example, a nucleotide transcript or protein encoded by or corresponding to a marker. Probes can be either synthesized by one skilled in the art, or derived from appropriate biological preparations. For purposes of detection of the target molecule, probes may be specifically designed to be

labeled, as described herein. Examples of molecules that can be utilized as probes include, but are not limited to, RNA, DNA, proteins, antibodies, and organic molecules.

An "ovary-associated" body fluid is a fluid which, when in the body of a patient, contacts or passes through ovarian cells or into which cells or proteins shed from  
5 ovarian cells *e.g.* ovarian epithelium, are capable of passing. Exemplary ovary-associated body fluids include blood fluids, lymph, ascites, gynecological fluids, cystic fluid, urine, and fluids collected by peritoneal rinsing.

The "normal" level of expression of a marker is the level of expression of the marker in ovarian cells of a human subject or patient not afflicted with ovarian  
10 cancer

An "over-expression" or "significantly higher level of expression" of a marker refers to an expression level in a test sample that is greater than the standard error of the assay employed to assess expression, and is preferably at least twice, and more preferably three, four, five or ten times the expression level of the marker in a  
15 control sample (*e.g.*, sample from a healthy subjects not having the marker associated disease) and preferably, the average expression level of the marker in several control samples.

As used herein, the term "promoter/regulatory sequence" means a nucleic acid sequence which is required for expression of a gene product operably linked to the  
20 promoter/regulatory sequence. In some instances, this sequence may be the core promoter sequence and in other instances, this sequence may also include an enhancer sequence and other regulatory elements which are required for expression of the gene product. The promoter/regulatory sequence may, for example, be one which expresses the gene product in a tissue-specific manner.

25 A "constitutive" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell under most or all physiological conditions of the cell.

An "inducible" promoter is a nucleotide sequence which, when operably  
30 linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell substantially only when an inducer which corresponds to the promoter is present in the cell.

A "tissue-specific" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell substantially only if the cell is a cell of the tissue type corresponding to the promoter.

5 A "transcribed polynucleotide" or "nucleotide transcript" is a polynucleotide (*e.g.* an mRNA, hnRNA, a cDNA, or an analog of such RNA or cDNA) which is complementary to or homologous with all or a portion of a mature mRNA made by transcription of a marker of the invention and normal post-transcriptional processing (*e.g.* splicing), if any, of the RNA transcript, and reverse transcription of the  
10 RNA transcript.

"Complementary" refers to the broad concept of sequence complementarity between regions of two nucleic acid strands or between two regions of the same nucleic acid strand. It is known that an adenine residue of a first nucleic acid region is capable of forming specific hydrogen bonds ("base pairing") with a residue of  
15 a second nucleic acid region which is antiparallel to the first region if the residue is thymine or uracil. Similarly, it is known that a cytosine residue of a first nucleic acid strand is capable of base pairing with a residue of a second nucleic acid strand which is antiparallel to the first strand if the residue is guanine. A first region of a nucleic acid is complementary to a second region of the same or a different nucleic acid if, when the  
20 two regions are arranged in an antiparallel fashion, at least one nucleotide residue of the first region is capable of base pairing with a residue of the second region. Preferably, the first region comprises a first portion and the second region comprises a second portion, whereby, when the first and second portions are arranged in an antiparallel fashion, at least about 50%, and preferably at least about 75%, at least about 90%, or at  
25 least about 95% of the nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion. More preferably, all nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion.

"Homologous" as used herein, refers to nucleotide sequence similarity  
30 between two regions of the same nucleic acid strand or between regions of two different nucleic acid strands. When a nucleotide residue position in both regions is occupied by the same nucleotide residue, then the regions are homologous at that position. A first



- 28 -

region is homologous to a second region if at least one nucleotide residue position of each region is occupied by the same residue. Homology between two regions is expressed in terms of the proportion of nucleotide residue positions of the two regions that are occupied by the same nucleotide residue. By way of example, a region having  
5 the nucleotide sequence 5'-ATTGCC-3' and a region having the nucleotide sequence 5'-TATGGC-3' share 50% homology. Preferably, the first region comprises a first portion and the second region comprises a second portion, whereby, at least about 50%, and preferably at least about 75%, at least about 90%, or at least about 95% of the nucleotide residue positions of each of the portions are occupied by the same nucleotide residue.  
10 More preferably, all nucleotide residue positions of each of the portions are occupied by the same nucleotide residue.

A molecule is "fixed" or "affixed" to a substrate if it is covalently or non-covalently associated with the substrate such the substrate can be rinsed with a fluid (e.g. standard saline citrate, pH 7.4) without a substantial fraction of the molecule  
15 dissociating from the substrate.

As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in an organism found in nature.

A cancer is "inhibited" if at least one symptom of the cancer is alleviated,  
20 terminated, slowed, or prevented. As used herein, ovarian cancer is also "inhibited" if recurrence or metastasis of the cancer is reduced, slowed, delayed, or prevented.

A kit is any manufacture (e.g. a package or container) comprising at least one reagent, e.g. a probe, for specifically detecting the expression of a marker of the invention. The kit may be promoted, distributed, or sold as a unit for performing the  
25 methods of the present invention.

"Proteins of the invention" encompass marker proteins and their fragments; variant marker proteins and their fragments; peptides and polypeptides comprising an at least 15 amino acid segment of a marker or variant marker protein; and fusion proteins comprising a marker or variant marker protein, or an at least 15 amino  
30 acid segment of a marker or variant marker protein.

Unless otherwise specified herewithin, the terms "antibody" and "antibodies" broadly encompass naturally-occurring forms of antibodies (*e.g.*, IgG, IgA, IgM, IgE) and recombinant antibodies such as single-chain antibodies, chimeric and humanized antibodies and multi-specific antibodies, as well as fragments and derivatives of all of the foregoing, which fragments and derivatives have at least an antigenic binding site. Antibody derivatives may comprise a protein or chemical moiety conjugated to an antibody moiety.

#### Description

The present invention is based, in part, on newly identified markers which are over-expressed in ovarian cancer cells as compared to their expression in normal (*i.e.* non-cancerous) ovarian cells. The enhanced expression of one or more of these markers in ovarian cells is herein correlated with the cancerous state of the tissue. The invention provides compositions, kits, and methods for assessing the cancerous state of ovarian cells (*e.g.* cells obtained from a human, cultured human cells, archived or preserved human cells and *in vivo* cells) as well as treating patients afflicted with ovarian cancer.

The compositions, kits, and methods of the invention have the following uses, among others:

- 1) assessing whether a patient is afflicted with ovarian cancer;
- 2) assessing the stage of ovarian cancer in a human patient;
- 3) assessing the grade of ovarian cancer in a patient;
- 4) assessing the benign or malignant nature of ovarian cancer in a patient;
- 5) assessing the metastatic potential of ovarian cancer in a patient;
- 6) assessing the histological type of neoplasm (*e.g.* serous, mucinous, endometrioid, or clear cell neoplasm) associated with ovarian cancer in a patient;
- 7) making antibodies, antibody fragments or antibody derivatives that are useful for treating ovarian cancer and/or assessing whether a patient is afflicted with ovarian cancer;

- 30 -

- 8) assessing the presence of ovarian cancer cells;
- 9) assessing the efficacy of one or more test compounds for inhibiting ovarian cancer in a patient;
- 10) assessing the efficacy of a therapy for inhibiting ovarian cancer in a patient;
- 11) monitoring the progression of ovarian cancer in a patient;
- 12) selecting a composition or therapy for inhibiting ovarian cancer in a patient;
- 13) treating a patient afflicted with ovarian cancer;
- 14) inhibiting ovarian cancer in a patient;
- 15) assessing the ovarian carcinogenic potential of a test compound; and
- 16) preventing the onset of ovarian cancer in a patient at risk for developing ovarian cancer.

The invention thus includes a method of assessing whether a patient is afflicted with ovarian cancer which includes assessing whether the patient has pre-metastasized ovarian cancer. This method comprises comparing the level of expression of a marker of the invention (listed in Table 1) in a patient sample and the normal level of expression of the marker in a control, *e.g.*, a non-ovarian cancer sample. A significantly higher level of expression of the marker in the patient sample as compared to the normal level is an indication that the patient is afflicted with ovarian cancer.

Gene delivery vehicles, host cells and compositions (all described herein) containing nucleic acids comprising the entirety, or a segment of 15 or more nucleotides, of any of the sequences listed in Tables 1-3 or the complement of such sequences, and polypeptides comprising the entirety, or a segment of 10 or more amino acids, of any of the sequences listed in Tables 1-3 are also provided by this invention.

As described herein, ovarian cancer in patients is associated with an increased level of expression of one or more markers of the invention. While, as discussed above, some of these changes in expression level result from occurrence of the ovarian cancer, others of these changes induce, maintain, and promote the cancerous state of ovarian cancer cells. Thus, ovarian cancer characterized by an increase in the level of expression of one or more markers of the invention can be inhibited by reducing

- 31 -

and/or interfering with the expression of the markers and/or function of the proteins encoded by those markers.

Expression of a marker of the invention can be inhibited in a number of ways generally known in the art. For example, an antisense oligonucleotide can be  
5 provided to the ovarian cancer cells in order to inhibit transcription, translation, or both, of the marker(s). Alternately, a polynucleotide encoding an antibody, an antibody derivative, or an antibody fragment which specifically binds a marker protein, and operably linked with an appropriate promoter/regulator region, can be provided to the cell in order to generate intracellular antibodies which will inhibit the function or  
10 activity of the protein. The expression and/or function of a marker may also be inhibited by treating the ovarian cancer cell with an antibody, antibody derivative or antibody fragment that specifically binds a marker protein. Using the methods described herein, a variety of molecules, particularly including molecules sufficiently small that they are able to cross the cell membrane, can be screened in order to identify molecules which  
15 inhibit expression of a marker or inhibit the function of a marker protein. The compound so identified can be provided to the patient in order to inhibit ovarian cancer cells of the patient.

Any marker or combination of markers of the invention, as well as any known markers in combination with the markers of the invention, may be used in the  
20 compositions, kits, and methods of the present invention. In general, it is preferable to use markers for which the difference between the level of expression of the marker in ovarian cancer cells and the level of expression of the same marker in normal ovarian cells is as great as possible. Although this difference can be as small as the limit of detection of the method for assessing expression of the marker, it is preferred that the  
25 difference be at least greater than the standard error of the assessment method, and preferably a difference of at least 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, 10-, 15-, 20-, 25-, 100-, 500-, 1000-fold or greater than the level of expression of the same marker in normal ovarian tissue.

It is recognized that certain marker proteins are secreted from ovarian  
30 cells (*i.e.* one or both of normal and cancerous cells) to the extracellular space surrounding the cells. These markers are preferably used in certain embodiments of the compositions, kits, and methods of the invention, owing to the fact that the such marker

- 32 -

proteins can be detected in an ovary-associated body fluid sample, which may be more easily collected from a human patient than a tissue biopsy sample. In addition, preferred *in vivo* techniques for detection of a marker protein include introducing into a subject a labeled antibody directed against the protein. For example, the antibody can be labeled  
5 with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

It is a simple matter for the skilled artisan to determine whether any particular marker protein is a secreted protein. In order to make this determination, the marker protein is expressed in, for example, a mammalian cell, preferably a human  
10 ovarian cell line, extracellular fluid is collected, and the presence or absence of the protein in the extracellular fluid is assessed (*e.g.* using a labeled antibody which binds specifically with the protein).

The following is an example of a method which can be used to detect secretion of a protein. About  $8 \times 10^5$  293T cells are incubated at 37°C in wells  
15 containing growth medium (Dulbecco's modified Eagle's medium {DMEM} supplemented with 10% fetal bovine serum) under a 5% (v/v) CO<sub>2</sub>, 95% air atmosphere to about 60-70% confluence. The cells are then transfected using a standard transfection mixture comprising 2 micrograms of DNA comprising an expression vector encoding the protein and 10 microliters of LipofectAMINE™ (GIBCO/BRL Catalog no. 18342-  
20 012) per well. The transfection mixture is maintained for about 5 hours, and then replaced with fresh growth medium and maintained in an air atmosphere. Each well is gently rinsed twice with DMEM which does not contain methionine or cysteine (DMEM-MC; ICN Catalog no. 16-424- 54). About 1 milliliter of DMEM-MC and about 50 microcuries of Trans-<sup>35</sup>S™ reagent (ICN Catalog no. 51006) are added to each  
25 well. The wells are maintained under the 5% CO<sub>2</sub> atmosphere described above and incubated at 37°C for a selected period. Following incubation, 150 microliters of conditioned medium is removed and centrifuged to remove floating cells and debris. The presence of the protein in the supernatant is an indication that the protein is secreted.

Examples of ovary-associated body fluids include blood fluids (*e.g.* whole blood, blood serum, blood having platelets removed therefrom, etc.), lymph, ascitic fluids, gynecological fluids (*e.g.* ovarian, fallopian, and uterine secretions, menses, vaginal douching fluids, fluids used to rinse ovarian cell samples, etc.), cystic  
5 fluid, urine, and fluids collected by peritoneal rinsing (*e.g.* fluids applied and collected during laparoscopy or fluids instilled into and withdrawn from the peritoneal cavity of a human patient). In these embodiments, the level of expression of the marker can be assessed by assessing the amount (*e.g.* absolute amount or concentration) of the marker protein in an ovary-associated body fluid obtained from a patient. The fluid can, of  
10 course, be subjected to a variety of well-known post-collection preparative and storage techniques (*e.g.* storage, freezing, ultrafiltration, concentration, evaporation, centrifugation, etc.) prior to assessing the amount of the marker in the fluid.

Many ovary-associated body fluids (*i.e.* usually excluding urine) can have ovarian cells, *e.g.* ovarian epithelium, therein, particularly when the ovarian cells  
15 are cancerous, and, more particularly, when the ovarian cancer is metastasizing. Cell-containing fluids which can contain ovarian cancer cells include, but are not limited to, peritoneal ascites, fluids collected by peritoneal rinsing, fluids collected by uterine rinsing, uterine fluids such as uterine exudate and menses, pleural fluid, and ovarian exudates. Thus, the compositions, kits, and methods of the invention can be used to  
20 detect expression of marker proteins having at least one portion which is displayed on the surface of cells which express it. It is a simple matter for the skilled artisan to determine whether a marker protein, or a portion thereof, is exposed on the cell surface. For example, immunological methods may be used to detect such proteins on whole cells, or well known computer-based sequence analysis methods (*e.g.* the SIGNALP  
25 program; Nielsen *et al.*, 1997, *Protein Engineering* 10:1-6) may be used to predict the presence of at least one extracellular domain (*i.e.* including both secreted proteins and proteins having at least one cell-surface domain). Expression of a marker protein having at least one portion which is displayed on the surface of a cell which expresses it may be detected without necessarily lysing the cell (*e.g.* using a labeled antibody which binds  
30 specifically with a cell-surface domain of the protein).

Expression of a marker of the invention may be assessed by any of a wide variety of well known methods for detecting expression of a transcribed nucleic acid or protein. Non-limiting examples of such methods include immunological methods for detection of secreted, cell-surface, cytoplasmic, or nuclear proteins, protein  
5 purification methods, protein function or activity assays, nucleic acid hybridization methods, nucleic acid reverse transcription methods, and nucleic acid amplification methods.

In a preferred embodiment, expression of a marker is assessed using an antibody (*e.g.* a radio-labeled, chromophore-labeled, fluorophore-labeled, or enzyme-  
10 labeled antibody), an antibody derivative (*e.g.* an antibody conjugated with a substrate or with the protein or ligand of a protein-ligand pair {*e.g.* biotin-streptavidin} ), or an antibody fragment (*e.g.* a single-chain antibody, an isolated antibody hypervariable domain, etc.) or derivative which binds specifically with a marker protein or fragment thereof, including a marker protein which has undergone all or a portion of its normal  
15 post-translational modification.

In another preferred embodiment, expression of a marker is assessed by preparing mRNA/cDNA (*i.e.* a transcribed polynucleotide) from cells in a patient sample, and by hybridizing the mRNA/cDNA with a reference polynucleotide which is a complement of a marker nucleic acid, or a fragment thereof. cDNA can, optionally, be  
20 amplified using any of a variety of polymerase chain reaction methods prior to hybridization with the reference polynucleotide; preferably, it is not amplified. Expression of one or more markers can likewise be detected using quantitative PCR to assess the level of expression of the marker(s). Alternatively, any of the many known methods of detecting mutations or variants (*e.g.* single nucleotide polymorphisms,  
25 deletions, etc.) of a marker of the invention may be used to detect occurrence of a marker in a patient.

In a related embodiment, a mixture of transcribed polynucleotides obtained from the sample is contacted with a substrate having fixed thereto a polynucleotide complementary to or homologous with at least a portion (*e.g.* at least 7,  
30 10, 15, 20, 25, 30, 40, 50, 100, 500, or more nucleotide residues) of a marker nucleic acid. If polynucleotides complementary to or homologous with several marker nucleic acids are differentially detectable on the substrate (*e.g.* detectable using different

chromophores or fluorophores, or fixed to different selected positions), then the levels of expression of a plurality of markers can be assessed simultaneously using a single substrate (e.g. a "gene chip" microarray of polynucleotides fixed at selected positions). When a method of assessing marker expression is used which involves hybridization of  
5 one nucleic acid with another, it is preferred that the hybridization be performed under stringent hybridization conditions.

Because the compositions, kits, and methods of the invention rely on detection of a difference in expression levels of one or more markers of the invention, it is preferable that the level of expression of the marker is significantly greater than the  
10 minimum detection limit of the method used to assess expression in at least one of normal ovarian cells and cancerous ovarian cells.

It is understood that by routine screening of additional patient samples using one or more of the markers of the invention, it will be realized that certain of the markers are over-expressed in cancers of various types, including specific ovarian  
15 cancers, as well as other cancers such as breast cancer, cervical cancer, etc. For example, it will be confirmed that some of the markers of the invention are over-expressed in most (i.e. 50% or more) or substantially all (i.e. 80% or more) of ovarian cancer. Furthermore, it will be confirmed that certain of the markers of the invention are associated with ovarian cancer of various stages (i.e. stage I, II, III, and IV ovarian  
20 cancers, as well as subclassifications IA, IB, IC, IIA, IIB, IIC, IIIA, IIIB, and IIIC, using the FIGO Stage Grouping system for primary carcinoma of the ovary; 1987, *Am. J. Obstet. Gynecol.* 156:236), of various histologic subtypes (e.g. serous, mucinous, endometrioid, and clear cell subtypes, as well as subclassifications and alternate classifications adenocarcinoma, papillary adenocarcinoma, papillary  
25 cystadenocarcinoma, surface papillary carcinoma, malignant adenofibroma, cystadenofibroma, adenocarcinoma, cystadenocarcinoma, adenoacanthoma, endometrioid stromal sarcoma, mesodermal (Müllerian) mixed tumor, mesonephroid tumor, malignant carcinoma, Brenner tumor, mixed epithelial tumor, and undifferentiated carcinoma, using the WHO/FIGO system for classification of malignant  
30 ovarian tumors; Scully, *Atlas of Tumor Pathology*, 3d series, Washington DC), and various grades (i.e. grade I {well differentiated} , grade II {moderately well differentiated}, and grade III {poorly differentiated from surrounding normal tissue} ).



In addition, as a greater number of patient samples are assessed for expression of the markers of the invention and the outcomes of the individual patients from whom the samples were obtained are correlated, it will also be confirmed that increased expression of certain of the markers of the invention are strongly correlated with malignant cancers and that increased expression of other markers of the invention are strongly correlated with benign tumors. The compositions, kits, and methods of the invention are thus useful for characterizing one or more of the stage, grade, histological type, and benign/malignant nature of ovarian cancer in patients. In addition, these compositions, kits, and methods can be used to detect and differentiate epithelial, stromal, and germ cell ovarian cancers.

When the compositions, kits, and methods of the invention are used for characterizing one or more of the stage, grade, histological type, and benign/malignant nature of ovarian cancer in a patient, it is preferred that the marker or panel of markers of the invention is selected such that a positive result is obtained in at least about 20%, and preferably at least about 40%, 60%, or 80%, and more preferably in substantially all patients afflicted with an ovarian cancer of the corresponding stage, grade, histological type, or benign/malignant nature. Preferably, the marker or panel of markers of the invention is selected such that a PPV of greater than about 10% is obtained for the general population (more preferably coupled with an assay specificity greater than 99.5%).

When a plurality of markers of the invention are used in the compositions, kits, and methods of the invention, the level of expression of each marker in a patient sample can be compared with the normal level of expression of each of the plurality of markers in non-cancerous samples of the same type, either in a single reaction mixture (*i.e.* using reagents, such as different fluorescent probes, for each marker) or in individual reaction mixtures corresponding to one or more of the markers. In one embodiment, a significantly increased level of expression of more than one of the plurality of markers in the sample, relative to the corresponding normal levels, is an indication that the patient is afflicted with ovarian cancer. When a plurality of markers is used, it is preferred that 2, 3, 4, 5, 8, 10, 12, 15, 20, 30, or 50 or more individual markers be used, wherein fewer markers are preferred.

In order to maximize the sensitivity of the compositions, kits, and methods of the invention (*i.e.* by interference attributable to cells of non-ovarian origin in a patient sample), it is preferable that the marker of the invention used therein be a marker which has a restricted tissue distribution, *e.g.*, normally not expressed in a non-epithelial tissue, and more preferably a marker which is normally not expressed in a non-ovarian tissue.

Only a small number of markers are known to be associated with ovarian cancers (*e.g.* *AKT2*, *Ki-RAS*, *ERBB2*, *c-MYC*, *RB1*, and *TP53*; Lynch, *supra*). These markers are not, of course, included among the markers of the invention, although they may be used together with one or more markers of the invention in a panel of markers, for example. It is well known that certain types of genes, such as oncogenes, tumor suppressor genes, growth factor-like genes, protease-like genes, and protein kinase-like genes are often involved with development of cancers of various types. Thus, among the markers of the invention, use of those which correspond to proteins which resemble proteins encoded by known oncogenes and tumor suppressor genes, and those which correspond to proteins which resemble growth factors, proteases, and protein kinases are preferred.

It is recognized that the compositions, kits, and methods of the invention will be of particular utility to patients having an enhanced risk of developing ovarian cancer and their medical advisors. Patients recognized as having an enhanced risk of developing ovarian cancer include, for example, patients having a familial history of ovarian cancer, patients identified as having a mutant oncogene (*i.e.* at least one allele), and patients of advancing age (*i.e.* women older than about 50 or 60 years).

The level of expression of a marker in normal (*i.e.* non-cancerous) human ovarian tissue can be assessed in a variety of ways. In one embodiment, this normal level of expression is assessed by assessing the level of expression of the marker in a portion of ovarian cells which appears to be non-cancerous and by comparing this normal level of expression with the level of expression in a portion of the ovarian cells which is suspected of being cancerous. For example, when laparoscopy or other medical procedure, reveals the presence of a lump on one portion of a patient's ovary, but not on another portion of the same ovary or on the other ovary, the normal level of expression of a marker may be assessed using one or both or the non-affected ovary and

a non-affected portion of the affected ovary, and this normal level of expression may be compared with the level of expression of the same marker in an affected portion (*i.e.* the lump) of the affected ovary. Alternately, and particularly as further information becomes available as a result of routine performance of the methods described herein,  
5 population-average values for normal expression of the markers of the invention may be used. In other embodiments, the 'normal' level of expression of a marker may be determined by assessing expression of the marker in a patient sample obtained from a non-cancer-afflicted patient, from a patient sample obtained from a patient before the suspected onset of ovarian cancer in the patient, from archived patient samples, and the  
10 like.

The invention includes compositions, kits, and methods for assessing the presence of ovarian cancer cells in a sample (*e.g.* an archived tissue sample or a sample obtained from a patient). These compositions, kits, and methods are substantially the same as those described above, except that, where necessary, the compositions, kits, and  
15 methods are adapted for use with samples other than patient samples. For example, when the sample to be used is a parafinized, archived human tissue sample, it can be necessary to adjust the ratio of compounds in the compositions of the invention, in the kits of the invention, or the methods used to assess levels of marker expression in the sample. Such methods are well known in the art and within the skill of the ordinary  
20 artisan.

The invention includes a kit for assessing the presence of ovarian cancer cells (*e.g.* in a sample such as a patient sample). The kit comprises a plurality of reagents, each of which is capable of binding specifically with a marker nucleic acid or protein. Suitable reagents for binding with a marker protein include antibodies,  
25 antibody derivatives, antibody fragments, and the like. Suitable reagents for binding with a marker nucleic acid (*e.g.* a genomic DNA, an mRNA, a spliced mRNA, a cDNA, or the like) include complementary nucleic acids. For example, the nucleic acid reagents may include oligonucleotides (labeled or non-labeled) fixed to a substrate, labeled oligonucleotides not bound with a substrate, pairs of PCR primers, molecular  
30 beacon probes, and the like.

The kit of the invention may optionally comprise additional components useful for performing the methods of the invention. By way of example, the kit may comprise fluids (*e.g.* SSC buffer) suitable for annealing complementary nucleic acids or for binding an antibody with a protein with which it specifically binds, one or more  
5 sample compartments, an instructional material which describes performance of a method of the invention, a sample of normal ovarian cells, a sample of ovarian cancer cells, and the like.

The invention also includes a method of making an isolated hybridoma which produces an antibody useful for assessing whether patient is afflicted with an  
10 ovarian cancer. In this method, a protein or peptide comprising the entirety or a segment of a marker protein is synthesized or isolated (*e.g.* by purification from a cell in which it is expressed or by transcription and translation of a nucleic acid encoding the protein or peptide *in vivo* or *in vitro* using known methods). A vertebrate, preferably a mammal such as a mouse, rat, rabbit, or sheep, is immunized using the protein or peptide. The  
15 vertebrate may optionally (and preferably) be immunized at least one additional time with the protein or peptide, so that the vertebrate exhibits a robust immune response to the protein or peptide. Splenocytes are isolated from the immunized vertebrate and fused with an immortalized cell line to form hybridomas, using any of a variety of methods well known in the art. Hybridomas formed in this manner are then screened  
20 using standard methods to identify one or more hybridomas which produce an antibody which specifically binds with the marker protein or a fragment thereof. The invention also includes hybridomas made by this method and antibodies made using such hybridomas.

The invention also includes a method of assessing the efficacy of a test  
25 compound for inhibiting ovarian cancer cells. As described above, differences in the level of expression of the markers of the invention correlate with the cancerous state of ovarian cells. Although it is recognized that changes in the levels of expression of certain of the markers of the invention likely result from the cancerous state of ovarian cells, it is likewise recognized that changes in the levels of expression of other of the  
30 markers of the invention induce, maintain, and promote the cancerous state of those cells. Thus, compounds which inhibit an ovarian cancer in a patient will cause the level of expression of one or more of the markers of the invention to change to a level nearer

the normal level of expression for that marker (*i.e.* the level of expression for the marker in non-cancerous ovarian cells).

This method thus comprises comparing expression of a marker in a first ovarian cell sample and maintained in the presence of the test compound and expression  
5 of the marker in a second ovarian cell sample and maintained in the absence of the test compound. A significantly reduced expression of a marker of the invention in the presence of the test compound is an indication that the test compound inhibits ovarian cancer. The ovarian cell samples may, for example, be aliquots of a single sample of normal ovarian cells obtained from a patient, pooled samples of normal ovarian cells  
10 obtained from a patient, cells of a normal ovarian cell line, aliquots of a single sample of ovarian cancer cells obtained from a patient, pooled samples of ovarian cancer cells obtained from a patient, cells of an ovarian cancer cell line, or the like. In one embodiment, the samples are ovarian cancer cells obtained from a patient and a plurality of compounds known to be effective for inhibiting various ovarian cancers are tested in  
15 order to identify the compound which is likely to best inhibit the ovarian cancer in the patient.

This method may likewise be used to assess the efficacy of a therapy for inhibiting ovarian cancer in a patient. In this method, the level of expression of one or more markers of the invention in a pair of samples (one subjected to the therapy, the  
20 other not subjected to the therapy) is assessed. As with the method of assessing the efficacy of test compounds, if the therapy induces a significantly lower level of expression of a marker of the invention then the therapy is efficacious for inhibiting ovarian cancer. As above, if samples from a selected patient are used in this method, then alternative therapies can be assessed *in vitro* in order to select a therapy most likely  
25 to be efficacious for inhibiting ovarian cancer in the patient.

As described above, the cancerous state of human ovarian cells is correlated with changes in the levels of expression of the markers of the invention. The invention includes a method for assessing the human ovarian cell carcinogenic potential of a test compound. This method comprises maintaining separate aliquots of human  
30 ovarian cells in the presence and absence of the test compound. Expression of a marker of the invention in each of the aliquots is compared. A significantly higher level of expression of a marker of the invention in the aliquot maintained in the presence of the

test compound (relative to the aliquot maintained in the absence of the test compound) is an indication that the test compound possesses human ovarian cell carcinogenic potential. The relative carcinogenic potentials of various test compounds can be assessed by comparing the degree of enhancement or inhibition of the level of  
5 expression of the relevant markers, by comparing the number of markers for which the level of expression is enhanced or inhibited, or by comparing both.

Various aspects of the invention are described in further detail in the following subsections.

#### 10 I. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules, including nucleic acids which encode a marker protein or a portion thereof. Isolated nucleic acids of the invention also include nucleic acid molecules sufficient for use as hybridization probes to identify marker nucleic acid molecules, and fragments of marker  
15 nucleic acid molecules, *e.g.*, those suitable for use as PCR primers for the amplification or mutation of marker nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-  
20 stranded, but preferably is double-stranded DNA.

An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid molecule. Preferably, an "isolated" nucleic acid molecule is free of sequences (preferably protein-encoding sequences) which naturally flank the nucleic acid (*i.e.*,  
25 sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kB, 4 kB, 3 kB, 2 kB, 1 kB, 0.5 kB or 0.1 kB of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover,  
30 an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques,

or substantially free of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention can be isolated using standard molecular biology techniques and the sequence information in the database records described herein. Using all or a portion of such nucleic acid sequences, nucleic acid molecules of the invention can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, ed., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

A nucleic acid molecule of the invention can be amplified using cDNA, mRNA, or genomic DNA as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, nucleotides corresponding to all or a portion of a nucleic acid molecule of the invention can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which has a nucleotide sequence complementary to the nucleotide sequence of a marker nucleic acid or to the nucleotide sequence of a nucleic acid encoding a marker protein. A nucleic acid molecule which is complementary to a given nucleotide sequence is one which is sufficiently complementary to the given nucleotide sequence that it can hybridize to the given nucleotide sequence thereby forming a stable duplex.

Moreover, a nucleic acid molecule of the invention can comprise only a portion of a nucleic acid sequence, wherein the full length nucleic acid sequence comprises a marker nucleic acid or which encodes a marker protein. Such nucleic acids can be used, for example, as a probe or primer. The probe/primer typically is used as one or more substantially purified oligonucleotides. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 7, preferably about 15, more preferably about 25, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, or 400 or more consecutive nucleotides of a nucleic acid of the invention.

Probes based on the sequence of a nucleic acid molecule of the invention can be used to detect transcripts or genomic sequences corresponding to one or more markers of the invention. The probe comprises a label group attached thereto, *e.g.*, a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes  
5 can be used as part of a diagnostic test kit for identifying cells or tissues which mis-express the protein, such as by measuring levels of a nucleic acid molecule encoding the protein in a sample of cells from a subject, *e.g.*, detecting mRNA levels or determining whether a gene encoding the protein has been mutated or deleted.

The invention further encompasses nucleic acid molecules that differ, due  
10 to degeneracy of the genetic code, from the nucleotide sequence of nucleic acids encoding a marker protein and thus encode the same protein.

It will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequence can exist within a population (*e.g.*, the human population). Such genetic polymorphisms can exist among  
15 individuals within a population due to natural allelic variation. An allele is one of a group of genes which occur alternatively at a given genetic locus. In addition, it will be appreciated that DNA polymorphisms that affect RNA expression levels can also exist that may affect the overall expression level of that gene (*e.g.*, by affecting regulation or degradation).

20 As used herein, the phrase "allelic variant" refers to a nucleotide sequence which occurs at a given locus or to a polypeptide encoded by the nucleotide sequence.

As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a polypeptide corresponding  
25 to a marker of the invention. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of a given gene. Alternative alleles can be identified by sequencing the gene of interest in a number of different individuals. This can be readily carried out by using hybridization probes to identify the same genetic locus in a variety of individuals. Any and all such nucleotide variations and resulting amino acid  
30 polymorphisms or variations that are the result of natural allelic variation and that do not alter the functional activity are intended to be within the scope of the invention.



In another embodiment, an isolated nucleic acid molecule of the invention is at least 7, 15, 20, 25, 30, 40, 60, 80, 100, 150, 200, 250, 300, 350, 400, 450, 550, 650, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2200, 2400, 2600, 2800, 3000, 3500, 4000, 4500, or more nucleotides in length and hybridizes under stringent  
5 conditions to a marker nucleic acid or to a nucleic acid encoding a marker protein. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% (65%, 70%, preferably 75%) identical to each other typically remain hybridized to each other. Such stringent conditions are known to those skilled in the art and can be found  
10 in sections 6.3.1-6.3.6 of *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989). A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C.

In addition to naturally-occurring allelic variants of a nucleic acid  
15 molecule of the invention that can exist in the population, the skilled artisan will further appreciate that sequence changes can be introduced by mutation thereby leading to changes in the amino acid sequence of the encoded protein, without altering the biological activity of the protein encoded thereby. For example, one can make nucleotide substitutions leading to amino acid substitutions at "non-essential" amino  
20 acid residues. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are not conserved or only semi-conserved among homologs of various species may be non-essential for activity and thus would be likely targets for alteration.  
25 Alternatively, amino acid residues that are conserved among the homologs of various species (*e.g.*, murine and human) may be essential for activity and thus would not be likely targets for alteration.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding a variant marker protein that contain changes in amino acid residues  
30 that are not essential for activity. Such variant marker proteins differ in amino acid sequence from the naturally-occurring marker proteins, yet retain biological activity. In one embodiment, such a variant marker protein has an amino acid sequence that is at

least about 40% identical, 50%, 60%, 70%, 80%, 90%, 95%, or 98% identical to the amino acid sequence of a marker protein.

An isolated nucleic acid molecule encoding a variant marker protein can be created by introducing one or more nucleotide substitutions, additions or deletions  
5 into the nucleotide sequence of marker nucleic acids, such that one or more amino acid residue substitutions, additions, or deletions are introduced into the encoded protein. Mutations can be introduced by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative  
10 amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine,  
15 serine, threonine, tyrosine, cysteine), non-polar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Alternatively, mutations can be introduced randomly along all or part of the coding sequence, such as by saturation mutagenesis,  
20 and the resultant mutants can be screened for biological activity to identify mutants that retain activity. Following mutagenesis, the encoded protein can be expressed recombinantly and the activity of the protein can be determined.

The present invention encompasses antisense nucleic acid molecules, *i.e.*, molecules which are complementary to a sense nucleic acid of the invention, *e.g.*,  
25 complementary to the coding strand of a double-stranded marker cDNA molecule or complementary to a marker mRNA sequence. Accordingly, an antisense nucleic acid of the invention can hydrogen bond to (*i.e.* anneal with) a sense nucleic acid of the invention. The antisense nucleic acid can be complementary to an entire coding strand, or to only a portion thereof, *e.g.*, all or part of the protein coding region (or open reading  
30 frame). An antisense nucleic acid molecule can also be antisense to all or part of a non-coding region of the coding strand of a nucleotide sequence encoding a marker protein.

The non-coding regions ("5' and 3' untranslated regions") are the 5' and 3' sequences which flank the coding region and are not translated into amino acids.

An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 or more nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been sub-cloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a marker protein to thereby inhibit expression of the marker, *e.g.*, by inhibiting transcription and/or translation. The

hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. Examples of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site or infusion of the antisense nucleic acid into an ovary-associated body fluid. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies which bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

An antisense nucleic acid molecule of the invention can be an  $\alpha$ -anomeric nucleic acid molecule. An  $\alpha$ -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\alpha$ -units, the strands run parallel to each other (Gaultier *et al.*, 1987, *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-O-methylribonucleotide (Inoue *et al.*, 1987, *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.*, 1987, *FEBS Lett.* 215:327-330).

The invention also encompasses ribozymes. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes as described in Haselhoff and Gerlach, 1988, *Nature* 334:585-591) can be used to catalytically cleave mRNA transcripts to thereby inhibit translation of the protein encoded by the mRNA. A ribozyme having specificity for a nucleic acid molecule encoding a marker protein can be designed based upon the nucleotide sequence of a cDNA corresponding to the marker. For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved

(see Cech *et al.* U.S. Patent No. 4,987,071; and Cech *et al.* U.S. Patent No. 5,116,742). Alternatively, an mRNA encoding a polypeptide of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules (see, *e.g.*, Bartel and Szostak, 1993, *Science* 261:1411-1418).

5                   The invention also encompasses nucleic acid molecules which form triple helical structures. For example, expression of a marker of the invention can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the gene encoding the marker nucleic acid or protein (*e.g.*, the promoter and/or enhancer) to form triple helical structures that prevent transcription of the gene in target cells. See  
10                   generally Helene (1991) *Anticancer Drug Des.* 6(6):569-84; Helene (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14(12):807-15.

                  In various embodiments, the nucleic acid molecules of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose  
15                   phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.*, 1996, *Bioorganic & Medicinal Chemistry* 4(1): 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral  
20                   backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996), *supra*; Perry-O'Keefe *et al.* (1996) *Proc. Natl. Acad. Sci. USA* 93:14670-675.

25                   PNAs can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction  
30                   enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup (1996), *supra*; or as probes or primers for DNA sequence and hybridization (Hyrup, 1996, *supra*; Perry-O'Keefe *et al.*, 1996, *Proc. Natl. Acad. Sci. USA* 93:14670-675).

In another embodiment, PNAs can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated  
5 which can combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and  
10 orientation (Hyrup, 1996, *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996), *supra*, and Finn *et al.* (1996) *Nucleic Acids Res.* 24(17):3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry and modified nucleoside analogs. Compounds such as 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite can  
15 be used as a link between the PNA and the 5' end of DNA (Mag *et al.*, 1989, *Nucleic Acids Res.* 17:5973-88). PNA monomers are then coupled in a step-wise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.*, 1996, *Nucleic Acids Res.* 24(17):3357-63). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment (Peterser *et al.*, 1975,  
20 *Bioorganic Med. Chem. Lett.* 5:1119-11124).

In other embodiments, the oligonucleotide can include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. USA* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci. USA*  
25 84:648-652; PCT Publication No. WO 88/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, 1988, *Bio/Techniques* 6:958-976) or intercalating agents (see, *e.g.*, Zon, 1988, *Pharm. Res.* 5:539-549). To this end, the oligonucleotide can be conjugated to another molecule, *e.g.*, a peptide,  
30 hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

- 50 -

The invention also includes molecular beacon nucleic acids having at least one region which is complementary to a nucleic acid of the invention, such that the molecular beacon is useful for quantitating the presence of the nucleic acid of the invention in a sample. A "molecular beacon" nucleic acid is a nucleic acid comprising a pair of complementary regions and having a fluorophore and a fluorescent quencher associated therewith. The fluorophore and quencher are associated with different portions of the nucleic acid in such an orientation that when the complementary regions are annealed with one another, fluorescence of the fluorophore is quenched by the quencher. When the complementary regions of the nucleic acid are not annealed with one another, fluorescence of the fluorophore is quenched to a lesser degree. Molecular beacon nucleic acids are described, for example, in U.S. Patent 5,876,930.

## II. Isolated Proteins and Antibodies

One aspect of the invention pertains to isolated marker proteins and biologically active portions thereof, as well as polypeptide fragments suitable for use as immunogens to raise antibodies directed against a marker protein or a fragment thereof. In one embodiment, the native marker protein can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, a protein or peptide comprising the whole or a segment of the marker protein is produced by recombinant DNA techniques. Alternative to recombinant expression, such protein or peptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the protein is derived, or substantially free of chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. Thus, protein that is substantially free of cellular material includes preparations of protein having less than about 30%, 20%, 10%, or 5% (by dry weight) of heterologous protein (also referred to herein as a "contaminating protein"). When the protein or biologically active portion thereof is recombinantly produced, it is

also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, 10%, or 5% of the volume of the protein preparation. When the protein is produced by chemical synthesis, it is preferably substantially free of chemical precursors or other chemicals, *i.e.*, it is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. Accordingly such preparations of the protein have less than about 30%, 20%, 10%, 5% (by dry weight) of chemical precursors or compounds other than the polypeptide of interest.

Biologically active portions of a marker protein include polypeptides comprising amino acid sequences sufficiently identical to or derived from the amino acid sequence of the marker protein, which include fewer amino acids than the full length protein, and exhibit at least one activity of the corresponding full-length protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the corresponding full-length protein. A biologically active portion of a marker protein of the invention can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length. Moreover, other biologically active portions, in which other regions of the marker protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of the native form of the marker protein.

Preferred marker proteins are encoded by nucleotide sequences comprising the sequences listed in Tables 1-3. Other useful proteins are substantially identical (*e.g.*, at least about 40%, preferably 50%, 60%, 70%, 80%, 90%, 95%, or 99%) to one of these sequences and retain the functional activity of the corresponding naturally-occurring marker protein yet differ in amino acid sequence due to natural allelic variation or mutagenesis.

To determine the percent identity of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences



is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = # of identical positions/total # of positions (*e.g.*, overlapping positions)  $\times 100$ ).

In one embodiment the two sequences are the same length.

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-2268, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-410. BLAST nucleotide searches can be performed with the BLASTN program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the BLASTP program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, a newer version of the BLAST algorithm called Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402, which is able to perform gapped local alignments for the programs BLASTN, BLASTP and BLASTX. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (*e.g.*, BLASTX and BLASTN) can be used. Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, (1988) *CABIOS* 4:11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Yet another useful algorithm for identifying regions of local sequence similarity and alignment is the FASTA algorithm as described in Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85:2444-2448. When using the FASTA algorithm for comparing nucleotide or amino acid sequences, a PAM120 weight residue table can, for example, be used with a *k*-tuple value of 2.

The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, only exact matches are counted.

The invention also provides chimeric or fusion proteins comprising a marker protein or a segment thereof. As used herein, a "chimeric protein" or "fusion protein" comprises all or part (preferably a biologically active part) of a marker protein operably linked to a heterologous polypeptide (*i.e.*, a polypeptide other than the marker protein). Within the fusion protein, the term "operably linked" is intended to indicate that the marker protein or segment thereof and the heterologous polypeptide are fused in-frame to each other. The heterologous polypeptide can be fused to the amino-terminus or the carboxyl-terminus of the marker protein or segment.

One useful fusion protein is a GST fusion protein in which a marker protein or segment is fused to the carboxyl terminus of GST sequences. Such fusion proteins can facilitate the purification of a recombinant polypeptide of the invention.

In another embodiment, the fusion protein contains a heterologous signal sequence at its amino terminus. For example, the native signal sequence of a marker protein can be removed and replaced with a signal sequence from another protein. For example, the gp67 secretory sequence of the baculovirus envelope protein can be used as a heterologous signal sequence (Ausubel *et al.*, ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, NY, 1992). Other examples of eukaryotic heterologous signal sequences include the secretory sequences of melittin and human placental alkaline phosphatase (Stratagene; La Jolla, California). In yet another example, useful prokaryotic heterologous signal sequences include the *phoA* secretory signal (Sambrook *et al.*, *supra*) and the protein A secretory signal (Pharmacia Biotech; Piscataway, New Jersey).

In yet another embodiment, the fusion protein is an immunoglobulin fusion protein in which all or part of a marker protein is fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand (soluble or membrane-bound) and a protein on the surface of a cell (receptor), to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion protein can be used to affect the bioavailability of a

cognate ligand of a marker protein. Inhibition of ligand/receptor interaction can be useful therapeutically, both for treating proliferative and differentiative disorders and for modulating (e.g. promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies  
5 directed against a marker protein in a subject, to purify ligands and in screening assays to identify molecules which inhibit the interaction of the marker protein with ligands.

Chimeric and fusion proteins of the invention can be produced by standard recombinant DNA techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.  
10 Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and re-amplified to generate a chimeric gene sequence (see, e.g., Ausubel *et al.*, *supra*). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide).  
15 A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the polypeptide of the invention.

A signal sequence can be used to facilitate secretion and isolation of marker proteins. Signal sequences are typically characterized by a core of hydrophobic  
20 amino acids which are generally cleaved from the mature protein during secretion in one or more cleavage events. Such signal peptides contain processing sites that allow cleavage of the signal sequence from the mature proteins as they pass through the secretory pathway. Thus, the invention pertains to marker proteins, fusion proteins or segments thereof having a signal sequence, as well as to such proteins from which the  
25 signal sequence has been proteolytically cleaved (*i.e.*, the cleavage products). In one embodiment, a nucleic acid sequence encoding a signal sequence can be operably linked in an expression vector to a protein of interest, such as a marker protein or a segment thereof. The signal sequence directs secretion of the protein, such as from a eukaryotic host into which the expression vector is transformed, and the signal sequence is  
30 subsequently or concurrently cleaved. The protein can then be readily purified from the extracellular medium by art recognized methods. Alternatively, the signal sequence can

be linked to the protein of interest using a sequence which facilitates purification, such as with a GST domain.

The present invention also pertains to variants of the marker proteins. Such variants have an altered amino acid sequence which can function as either agonists  
5 (mimetics) or as antagonists. Variants can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation. An agonist can retain substantially the same, or a subset, of the biological activities of the naturally occurring form of the protein. An antagonist of a protein can inhibit one or more of the activities of the naturally occurring form of the protein by, for example, competitively binding to a downstream or upstream member  
10 of a cellular signaling cascade which includes the protein of interest. Thus, specific biological effects can be elicited by treatment with a variant of limited function. Treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein can have fewer side effects in a subject relative to treatment with the naturally occurring form of the protein.

15 Variants of a marker protein which function as either agonists (mimetics) or as antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the protein of the invention for agonist or antagonist activity. In one embodiment, a variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A  
20 variegated library of variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential protein sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display). There are a variety of methods which can be used to produce libraries of potential variants of the marker proteins from  
25 a degenerate oligonucleotide sequence. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, 1983, *Tetrahedron* 39:3; Itakura *et al.*, 1984, *Annu. Rev. Biochem.* 53:323; Itakura *et al.*, 1984, *Science* 198:1056; Ike *et al.*, 1983 *Nucleic Acid Res.* 11:477).

In addition, libraries of segments of a marker protein can be used to  
30 generate a variegated population of polypeptides for screening and subsequent selection of variant marker proteins or segments thereof. For example, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of the

coding sequence of interest with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by  
5 treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes amino terminal and internal fragments of various sizes of the protein of interest.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA  
10 libraries for gene products having a selected property. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates  
15 isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify variants of a protein of the invention (Arkin and Yourvan, 1992, *Proc. Natl. Acad. Sci. USA* 89:7811-7815; Delgrave *et al.*, 1993, *Protein Engineering* 6(3):327- 331).

20 Another aspect of the invention pertains to antibodies directed against a protein of the invention. In preferred embodiments, the antibodies specifically bind a marker protein or a fragment thereof. The terms "antibody" and "antibodies" as used interchangeably herein refer to immunoglobulin molecules as well as fragments and derivatives thereof that comprise an immunologically active portion of an  
25 immunoglobulin molecule, (*i.e.*, such a portion contains an antigen binding site which specifically binds an antigen, such as a marker protein, *e.g.*, an epitope of a marker protein). An antibody which specifically binds to a protein of the invention is an antibody which binds the protein, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the protein. Examples of an  
30 immunologically active portion of an immunoglobulin molecule include, but are not limited to, single-chain antibodies (scAb), F(ab) and F(ab')<sub>2</sub> fragments.

An isolated protein of the invention or a fragment thereof can be used as an immunogen to generate antibodies. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments for use as immunogens. The antigenic peptide of a protein of the invention comprises at least 8 (preferably 10, 15, 20, or 30 or more) amino acid residues of the amino acid sequence of one of the proteins of the invention, and encompasses at least one epitope of the protein such that an antibody raised against the peptide forms a specific immune complex with the protein. Preferred epitopes encompassed by the antigenic peptide are regions that are located on the surface of the protein, *e.g.*, hydrophilic regions. Hydrophobicity sequence analysis, hydrophilicity sequence analysis, or similar analyses can be used to identify hydrophilic regions. In preferred embodiments, an isolated marker protein or fragment thereof is used as an immunogen.

An immunogen typically is used to prepare antibodies by immunizing a suitable (*i.e.* immunocompetent) subject such as a rabbit, goat, mouse, or other mammal or vertebrate. An appropriate immunogenic preparation can contain, for example, recombinantly-expressed or chemically-synthesized protein or peptide. The preparation can further include an adjuvant, such as Freund's complete or incomplete adjuvant, or a similar immunostimulatory agent. Preferred immunogen compositions are those that contain no other human proteins such as, for example, immunogen compositions made using a non-human host cell for recombinant expression of a protein of the invention. In such a manner, the resulting antibody compositions have reduced or no binding of human proteins other than a protein of the invention.

The invention provides polyclonal and monoclonal antibodies. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope. Preferred polyclonal and monoclonal antibody compositions are ones that have been selected for antibodies directed against a protein of the invention. Particularly preferred polyclonal and monoclonal antibody preparations are ones that contain only antibodies directed against a marker protein or fragment thereof.

Polyclonal antibodies can be prepared by immunizing a suitable subject with a protein of the invention as an immunogen. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. At an appropriate  
5 time after immunization, *e.g.*, when the specific antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies (mAb) by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein (1975) *Nature* 256:495-497, the human B cell hybridoma technique (see Kozbor *et al.*, 1983, *Immunol. Today* 4:72), the EBV-  
10 hybridoma technique (see Cole *et al.*, pp. 77-96 In *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., 1985) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology*, Coligan *et al.* ed., John Wiley & Sons, New York, 1994). Hybridoma cells producing a monoclonal antibody of the invention are detected by screening the hybridoma culture  
15 supernatants for antibodies that bind the polypeptide of interest, *e.g.*, using a standard ELISA assay.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody directed against a protein of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (*e.g.*, an  
20 antibody phage display library) with the polypeptide of interest. Kits for generating and screening phage display libraries are commercially available (*e.g.*, the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene *SurfZAP Phage Display Kit*, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display  
25 library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT  
Publication No. WO 90/02809; Fuchs *et al.* (1991) *Bio/Technology* 9:1370-1372; Hay *et al.* (1992) *Hum. Antibod. Hybridomas* 3:81-85; Huse *et al.* (1989) *Science* 246:1275-  
30 1281; Griffiths *et al.* (1993) *EMBO J.* 12:725-734.

The invention also provides recombinant antibodies that specifically bind a protein of the invention. In preferred embodiments, the recombinant antibodies specifically binds a marker protein or fragment thereof. Recombinant antibodies include, but are not limited to, chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, single-chain antibodies and multi-specific antibodies. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. (See, *e.g.*, Cabilly et al., U.S. Patent No. 4,816,567; and Boss et al., U.S. Patent No. 4,816,397, which are incorporated herein by reference in their entirety.) Single-chain antibodies have an antigen binding site and consist of single polypeptides. They can be produced by techniques known in the art, for example using methods described in Ladner *et. al* U.S. Pat. No. 4,946,778 (which is incorporated herein by reference in its entirety); Bird *et al.*, (1988) *Science* 242:423-426; Whitlow *et al.*, (1991) *Methods in Enzymology* 2:1-9; Whitlow *et al.*, (1991) *Methods in Enzymology* 2:97-105; and Huston *et al.*, (1991) *Methods in Enzymology Molecular Design and Modeling: Concepts and Applications* 203:46-88. Multi-specific antibodies are antibody molecules having at least two antigen-binding sites that specifically bind different antigens. Such molecules can be produced by techniques known in the art, for example using methods described in Segal, U.S. Patent No. 4,676,980 (the disclosure of which is incorporated herein by reference in its entirety); Holliger et al., (1993) *Proc. Natl. Acad. Sci. USA* 90:6444-6448; Whitlow *et al.*, (1994) *Protein Eng.* 7:1017-1026 and U.S. Pat. No. 6,121,424.

Humanized antibodies are antibody molecules from non-human species having one or more complementarity determining regions (CDRs) from the non-human species and a framework region from a human immunoglobulin molecule. (See, *e.g.*, Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) Humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Patent No. 4,816,567; European Patent Application 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Liu



- et al.* (1987) *J. Immunol.* 139:3521- 3526; Sun *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:214-218; Nishimura *et al.* (1987) *Cancer Res.* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; and Shaw *et al.* (1988) *J. Natl. Cancer Inst.* 80:1553-1559); Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *Bio/Techniques* 4:214; U.S. Patent 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525; Verhoevan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J. Immunol.* 141:4053-4060.

More particularly, humanized antibodies can be produced, for example, using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes.

10 The transgenic mice are immunized in the normal fashion with a selected antigen, *e.g.*, all or a portion of a polypeptide corresponding to a marker of the invention. Monoclonal antibodies directed against the antigen can be obtained using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class

15 switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar (1995) *Int. Rev. Immunol.* 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, *e.g.*,

20 U.S. Patent 5,625,126; U.S. Patent 5,633,425; U.S. Patent 5,569,825; U.S. Patent 5,661,016; and U.S. Patent 5,545,806. In addition, companies such as Abgenix, Inc. (Freemont, CA), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be

25 generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, *e.g.*, a murine antibody, is used to guide the selection of a completely human antibody recognizing the same epitope (Jespers *et al.*, 1994, *Bio/technology* 12:899-903).

The antibodies of the invention can be isolated after production (*e.g.*,

30 from the blood or serum of the subject) or synthesis and further purified by well-known techniques. For example, IgG antibodies can be purified using protein A chromatography. Antibodies specific for a protein of the invention can be selected or

(*e.g.*, partially purified) or purified by, *e.g.*, affinity chromatography. For example, a recombinantly expressed and purified (or partially purified) protein of the invention is produced as described herein, and covalently or non-covalently coupled to a solid support such as, for example, a chromatography column. The column can then be used to affinity purify antibodies specific for the proteins of the invention from a sample containing antibodies directed against a large number of different epitopes, thereby generating a substantially purified antibody composition, *i.e.*, one that is substantially free of contaminating antibodies. By a substantially purified antibody composition is meant, in this context, that the antibody sample contains at most only 30% (by dry weight) of contaminating antibodies directed against epitopes other than those of the desired protein of the invention, and preferably at most 20%, yet more preferably at most 10%, and most preferably at most 5% (by dry weight) of the sample is contaminating antibodies. A purified antibody composition means that at least 99% of the antibodies in the composition are directed against the desired protein of the invention.

In a preferred embodiment, the substantially purified antibodies of the invention may specifically bind to a signal peptide, a secreted sequence, an extracellular domain, a transmembrane or a cytoplasmic domain or cytoplasmic membrane of a protein of the invention. In a particularly preferred embodiment, the substantially purified antibodies of the invention specifically bind to a secreted sequence or an extracellular domain of the amino acid sequences of a protein of the invention. In a more preferred embodiment, the substantially purified antibodies of the invention specifically bind to a secreted sequence or an extracellular domain of the amino acid sequences of a marker protein.

An antibody directed against a protein of the invention can be used to isolate the protein by standard techniques, such as affinity chromatography or immunoprecipitation. Moreover, such an antibody can be used to detect the marker protein or fragment thereof (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the level and pattern of expression of the marker. The antibodies can also be used diagnostically to monitor protein levels in tissues or body fluids (*e.g.* in an ovary-associated body fluid) as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by the

use of an antibody derivative, which comprises an antibody of the invention coupled to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish  
5 peroxidase, alkaline phosphatase,  $\beta$ -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol;  
10 examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$  or  $^3\text{H}$ .

Antibodies of the invention may also be used as therapeutic agents in treating cancers. In a preferred embodiment, completely human antibodies of the invention are used for therapeutic treatment of human cancer patients, particularly those  
15 having an ovarian cancer. In another preferred embodiment, antibodies that bind specifically to a marker protein or fragment thereof are used for therapeutic treatment. Further, such therapeutic antibody may be an antibody derivative or immunotoxin comprising an antibody conjugated to a therapeutic moiety such as a cytotoxin, a therapeutic agent or a radioactive metal ion. A cytotoxin or cytotoxic agent includes any  
20 agent that is detrimental to cells. Examples include taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof.  
25 Therapeutic agents include, but are not limited to, antimetabolites (*e.g.*, methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (*e.g.*, mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclophosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines  
30 (*e.g.*, daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (*e.g.*, dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (*e.g.*, vincristine and vinblastine).

The conjugated antibodies of the invention can be used for modifying a given biological response, for the drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as ribosome-inhibiting protein (see Better et al., U.S. Patent No. 6,146,631, the disclosure of which is incorporated herein in its entirety), abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a protein such as tumor necrosis factor, .alpha.-interferon, .beta.-interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophase colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

Techniques for conjugating such therapeutic moiety to antibodies are well known, see, *e.g.*, Arnon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in Monoclonal Antibodies And Cancer Therapy, Reisfeld et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For Drug Delivery", in Controlled Drug Delivery (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in Monoclonal Antibodies '84: Biological And Clinical Applications, Pinchera et al. (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in Monoclonal Antibodies For Cancer Detection And Therapy, Baldwin et al. (eds.), pp. 303-16 (Academic Press 1985), and Thorpe et al., "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", Immunol. Rev., 62:119-58 (1982).

Accordingly, in one aspect, the invention provides substantially purified antibodies, antibody fragments and derivatives, all of which specifically bind to a protein of the invention and preferably, a marker protein. In various embodiments, the substantially purified antibodies of the invention, or fragments or derivatives thereof, can be human, non-human, chimeric and/or humanized antibodies. In another aspect, the invention provides non-human antibodies, antibody fragments and derivatives, all of which specifically bind to a protein of the invention and preferably, a marker protein. Such non-human antibodies can be goat, mouse, sheep, horse, chicken, rabbit, or rat

antibodies. Alternatively, the non-human antibodies of the invention can be chimeric and/or humanized antibodies. In addition, the non-human antibodies of the invention can be polyclonal antibodies or monoclonal antibodies. In still a further aspect, the invention provides monoclonal antibodies, antibody fragments and derivatives, all of which specifically bind to a protein of the invention and preferably, a marker protein. The monoclonal antibodies can be human, humanized, chimeric and/or non-human antibodies.

The invention also provides a kit containing an antibody of the invention conjugated to a detectable substance, and instructions for use. Still another aspect of the invention is a pharmaceutical composition comprising an antibody of the invention and a pharmaceutically acceptable carrier. In preferred embodiments, the pharmaceutical composition contains an antibody of the invention, a therapeutic moiety, and a pharmaceutically acceptable carrier.

### 15 III. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding a marker protein (or a portion of such a protein). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors, namely expression vectors, are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids (vectors). However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective

- 65 -

retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell.

5 This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression  
10 of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, *Methods in Enzymology: Gene Expression Technology* vol.185,  
15 Academic Press, San Diego, CA (1991). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the  
20 host cell to be transformed, the level of expression of protein desired, and the like. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein.

The recombinant expression vectors of the invention can be designed for  
25 expression of a marker protein or a segment thereof in prokaryotic (*e.g.*, *E. coli*) or eukaryotic cells (*e.g.*, insect cells {using baculovirus expression vectors}, yeast cells or mammalian cells). Suitable host cells are discussed further in Goeddel, *supra*. Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

30 Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a

protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification.

- 5 Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX
- 10 (Pharmacia Biotech Inc; Smith and Johnson, 1988, *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

- Examples of suitable inducible non-fusion *E. coli* expression vectors
- 15 include pTrc (Amann *et al.*, 1988, *Gene* 69:301-315) and pET 11d (Studier *et al.*, p. 60-89, In *Gene Expression Technology: Methods in Enzymology* vol.185, Academic Press, San Diego, CA, 1991). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter
- 20 mediated by a co-expressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter.

- One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave
- 25 the recombinant protein (Gottesman, p. 119-128, In *Gene Expression Technology: Methods in Enzymology* vol. 185, Academic Press, San Diego, CA, 1990. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, 1992, *Nucleic Acids Res.* 20:2111-2118).
- 30 Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari *et al.*, 1987, *EMBO J.* 6:229-234), pMFa (Kurjan and Herskowitz, 1982, *Cell* 30:933-943), pJRY88 (Schultz *et al.*, 1987, *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, CA), and pPicZ (Invitrogen Corp, San Diego, CA).

Alternatively, the expression vector is a baculovirus expression vector. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.*, 1983, *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers, 1989, *Virology* 170:31-39).

10 In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, 1987, *Nature* 329:840) and pMT2PC (Kaufman *et al.*, 1987, *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements.

15 For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook *et al.*, *supra*.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type

20 (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.*, 1987, *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton, 1988, *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and

25 Baltimore, 1989, *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.*, 1983, *Cell* 33:729-740; Queen and Baltimore, 1983, *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle, 1989, *Proc. Natl. Acad. Sci. USA* 86:5473-5477), pancreas-specific promoters (Edlund *et al.*, 1985, *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No.

30 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters



(Kessel and Gruss, 1990, *Science* 249:374-379) and the  $\alpha$ -fetoprotein promoter (Camper and Tilghman, 1989, *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operably linked to a regulatory  
5 sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to the mRNA encoding a polypeptide of the invention. Regulatory sequences operably linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the  
10 antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue-specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid, or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency  
15 regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, 1986, *Trends in Genetics*, Vol. 1(1).

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host  
20 cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term  
25 as used herein.

A host cell can be any prokaryotic (*e.g.*, *E. coli*) or eukaryotic cell (*e.g.*, insect cells, yeast or mammalian cells).

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms  
30 "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection,

lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*supra*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells  
5 may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Cells stably transfected with the introduced nucleic acid  
10 can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce a marker protein or a segment thereof. Accordingly, the invention further provides methods for producing a marker protein or a segment  
15 thereof using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of the invention (into which a recombinant expression vector encoding a marker protein or a segment thereof has been introduced) in a suitable medium such that the is produced. In another embodiment, the method further comprises isolating the a marker protein or a segment thereof from the medium or the  
20 host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which a sequences encoding a marker protein or a segment thereof have been introduced. Such host cells can then be used to  
25 create non-human transgenic animals in which exogenous sequences encoding a marker protein of the invention have been introduced into their genome or homologous recombinant animals in which endogenous gene(s) encoding a marker protein have been altered. Such animals are useful for studying the function and/or activity of the marker protein and for identifying and/or evaluating modulators of marker protein. As used  
30 herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human

primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

10 A transgenic animal of the invention can be created by introducing a nucleic acid encoding a marker protein into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the transgene to direct expression of the polypeptide of the invention to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, U.S. Patent No. 15 4,873,191 and in Hogan, *Manipulating the Mouse Embryo*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the transgene in its genome and/or expression of mRNA encoding the transgene in tissues or cells of the animals. A transgenic founder animal 20 can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying the transgene can further be bred to other transgenic animals carrying other transgenes.

To create an homologous recombinant animal, a vector is prepared which contains at least a portion of a gene encoding a marker protein into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the gene. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous gene is functionally disrupted (*i.e.*, no longer encodes a 30

functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous protein). In the homologous recombination vector, the altered portion of the gene is flanked at its 5' and 3' ends by additional nucleic acid of the gene to allow for homologous recombination to occur between the exogenous gene carried by the vector and an endogenous gene in an embryonic stem cell. The additional flanking nucleic acid sequences are of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see, *e.g.*, Thomas and Capecchi, 1987, *Cell* 51:503 for a description of homologous recombination vectors). The vector is introduced into an embryonic stem cell line (*e.g.*, by electroporation) and cells in which the introduced gene has homologously recombined with the endogenous gene are selected (see, *e.g.*, Li *et al.*, 1992, *Cell* 69:915). The selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse) to form aggregation chimeras (see, *e.g.*, Bradley, *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, Robertson, Ed., IRL, Oxford, 1987, pp. 113-152). A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Current Opinion in Bio/Technology* 2:823-829 and in PCT Publication NOS. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169.

In another embodiment, transgenic non-human animals can be produced which contain selected systems which allow for regulated expression of the transgene. One example of such a system is the *cre/loxP* recombinase system of bacteriophage P1. For a description of the *cre/loxP* recombinase system, see, *e.g.*, Lakso *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.*, 1991, *Science* 251:1351-1355). If a *cre/loxP* recombinase system is used to regulate expression of the

- 72 -

transgene, animals containing transgenes encoding both the *Cre* recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, *e.g.*, by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813 and PCT Publication NOS. WO 97/07668 and WO 97/07669.

#### 10 IV. Pharmaceutical Compositions

The nucleic acid molecules, polypeptides, and antibodies (also referred to herein as "active compounds") of the invention can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier.

15 As used herein the language "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

The invention includes methods for preparing pharmaceutical compositions for modulating the expression or activity of a marker nucleic acid or protein. Such methods comprise formulating a pharmaceutically acceptable carrier with an agent which modulates expression or activity of a marker nucleic acid or protein. Such compositions can further include additional active agents. Thus, the invention further includes methods for preparing a pharmaceutical composition by formulating a pharmaceutically acceptable carrier with an agent which modulates expression or activity of a marker nucleic acid or protein and one or more additional active compounds.

The invention also provides methods (also referred to herein as "screening assays") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, peptoids, small molecules or other drugs) which (a) bind to the marker, or (b) have a modulatory (*e.g.*, stimulatory or inhibitory) effect on the activity of the marker or, more specifically, (c) have a modulatory effect on the interactions of the marker with one or more of its natural substrates (*e.g.*, peptide, protein, hormone, co-factor, or nucleic acid), or (d) have a modulatory effect on the expression of the marker. Such assays typically comprise a reaction between the marker and one or more assay components. The other components may be either the test compound itself, or a combination of test compound and a natural binding partner of the marker.

The test compounds of the present invention may be obtained from any available source, including systematic libraries of natural and/or synthetic compounds. Test compounds may also be obtained by any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; peptoid libraries (libraries of molecules having the functionalities of peptides, but with a novel, non-peptide backbone which are resistant to enzymatic degradation but which nevertheless remain bioactive; see, *e.g.*, Zuckermann *et al.*, 1994, *J. Med. Chem.* 37:2678-85); spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library and peptoid library approaches are limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, 1997, *Anticancer Drug Des.* 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc. Natl. Acad. Sci. U.S.A.* 90:6909; Erb *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:11422; Zuckermann *et al.* (1994). *J. Med. Chem.* 37:2678; Cho *et al.* (1993) *Science* 261:1303; Carrell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2059; Carell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2061; and in Gallop *et al.* (1994) *J. Med. Chem.* 37:1233.

Libraries of compounds may be presented in solution (e.g., Houghten, 1992, *Biotechniques* 13:412-421), or on beads (Lam, 1991, *Nature* 354:82-84), chips (Fodor, 1993, *Nature* 364:555-556), bacteria and/or spores, (Ladner, USP 5,223,409), plasmids (Cull *et al*, 1992, *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott  
5 and Smith, 1990, *Science* 249:386-390; Devlin, 1990, *Science* 249:404-406; Cwirla *et al*, 1990, *Proc. Natl. Acad. Sci.* 87:6378-6382; Felici, 1991, *J. Mol. Biol.* 222:301-310; Ladner, *supra*).

In one embodiment, the invention provides assays for screening candidate or test compounds which are substrates of a protein encoded by or  
10 corresponding to a marker or biologically active portion thereof. In another embodiment, the invention provides assays for screening candidate or test compounds which bind to a protein encoded by or corresponding to a marker or biologically active portion thereof. Determining the ability of the test compound to directly bind to a protein can be accomplished, for example, by coupling the compound with a  
15 radioisotope or enzymatic label such that binding of the compound to the marker can be determined by detecting the labeled marker compound in a complex. For example, compounds (e.g., marker substrates) can be labeled with  $^{125}\text{I}$ ,  $^{35}\text{S}$ ,  $^{14}\text{C}$ , or  $^3\text{H}$ , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, assay components can be enzymatically  
20 labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product.

In another embodiment, the invention provides assays for screening candidate or test compounds which modulate the expression of a marker or the activity  
25 of a protein encoded by or corresponding to a marker, or a biologically active portion thereof. In all likelihood, the protein encoded by or corresponding to the marker can, *in vivo*, interact with one or more molecules, such as but not limited to, peptides, proteins, hormones, cofactors and nucleic acids. For the purposes of this discussion, such cellular and extracellular molecules are referred to herein as "binding partners" or marker  
30 "substrate".

One necessary embodiment of the invention in order to facilitate such screening is the use of a protein encoded by or corresponding to marker to identify the protein's natural *in vivo* binding partners. There are many ways to accomplish this which are known to one skilled in the art. One example is the use of the marker protein as "bait protein" in a two-hybrid assay or three-hybrid assay (see, *e.g.*, U.S. Patent No. 5,283,317; Zervos *et al*, 1993, *Cell* 72:223-232; Madura *et al*, 1993, *J. Biol. Chem.* 268:12046-12054; Bartel *et al*, 1993, *Biotechniques* 14:920-924; Iwabuchi *et al*, 1993 *Oncogene* 8:1693-1696; Brent WO94/10300) in order to identify other proteins which bind to or interact with the marker (binding partners) and, therefore, are possibly involved in the natural function of the marker. Such marker binding partners are also likely to be involved in the propagation of signals by the marker protein or downstream elements of a marker protein-mediated signaling pathway. Alternatively, such marker protein binding partners may also be found to be inhibitors of the marker protein.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that encodes a marker protein fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a marker-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) which is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be readily detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene which encodes the protein which interacts with the marker protein.

In a further embodiment, assays may be devised through the use of the invention for the purpose of identifying compounds which modulate (*e.g.*, affect either positively or negatively) interactions between a marker protein and its substrates and/or binding partners. Such compounds can include, but are not limited to, molecules such as antibodies, peptides, hormones, oligonucleotides, nucleic acids, and analogs thereof.



- 76 -

Such compounds may also be obtained from any available source, including systematic libraries of natural and/or synthetic compounds. The preferred assay components for use in this embodiment is an ovarian cancer marker protein identified herein, the known binding partner and/or substrate of same, and the test compound. Test compounds can be  
5 supplied from any source.

The basic principle of the assay systems used to identify compounds that interfere with the interaction between the marker protein and its binding partner involves preparing a reaction mixture containing the marker protein and its binding partner under conditions and for a time sufficient to allow the two products to interact  
10 and bind, thus forming a complex. In order to test an agent for inhibitory activity, the reaction mixture is prepared in the presence and absence of the test compound. The test compound can be initially included in the reaction mixture, or can be added at a time subsequent to the addition of the marker protein and its binding partner. Control reaction mixtures are incubated without the test compound or with a placebo. The  
15 formation of any complexes between the marker protein and its binding partner is then detected. The formation of a complex in the control reaction, but less or no such formation in the reaction mixture containing the test compound, indicates that the compound interferes with the interaction of the marker protein and its binding partner. Conversely, the formation of more complex in the presence of compound than in the  
20 control reaction indicates that the compound may enhance interaction of the marker protein and its binding partner.

The assay for compounds that interfere with the interaction of the marker protein with its binding partner may be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring either the marker protein or its binding  
25 partner onto a solid phase and detecting complexes anchored to the solid phase at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the marker proteins and the binding partners  
30 (*e.g.*, by competition) can be identified by conducting the reaction in the presence of the test substance, *i.e.*, by adding the test substance to the reaction mixture prior to or simultaneously with the marker and its interactive binding partner. Alternatively, test

compounds that disrupt preformed complexes, *e.g.*, compounds with higher binding constants that displace one of the components from the complex, can be tested by adding the test compound to the reaction mixture after complexes have been formed. The various formats are briefly described below.

5                   In a heterogeneous assay system, either the marker protein or its binding partner is anchored onto a solid surface or matrix, while the other corresponding non-anchored component may be labeled, either directly or indirectly. In practice, microtitre plates are often utilized for this approach. The anchored species can be immobilized by a number of methods, either non-covalent or covalent, that are typically well known to  
10 one who practices the art. Non-covalent attachment can often be accomplished simply by coating the solid surface with a solution of the marker protein or its binding partner and drying. Alternatively, an immobilized antibody specific for the assay component to be anchored can be used for this purpose. Such surfaces can often be prepared in advance and stored.

15                   In related embodiments, a fusion protein can be provided which adds a domain that allows one or both of the assay components to be anchored to a matrix. For example, glutathione-S-transferase/marker fusion proteins or glutathione-S-transferase/binding partner can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, which are then  
20 combined with the test compound or the test compound and either the non-adsorbed marker or its binding partner, and the mixture incubated under conditions conducive to complex formation (*e.g.*, physiological conditions). Following incubation, the beads or microtiter plate wells are washed to remove any unbound assay components, the immobilized complex assessed either directly or indirectly, for example, as described  
25 above. Alternatively, the complexes can be dissociated from the matrix, and the level of marker binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either a marker protein or a marker protein binding partner can be immobilized utilizing conjugation of biotin and  
30 streptavidin. Biotinylated marker protein or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of

streptavidin-coated 96 well plates (Pierce Chemical). In certain embodiments, the protein-immobilized surfaces can be prepared in advance and stored.

In order to conduct the assay, the corresponding partner of the immobilized assay component is exposed to the coated surface with or without the test compound. After the reaction is complete, unreacted assay components are removed (e.g., by washing) and any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the non-immobilized component is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed.

Where the non-immobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the initially non-immobilized species (the antibody, in turn, can be directly labeled or indirectly labeled with, e.g., a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which modulate (inhibit or enhance) complex formation or which disrupt preformed complexes can be detected.

In an alternate embodiment of the invention, a homogeneous assay may be used. This is typically a reaction, analogous to those mentioned above, which is conducted in a liquid phase in the presence or absence of the test compound. The formed complexes are then separated from unreacted components, and the amount of complex formed is determined. As mentioned for heterogeneous assay systems, the order of addition of reactants to the liquid phase can yield information about which test compounds modulate (inhibit or enhance) complex formation and which disrupt preformed complexes.

In such a homogeneous assay, the reaction products may be separated from unreacted assay components by any of a number of standard techniques, including but not limited to: differential centrifugation, chromatography, electrophoresis and immunoprecipitation. In differential centrifugation, complexes of molecules may be separated from uncomplexed molecules through a series of centrifugal steps, due to the different sedimentation equilibria of complexes based on their different sizes and densities (see, for example, Rivas, G., and Minton, A.P., *Trends Biochem Sci* 1993 Aug;18(8):284-7). Standard chromatographic techniques may also be utilized to separate complexed molecules from uncomplexed ones. For example, gel filtration

chromatography separates molecules based on size, and through the utilization of an appropriate gel filtration resin in a column format, for example, the relatively larger complex may be separated from the relatively smaller uncomplexed components. Similarly, the relatively different charge properties of the complex as compared to the uncomplexed molecules may be exploited to differentially separate the complex from the remaining individual reactants, for example through the use of ion-exchange chromatography resins. Such resins and chromatographic techniques are well known to one skilled in the art (see, *e.g.*, Heegaard, 1998, *J Mol. Recognit.* 11:141-148; Hage and Tweed, 1997, *J. Chromatogr. B. Biomed. Sci. Appl.*, 699:499-525). Gel electrophoresis may also be employed to separate complexed molecules from unbound species (see, *e.g.*, Ausubel *et al* (eds.), as described in : Current Protocols in Molecular Biology, J. Wiley & Sons, New York. 1999). In this technique, protein or nucleic acid complexes are separated based on size or charge, for example. In order to maintain the binding interaction during the electrophoretic process, nondenaturing gels in the absence of reducing agent are typically preferred, but conditions appropriate to the particular interactants will be well known to one skilled in the art. Immunoprecipitation is another common technique utilized for the isolation of a protein-protein complex from solution (see, *e.g.*, Ausubel *et al* (eds.), In: Current Protocols in Molecular Biology, J. Wiley & Sons, New York. 1999). In this technique, all proteins binding to an antibody specific to one of the binding molecules are precipitated from solution by conjugating the antibody to a polymer bead that may be readily collected by centrifugation. The bound assay components are released from the beads (through a specific proteolysis event or other technique well known in the art which will not disturb the protein-protein interaction in the complex), and a second immunoprecipitation step is performed, this time utilizing antibodies specific for the correspondingly different interacting assay component. In this manner, only formed complexes should remain attached to the beads. Variations in complex formation in both the presence and the absence of a test compound can be compared, thus offering information about the ability of the compound to modulate interactions between the marker protein and its binding partner.

Also within the scope of the present invention are methods for direct detection of interactions between the marker protein and its natural binding partner and/or a test compound in a homogeneous or heterogeneous assay system without

further sample manipulation. For example, the technique of fluorescence energy transfer may be utilized (see, *e.g.*, Lakowicz *et al*, U.S. Patent No. 5,631,169; Stavrianopoulos *et al*, U.S. Patent No. 4,868,103). Generally, this technique involves the addition of a fluorophore label on a first 'donor' molecule (*e.g.*, marker or test compound) such that  
5 its emitted fluorescent energy will be absorbed by a fluorescent label on a second, 'acceptor' molecule (*e.g.*, marker or test compound), which in turn is able to fluoresce due to the absorbed energy. Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the 'acceptor' molecule label may be  
10 differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, spatial relationships between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label in the assay should be maximal. An FET binding event can be conveniently measured through  
15 standard fluorometric detection means well known in the art (*e.g.*, using a fluorimeter). A test substance which either enhances or hinders participation of one of the species in the preformed complex will result in the generation of a signal variant to that of background. In this way, test substances that modulate interactions between a marker and its binding partner can be identified in controlled assays.

20 In another embodiment, modulators of marker expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of marker mRNA or protein in the cell, is determined. The level of expression of marker mRNA or protein in the presence of the candidate compound is compared to the level of expression of marker mRNA or protein in the absence of the candidate  
25 compound. The candidate compound can then be identified as a modulator of marker expression based on this comparison. For example, when expression of marker mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of marker mRNA or protein expression. Conversely, when expression of marker mRNA  
30 or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of marker mRNA or protein expression. The level of marker mRNA or protein expression

in the cells can be determined by methods described herein for detecting marker mRNA or protein.

In another aspect, the invention pertains to a combination of two or more of the assays described herein. For example, a modulating agent can be identified using  
5 a cell-based or a cell free assay, and the ability of the agent to modulate the activity of a marker protein can be further confirmed *in vivo*, *e.g.*, in a whole animal model for cellular transformation and/or tumorigenesis.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to  
10 further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, an marker modulating agent, an antisense marker nucleic acid molecule, an marker-specific antibody, or an marker-binding partner) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as  
15 described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein.

It is understood that appropriate doses of small molecule agents and protein or polypeptide agents depends upon a number of factors within the knowledge of  
20 the ordinarily skilled physician, veterinarian, or researcher. The dose(s) of these agents will vary, for example, depending upon the identity, size, and condition of the subject or sample being treated, further depending upon the route by which the composition is to be administered, if applicable, and the effect which the practitioner desires the agent to have upon the nucleic acid or polypeptide of the invention. Exemplary doses of a small  
25 molecule include milligram or microgram amounts per kilogram of subject or sample weight (*e.g.* about 1 microgram per kilogram to about 500 milligrams per kilogram, about 100 micrograms per kilogram to about 5 milligrams per kilogram, or about 1 microgram per kilogram to about 50 micrograms per kilogram). Exemplary doses of a protein or polypeptide include gram, milligram or microgram amounts per kilogram of  
30 subject or sample weight (*e.g.* about 1 microgram per kilogram to about 5 grams per kilogram, about 100 micrograms per kilogram to about 500 milligrams per kilogram, or about 1 milligram per kilogram to about 50 milligrams per kilogram). It is furthermore

understood that appropriate doses of one of these agents depend upon the potency of the agent with respect to the expression or activity to be modulated. Such appropriate doses can be determined using the assays described herein. When one or more of these agents is to be administered to an animal (*e.g.* a human) in order to modulate expression or activity of a polypeptide or nucleic acid of the invention, a physician, veterinarian, or researcher can, for example, prescribe a relatively low dose at first, subsequently increasing the dose until an appropriate response is obtained. In addition, it is understood that the specific dose level for any particular animal subject will depend upon a variety of factors including the activity of the specific agent employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of administration, the rate of excretion, any drug combination, and the degree of expression or activity to be modulated.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediamine-tetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL (BASF; Parsippany, NJ) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy

syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can  
5 be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid,  
10 thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

15 Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, a polypeptide or antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium,  
20 and then incorporating the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

25 Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid  
30 carrier is applied orally and swished and expectorated or swallowed.



Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches, and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a  
5 lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the  
10 form of an aerosol spray from a pressurized container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally  
15 known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

20 The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled  
25 release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova  
30 Pharmaceuticals, Inc. Liposomal suspensions (including liposomes having monoclonal antibodies incorporated therein or thereon) can also be used as pharmaceutically

acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit  
5 form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound  
10 and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

For antibodies, the preferred dosage is 0.1 mg/kg to 100 mg/kg of body weight (generally 10 mg/kg to 20 mg/kg). If the antibody is to act in the brain, a dosage of 50 mg/kg to 100 mg/kg is usually appropriate. Generally, partially human antibodies  
15 and fully human antibodies have a longer half-life within the human body than other antibodies. Accordingly, lower dosages and less frequent administration is often possible. Modifications such as lipitation can be used to stabilize antibodies and to enhance uptake and tissue penetration (*e.g.*, into the ovarian epithelium). A method for lipitation of antibodies is described by Cruikshank *et al.* (1997) *J. Acquired Immune*  
20 *Deficiency Syndromes and Human Retrovirology* 14:193.

The invention also provides vaccine compositions for the prevention and/or treatment of ovarian cancer. The invention provides ovarian cancer vaccine compositions in which a protein of a marker of Table 1, or a combination of proteins of the markers of Table 1, are introduced into a subject in order to stimulate an immune  
25 response against the ovarian cancer. The invention also provides ovarian cancer vaccine compositions in which a gene expression construct, which expresses a marker or fragment of a marker identified in Table 1, is introduced into the subject such that a protein or fragment of a protein encoded by a marker of Table 1 is produced by transfected cells in the subject at a higher than normal level and elicits an immune  
30 response.

In one embodiment, an ovarian cancer vaccine is provided and employed as an immunotherapeutic agent for the prevention of ovarian cancer. In another embodiment, an ovarian cancer vaccine is provided and employed as an immunotherapeutic agent for the treatment of ovarian cancer.

5 By way of example, an ovarian cancer vaccine comprised of the proteins of the markers of Table 1, may be employed for the prevention and/or treatment of ovarian cancer in a subject by administering the vaccine by a variety of routes, *e.g.*, intradermally, subcutaneously, or intramuscularly. In addition, the ovarian cancer vaccine can be administered together with adjuvants and/or immunomodulators to boost  
10 the activity of the vaccine and the subject's response. In one embodiment, devices and/or compositions containing the vaccine, suitable for sustained or intermittent release could be, implanted in the body or topically applied thereto for the relatively slow release of such materials into the body. The ovarian cancer vaccine can be introduced along with immunomodulatory compounds, which can alter the type of immune  
15 response produced in order to produce a response which will be more effective in eliminating the cancer.

In another embodiment, an ovarian cancer vaccine comprised of an expression construct of the markers of Table 1, may be introduced by injection into muscle or by coating onto microprojectiles and using a device designed for the purpose  
20 to fire the projectiles at high speed into the skin. The cells of the subject will then express the protein(s) or fragments of proteins of the markers of Table 1 and induce an immune response. In addition, the ovarian cancer vaccine may be introduced along with expression constructs for immunomodulatory molecules, such as cytokines, which may increase the immune response or modulate the type of immune response produced in  
25 order to produce a response which will be more effective in eliminating the cancer.

The marker nucleic acid molecules of the present invention can also be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (U.S. Patent 5,328,470), or by stereotactic injection (see, *e.g.*, Chen *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91:3054-3057).  
30 The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively,

where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.* retroviral vectors, the pharmaceutical preparation can include one or more cells which produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or  
5 dispenser together with instructions for administration.

## V. Predictive Medicine

The present invention pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical  
10 trails are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining the level of expression of one or more marker proteins or nucleic acids, in order to determine whether an individual is at risk of developing ovarian cancer. Such assays can be used for prognostic or predictive purposes to thereby  
15 prophylactically treat an individual prior to the onset of the cancer.

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs or other compounds administered either to inhibit ovarian cancer or to treat or prevent any other disorder {*i.e.* in order to understand any ovarian carcinogenic effects that such treatment may have} ) on the expression or activity of a  
20 marker of the invention in clinical trials. These and other agents are described in further detail in the following sections.

### A. Diagnostic Assays

An exemplary method for detecting the presence or absence of a marker  
25 protein or nucleic acid in a biological sample involves obtaining a biological sample (*e.g.* an ovary-associated body fluid) from a test subject and contacting the biological sample with a compound or an agent capable of detecting the polypeptide or nucleic acid (*e.g.*, mRNA, genomic DNA, or cDNA). The detection methods of the invention can thus be used to detect mRNA, protein, cDNA, or genomic DNA, for example, in a  
30 biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of a marker protein include enzyme linked immunosorbent

assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of a marker protein include introducing into a subject a labeled antibody directed against the protein or fragment thereof. For  
5 example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

A general principle of such diagnostic and prognostic assays involves preparing a sample or reaction mixture that may contain a marker, and a probe, under appropriate conditions and for a time sufficient to allow the marker and probe to interact  
10 and bind, thus forming a complex that can be removed and/or detected in the reaction mixture. These assays can be conducted in a variety of ways.

For example, one method to conduct such an assay would involve anchoring the marker or probe onto a solid phase support, also referred to as a substrate, and detecting target marker/probe complexes anchored on the solid phase at the end of  
15 the reaction. In one embodiment of such a method, a sample from a subject, which is to be assayed for presence and/or concentration of marker, can be anchored onto a carrier or solid phase support. In another embodiment, the reverse situation is possible, in which the probe can be anchored to a solid phase and a sample from a subject can be allowed to react as an unanchored component of the assay.

20 There are many established methods for anchoring assay components to a solid phase. These include, without limitation, marker or probe molecules which are immobilized through conjugation of biotin and streptavidin. Such biotinylated assay components can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, IL), and  
25 immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). In certain embodiments, the surfaces with immobilized assay components can be prepared in advance and stored.

Other suitable carriers or solid phase supports for such assays include any material capable of binding the class of molecule to which the marker or probe belongs.  
30 Well-known supports or carriers include, but are not limited to, glass, polystyrene, nylon, polypropylene, nylon, polyethylene, dextran, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite.

In order to conduct assays with the above mentioned approaches, the non-immobilized component is added to the solid phase upon which the second component is anchored. After the reaction is complete, uncomplexed components may be removed (*e.g.*, by washing) under conditions such that any complexes formed will remain immobilized upon the solid phase. The detection of marker/probe complexes anchored to the solid phase can be accomplished in a number of methods outlined herein.

In a preferred embodiment, the probe, when it is the unanchored assay component, can be labeled for the purpose of detection and readout of the assay, either directly or indirectly, with detectable labels discussed herein and which are well-known to one skilled in the art.

It is also possible to directly detect marker/probe complex formation without further manipulation or labeling of either component (marker or probe), for example by utilizing the technique of fluorescence energy transfer (see, for example, Lakowicz *et al.*, U.S. Patent No. 5,631,169; Stavrianopoulos, *et al.*, U.S. Patent No. 4,868,103). A fluorophore label on the first, 'donor' molecule is selected such that, upon excitation with incident light of appropriate wavelength, its emitted fluorescent energy will be absorbed by a fluorescent label on a second 'acceptor' molecule, which in turn is able to fluoresce due to the absorbed energy. Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the 'acceptor' molecule label may be differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, spatial relationships between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label in the assay should be maximal. An FET binding event can be conveniently measured through standard fluorometric detection means well known in the art (*e.g.*, using a fluorimeter).

In another embodiment, determination of the ability of a probe to recognize a marker can be accomplished without labeling either assay component (probe or marker) by utilizing a technology such as real-time Biomolecular Interaction Analysis (BIA) (see, *e.g.*, Sjolander, S. and Urbaniczky, C., 1991, *Anal. Chem.* 63:2338-2345

and Szabo *et al.*, 1995, *Curr. Opin. Struct. Biol.* 5:699-705). As used herein, "BIA" or "surface plasmon resonance" is a technology for studying biospecific interactions in real time, without labeling any of the interactants (*e.g.*, BIAcore). Changes in the mass at the binding surface (indicative of a binding event) result in alterations of the refractive index of light near the surface (the optical phenomenon of surface plasmon resonance (SPR)),  
5 resulting in a detectable signal which can be used as an indication of real-time reactions between biological molecules.

Alternatively, in another embodiment, analogous diagnostic and prognostic assays can be conducted with marker and probe as solutes in a liquid phase.

10 In such an assay, the complexed marker and probe are separated from uncomplexed components by any of a number of standard techniques, including but not limited to: differential centrifugation, chromatography, electrophoresis and immunoprecipitation. In differential centrifugation, marker/probe complexes may be separated from uncomplexed assay components through a series of centrifugal steps, due to the different  
15 sedimentation equilibria of complexes based on their different sizes and densities (see, for example, Rivas, G., and Minton, A.P., 1993, *Trends Biochem Sci.* 18(8):284-7). Standard chromatographic techniques may also be utilized to separate complexed molecules from uncomplexed ones. For example, gel filtration chromatography separates molecules based on size, and through the utilization of an appropriate gel  
20 filtration resin in a column format, for example, the relatively larger complex may be separated from the relatively smaller uncomplexed components. Similarly, the relatively different charge properties of the marker/probe complex as compared to the uncomplexed components may be exploited to differentiate the complex from uncomplexed components, for example through the utilization of ion-exchange  
25 chromatography resins. Such resins and chromatographic techniques are well known to one skilled in the art (see, *e.g.*, Heegaard, N.H., 1998, *J. Mol. Recognit.* Winter 11(1-6):141-8; Hage, D.S., and Tweed, S.A. *J Chromatogr B Biomed Sci Appl* 1997 Oct 10;699(1-2):499-525). Gel electrophoresis may also be employed to separate complexed assay components from unbound components (see, *e.g.*, Ausubel *et al.*, ed.,  
30 *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, 1987-1999). In this technique, protein or nucleic acid complexes are separated based on size or charge, for example. In order to maintain the binding interaction during the

electrophoretic process, non-denaturing gel matrix materials and conditions in the absence of reducing agent are typically preferred. Appropriate conditions to the particular assay and components thereof will be well known to one skilled in the art.

In a particular embodiment, the level of marker mRNA can be  
5 determined both by *in situ* and by *in vitro* formats in a biological sample using methods known in the art. The term "biological sample" is intended to include tissues, cells, biological fluids and isolates thereof, isolated from a subject, as well as tissues, cells and fluids present within a subject. Many expression detection methods use isolated RNA. For *in vitro* methods, any RNA isolation technique that does not select against the  
10 isolation of mRNA can be utilized for the purification of RNA from ovarian cells (see, e.g., Ausubel *et al.*, ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York 1987-1999). Additionally, large numbers of tissue samples can readily be processed using techniques well known to those of skill in the art, such as, for example, the single-step RNA isolation process of Chomczynski (1989, U.S. Patent No.  
15 4,843,155).

The isolated mRNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or Northern analyses, polymerase chain reaction analyses and probe arrays. One preferred diagnostic method for the detection of mRNA levels involves contacting the isolated mRNA with a nucleic acid molecule  
20 (probe) that can hybridize to the mRNA encoded by the gene being detected. The nucleic acid probe can be, for example, a full-length cDNA, or a portion thereof, such as an oligonucleotide of at least 7, 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to a mRNA or genomic DNA encoding a marker of the present invention. Other suitable probes for use in the  
25 diagnostic assays of the invention are described herein. Hybridization of an mRNA with the probe indicates that the marker in question is being expressed.

In one format, the mRNA is immobilized on a solid surface and contacted with a probe, for example by running the isolated mRNA on an agarose gel and transferring the mRNA from the gel to a membrane, such as nitrocellulose. In an  
30 alternative format, the probe(s) are immobilized on a solid surface and the mRNA is contacted with the probe(s), for example, in an Affymetrix gene chip array. A skilled



artisan can readily adapt known mRNA detection methods for use in detecting the level of mRNA encoded by the markers of the present invention.

An alternative method for determining the level of mRNA marker in a sample involves the process of nucleic acid amplification, *e.g.*, by rtPCR (the  
5 experimental embodiment set forth in Mullis, 1987, U.S. Patent No. 4,683,202), ligase chain reaction (Barany, 1991, *Proc. Natl. Acad. Sci. USA*, 88:189-193), self sustained sequence replication (Guatelli *et al.*, 1990, *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh *et al.*, 1989, *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.*, 1988, *Bio/Technology* 6:1197), rolling  
10 circle replication (Lizardi *et al.*, U.S. Patent No. 5,854,033) or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers. As used herein, amplification primers are defined as being  
15 a pair of nucleic acid molecules that can anneal to 5' or 3' regions of a gene (plus and minus strands, respectively, or vice-versa) and contain a short region in between. In general, amplification primers are from about 10 to 30 nucleotides in length and flank a region from about 50 to 200 nucleotides in length. Under appropriate conditions and with appropriate reagents, such primers permit the amplification of a nucleic acid  
20 molecule comprising the nucleotide sequence flanked by the primers.

For *in situ* methods, mRNA does not need to be isolated from the ovarian cells prior to detection. In such methods, a cell or tissue sample is prepared/processed using known histological methods. The sample is then immobilized on a support, typically a glass slide, and then contacted with a probe that can hybridize to mRNA that  
25 encodes the marker.

As an alternative to making determinations based on the absolute expression level of the marker, determinations may be based on the normalized expression level of the marker. Expression levels are normalized by correcting the absolute expression level of a marker by comparing its expression to the expression of a  
30 gene that is not a marker, *e.g.*, a housekeeping gene that is constitutively expressed. Suitable genes for normalization include housekeeping genes such as the actin gene, or epithelial cell-specific genes. This normalization allows the comparison of the

expression level in one sample, *e.g.*, a patient sample, to another sample, *e.g.*, a non-ovarian cancer sample, or between samples from different sources.

Alternatively, the expression level can be provided as a relative expression level. To determine a relative expression level of a marker, the level of  
5 expression of the marker is determined for 10 or more samples of normal versus cancer cell isolates, preferably 50 or more samples, prior to the determination of the expression level for the sample in question. The mean expression level of each of the genes assayed in the larger number of samples is determined and this is used as a baseline expression level for the marker. The expression level of the marker determined for the  
10 test sample (absolute level of expression) is then divided by the mean expression value obtained for that marker. This provides a relative expression level.

Preferably, the samples used in the baseline determination will be from ovarian cancer or from non-ovarian cancer cells of ovarian tissue. The choice of the cell source is dependent on the use of the relative expression level. Using expression found  
15 in normal tissues as a mean expression score aids in validating whether the marker assayed is ovarian specific (versus normal cells). In addition, as more data is accumulated, the mean expression value can be revised, providing improved relative expression values based on accumulated data. Expression data from ovarian cells provides a means for grading the severity of the ovarian cancer state.

20 In another embodiment of the present invention, a marker protein is detected. A preferred agent for detecting marker protein of the invention is an antibody capable of binding to such a protein or a fragment thereof, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment or derivatives thereof (*e.g.*, Fab or F(ab')<sub>2</sub>) can be used.  
25 The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody  
30 and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

Proteins from ovarian cells can be isolated using techniques that are well known to those of skill in the art. The protein isolation methods employed can, for example, be such as those described in Harlow and Lane (Harlow and Lane, 1988, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York).

A variety of formats can be employed to determine whether a sample contains a protein that binds to a given antibody. Examples of such formats include, but are not limited to, enzyme immunoassay (EIA), radioimmunoassay (RIA), Western blot analysis and enzyme linked immunoabsorbant assay (ELISA). A skilled artisan can readily adapt known protein/antibody detection methods for use in determining whether ovarian cells express a marker of the present invention.

In one format, antibodies, or antibody fragments or derivatives, can be used in methods such as Western blots or immunofluorescence techniques to detect the expressed proteins. In such uses, it is generally preferable to immobilize either the antibody or proteins on a solid support. Suitable solid phase supports or carriers include any support capable of binding an antigen or an antibody. Well-known supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite.

One skilled in the art will know many other suitable carriers for binding antibody or antigen, and will be able to adapt such support for use with the present invention. For example, protein isolated from ovarian cells can be run on a polyacrylamide gel electrophoresis and immobilized onto a solid phase support such as nitrocellulose. The support can then be washed with suitable buffers followed by treatment with the detectably labeled antibody. The solid phase support can then be washed with the buffer a second time to remove unbound antibody. The amount of bound label on the solid support can then be detected by conventional means.

The invention also encompasses kits for detecting the presence of a marker protein or nucleic acid in a biological sample (e.g. an ovary-associated body fluid such as a urine sample). Such kits can be used to determine if a subject is suffering from or is at increased risk of developing ovarian cancer. For example, the kit can comprise a labeled compound or agent capable of detecting a marker protein or nucleic acid in a biological sample and means for determining the amount of the protein or

mRNA in the sample (*e.g.*, an antibody which binds the protein or a fragment thereof, or an oligonucleotide probe which binds to DNA or mRNA encoding the protein). Kits can also include instructions for interpreting the results obtained using the kit.

For antibody-based kits, the kit can comprise, for example: (1) a first  
5 antibody (*e.g.*, attached to a solid support) which binds to a marker protein; and, optionally, (2) a second, different antibody which binds to either the protein or the first antibody and is conjugated to a detectable label.

For oligonucleotide-based kits, the kit can comprise, for example: (1) an oligonucleotide, *e.g.*, a detectably labeled oligonucleotide, which hybridizes to a nucleic  
10 acid sequence encoding a marker protein or (2) a pair of primers useful for amplifying a marker nucleic acid molecule. The kit can also comprise, *e.g.*, a buffering agent, a preservative, or a protein stabilizing agent. The kit can further comprise components necessary for detecting the detectable label (*e.g.*, an enzyme or a substrate). The kit can also contain a control sample or a series of control samples which can be assayed and  
15 compared to the test sample. Each component of the kit can be enclosed within an individual container and all of the various containers can be within a single package, along with instructions for interpreting the results of the assays performed using the kit.

#### B. Pharmacogenomics

20 Agents or modulators which have a stimulatory or inhibitory effect on expression of a marker of the invention can be administered to individuals to treat (prophylactically or therapeutically) ovarian cancer in the patient. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of  
25 the individual may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such  
30 pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the level of expression of a marker of the invention in an

individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

Pharmacogenomics deals with clinically significant variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See, e.g., Linder (1997) *Clin. Chem.* 43(2):254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body are referred to as "altered drug action." Genetic conditions transmitted as single factors altering the way the body acts on drugs are referred to as "altered drug metabolism". These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (antimalarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (e.g., N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, a PM will show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the level of expression of a marker of the invention in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the  
5 identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a modulator of expression of a marker of the invention.

10                    C. Monitoring Clinical Trials

Monitoring the influence of agents (*e.g.*, drug compounds) on the level of expression of a marker of the invention can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent to affect marker expression can be monitored in clinical trials of subjects receiving treatment for ovarian  
15 cancer. In a preferred embodiment, the present invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of one  
20 or more selected markers of the invention in the pre-administration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the level of expression of the marker(s) in the post-administration samples; (v) comparing the level of expression of the marker(s) in the pre-administration sample with the level of expression of the marker(s) in the post-administration sample or samples; and (vi)  
25 altering the administration of the agent to the subject accordingly. For example, increased administration of the agent can be desirable to increase expression of the marker(s) to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent can be desirable to decrease expression of the marker(s) to lower levels than detected, *i.e.*, to decrease the  
30 effectiveness of the agent.

#### D. Electronic Apparatus Readable Media and Arrays

Electronic apparatus readable media comprising a marker of the present invention is also provided. As used herein, "electronic apparatus readable media" refers to any suitable medium for storing, holding or containing data or information that can be  
5 read and accessed directly by an electronic apparatus. Such media can include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as compact disc; electronic storage media such as RAM, ROM, EPROM, EEPROM and the like; general hard disks and hybrids of these categories such as magnetic/optical storage media. The medium is adapted or  
10 configured for having recorded thereon a marker of the present invention.

As used herein, the term "electronic apparatus" is intended to include any suitable computing or processing apparatus or other device configured or adapted for storing data or information. Examples of electronic apparatus suitable for use with the present invention include stand-alone computing apparatus; networks, including a local  
15 area network (LAN), a wide area network (WAN) Internet, Intranet, and Extranet; electronic appliances such as a personal digital assistants (PDAs), cellular phone, pager and the like; and local and distributed processing systems.

As used herein, "recorded" refers to a process for storing or encoding information on the electronic apparatus readable medium. Those skilled in the art can  
20 readily adopt any of the presently known methods for recording information on known media to generate manufactures comprising the markers of the present invention.

A variety of software programs and formats can be used to store the marker information of the present invention on the electronic apparatus readable medium. For example, the marker nucleic acid sequence can be represented in a word  
25 processing text file, formatted in commercially-available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like, as well as in other forms. Any number of data processor structuring formats (e.g., text file or database) may be employed in order to obtain or create a medium having recorded thereon the the markers  
30 of the present invention.

By providing the markers of the invention in readable form, one can routinely access the marker sequence information for a variety of purposes. For example, one skilled in the art can use the nucleotide or amino acid sequences of the present invention in readable form to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the sequences of the invention which match a particular target sequence or target motif.

The present invention therefore provides a medium for holding instructions for performing a method for determining whether a subject has ovarian cancer or a pre-disposition to ovarian cancer, wherein the method comprises the steps of determining the presence or absence of a marker and based on the presence or absence of the marker, determining whether the subject has ovarian cancer or a pre-disposition to ovarian cancer and/or recommending a particular treatment for ovarian cancer or pre-ovarian cancer condition.

The present invention further provides in an electronic system and/or in a network, a method for determining whether a subject has ovarian cancer or a pre-disposition to ovarian cancer associated with a marker wherein the method comprises the steps of determining the presence or absence of the marker, and based on the presence or absence of the marker, determining whether the subject has ovarian cancer or a pre-disposition to ovarian cancer, and/or recommending a particular treatment for the ovarian cancer or pre-ovarian cancer condition. The method may further comprise the step of receiving phenotypic information associated with the subject and/or acquiring from a network phenotypic information associated with the subject.

The present invention also provides in a network, a method for determining whether a subject has ovarian cancer or a pre-disposition to ovarian cancer associated with a marker; said method comprising the steps of receiving information associated with the marker receiving phenotypic information associated with the subject, acquiring information from the network corresponding to the marker and/or ovarian cancer, and based on one or more of the phenotypic information, the marker, and the acquired information, determining whether the subject has a ovarian cancer or a pre-disposition to ovarian cancer. The method may further comprise the step of



recommending a particular treatment for the ovarian cancer or pre-ovarian cancer condition.

The present invention also provides a business method for determining whether a subject has ovarian cancer or a pre-disposition to ovarian cancer, said method  
5 comprising the steps of receiving information associated with the marker, receiving phenotypic information associated with the subject, acquiring information from the network corresponding to the marker and/or ovarian cancer, and based on one or more of the phenotypic information, the marker, and the acquired information, determining whether the subject has ovarian cancer or a pre-disposition to ovarian cancer. The  
10 method may further comprise the step of recommending a particular treatment for the ovarian cancer or pre-ovarian cancer condition.

The invention also includes an array comprising a marker of the present invention. The array can be used to assay expression of one or more genes in the array. In one embodiment, the array can be used to assay gene expression in a tissue to  
15 ascertain tissue specificity of genes in the array. In this manner, up to about 7600 genes can be simultaneously assayed for expression. This allows a profile to be developed showing a battery of genes specifically expressed in one or more tissues.

In addition to such qualitative determination, the invention allows the quantitation of gene expression. Thus, not only tissue specificity, but also the level of  
20 expression of a battery of genes in the tissue is ascertainable. Thus, genes can be grouped on the basis of their tissue expression *per se* and level of expression in that tissue. This is useful, for example, in ascertaining the relationship of gene expression between or among tissues. Thus, one tissue can be perturbed and the effect on gene expression in a second tissue can be determined. In this context, the effect of one cell  
25 type on another cell type in response to a biological stimulus can be determined. Such a determination is useful, for example, to know the effect of cell-cell interaction at the level of gene expression. If an agent is administered therapeutically to treat one cell type but has an undesirable effect on another cell type, the invention provides an assay to determine the molecular basis of the undesirable effect and thus provides the  
30 opportunity to co-administer a counteracting agent or otherwise treat the undesired effect. Similarly, even within a single cell type, undesirable biological effects can be

determined at the molecular level. Thus, the effects of an agent on expression of other than the target gene can be ascertained and counteracted.

In another embodiment, the array can be used to monitor the time course of expression of one or more genes in the array. This can occur in various biological contexts, as disclosed herein, for example development of ovarian cancer, progression of ovarian cancer, and processes, such a cellular transformation associated with ovarian cancer.

The array is also useful for ascertaining the effect of the expression of a gene on the expression of other genes in the same cell or in different cells. This provides, for example, for a selection of alternate molecular targets for therapeutic intervention if the ultimate or downstream target cannot be regulated.

The array is also useful for ascertaining differential expression patterns of one or more genes in normal and abnormal cells. This provides a battery of genes that could serve as a molecular target for diagnosis or therapeutic intervention.

15

#### E. Surrogate Markers

The markers of the invention may serve as surrogate markers for one or more disorders or disease states or for conditions leading up to disease states, and in particular, ovarian cancer. As used herein, a "surrogate marker" is an objective biochemical marker which correlates with the absence or presence of a disease or disorder, or with the progression of a disease or disorder (*e.g.*, with the presence or absence of a tumor). The presence or quantity of such markers is independent of the disease. Therefore, these markers may serve to indicate whether a particular course of treatment is effective in lessening a disease state or disorder. Surrogate markers are of particular use when the presence or extent of a disease state or disorder is difficult to assess through standard methodologies (*e.g.*, early stage tumors), or when an assessment of disease progression is desired before a potentially dangerous clinical endpoint is reached (*e.g.*, an assessment of cardiovascular disease may be made using cholesterol levels as a surrogate marker, and an analysis of HIV infection may be made using HIV RNA levels as a surrogate marker, well in advance of the undesirable clinical outcomes of myocardial infarction or fully-developed AIDS). Examples of the use of surrogate

30

- 102 -

markers in the art include: Koomen *et al.* (2000) *J. Mass. Spectrom.* 35: 258-264; and James (1994) *AIDS Treatment News Archive* 209.

The markers of the invention are also useful as pharmacodynamic markers. As used herein, a "pharmacodynamic marker" is an objective biochemical marker which correlates specifically with drug effects. The presence or quantity of a pharmacodynamic marker is not related to the disease state or disorder for which the drug is being administered; therefore, the presence or quantity of the marker is indicative of the presence or activity of the drug in a subject. For example, a pharmacodynamic marker may be indicative of the concentration of the drug in a biological tissue, in that the marker is either expressed or transcribed or not expressed or transcribed in that tissue in relationship to the level of the drug. In this fashion, the distribution or uptake of the drug may be monitored by the pharmacodynamic marker. Similarly, the presence or quantity of the pharmacodynamic marker may be related to the presence or quantity of the metabolic product of a drug, such that the presence or quantity of the marker is indicative of the relative breakdown rate of the drug *in vivo*. Pharmacodynamic markers are of particular use in increasing the sensitivity of detection of drug effects, particularly when the drug is administered in low doses. Since even a small amount of a drug may be sufficient to activate multiple rounds of marker transcription or expression, the amplified marker may be in a quantity which is more readily detectable than the drug itself. Also, the marker may be more easily detected due to the nature of the marker itself; for example, using the methods described herein, antibodies may be employed in an immune-based detection system for a protein marker, or marker-specific radiolabeled probes may be used to detect a mRNA marker. Furthermore, the use of a pharmacodynamic marker may offer mechanism-based prediction of risk due to drug treatment beyond the range of possible direct observations. Examples of the use of pharmacodynamic markers in the art include: Matsuda *et al.* US 6,033,862; Hattis *et al.* (1991) *Env. Health Perspect.* 90: 229-238; Schentag (1999) *Am. J. Health-Syst. Pharm.* 56 Suppl. 3: S21-S24; and Nicolau (1999) *Am. J. Health-Syst. Pharm.* 56 Suppl. 3: S16-S20.

## VI. Experimental Protocol for all OV markers and M352 - M360

### A. Identification of markers

The markers of the present invention were identified by transcriptional  
5 profiling using mRNA from 9 normal ovarian epithelia, 11 stage I/II ovarian cancer  
tumors and 25 stage III/IV tumors. Clones having expression at least two-fold higher in  
ovarian tumors as compared to their expression in non-ovarian tumor tissues in at least 4  
tumor samples were selected to have their protein-encoding transcript sequences  
determined.

10

### B. Identification of Markers and Assembly of Their Sequences

Clones which displayed an increase in expression in ovarian tumor  
samples over the corresponding average expression of non-tumor samples were used for  
further study. Briefly, BLAST analysis, against both public and proprietary sequence  
15 databases, of EST sequences known to be associated with each clone was performed,  
either directly or in the context of automatically, high-stringency assembled contiguous  
sequences. An identification of protein sequence corresponding to the clone was  
accomplished by obtaining one of the following:

- a) a direct match between the protein sequence and at least one EST  
20 sequence in one of its 6 possible translations;
- b) a direct match between the nucleotide sequence for the mRNA  
corresponding to the protein sequence and at least one EST sequence;
- c) a match between the protein sequence and a contiguous assembly  
(contig) of the EST sequences with other available EST sequences in the databases in  
25 one of its 6 possible translations; or
- d) a match between the nucleotide sequence for the mRNA  
corresponding to the protein sequence and a contiguous assembly of the EST sequences  
with other available EST sequences in the databases in one of its 6 possible translations.

C. Identification of Markers Having Newly-Identified Nucleotide and Amino Acid Sequences.

The markers of Table 2 include newly-identified amino acid sequences.

- 5 These sequences were found to be novel based on one of the following criteria:
- a) the protein sequence found within available public databases was incomplete or erroneous, leading to the construction of an additional completed/corrected protein sequence that is not found as such in the public domain;
  - b) based on nucleotide evidence, variants of the protein sequence were
  - 10 additionally constructed that are not found as such in the public domain; or
  - c) the contig for the EST sequences did not match any known protein, so that a novel protein sequence was derived from an open reading frame of the contig.

- 15 VII. Experimental Protocol for M68, M103, M138, M185, M312, M327-M328, M400, M430-M480, M559, M571-M573, M575-M576, M578-M583, M585-594, and M604-M617

A. Identification of Markers and Assembly of Their Sequences

- 20 The markers of the present invention were identified by transcription profiling using mRNA from 67 ovarian tumors of various histotypes and stage and 96 non-ovarian tumor tissues including normal ovarian epithelium, benign conditions, other normal tissues, and other abnormal tissues. Clones having expression at least three-fold higher in at least 10% of ovarian tumors, as compared to their expression in non-ovarian
- 25 tumor tissue, were designated as ovarian cancer specific markers. These cDNA clones were selected to have their protein-encoding transcript sequences determined. Briefly, BLAST analysis, against both public and proprietary sequence databases, of EST sequences known to be associated with each clone was performed, either directly or in the context of automatically, high-stringency assembled contiguous sequences. An
- 30 identification of protein sequence corresponding to the clone was accomplished by obtaining one of the following:
- a) a direct match between the protein sequence and at least one EST sequence in one of its 6 possible translations;

- 105 -

- b) a direct match between the nucleotide sequence for the mRNA corresponding to the protein sequence and at least one EST sequence;
- c) a match between the protein sequence and a contiguous assembly (contig) of the EST sequences with other available EST sequences in the databases in one of its 6 possible translations; or
- d) a match between the nucleotide sequence for the mRNA corresponding to the protein sequence and a contiguous assembly of the EST sequences with other available EST sequences in the databases in one of its 6 possible translations.

10                    B. Identification of Markers Having Newly-Identified Amino Acid Sequences.

The markers of Table 2 include newly-identified amino acid sequences. These sequences were found to be novel based on one of the following criteria:

- a) the protein sequence found within available public databases was incomplete or erroneous, leading to the construction of an additional completed/corrected protein sequence that is not found as such in the public domain;
- b) based on nucleotide evidence, variants of the protein sequence were additionally constructed that are not found as such in the public domain; or
- c) the contig for the EST sequences did not match any known protein, so that a novel protein sequence was derived from an open reading frame of the contig.

VIII. Gene Expression Analysis

Total RNA from normal human tissue was obtained from commercial sources. The integrity of the RNA was verified by agarose gel electrophoresis and ethidium bromide staining. Cell lines were purchased from ATCC and grown under the conditions recommended by ATCC. Total RNA from a number of various cell lines was prepared using commercial kits (Qiagen). First strand cDNA was prepared using oligo-dT primer and standard conditions. Each RNA preparation was treated with DNase I (Ambion) at 37°C for 1 hour.

30                    Novel gene expression was measured by TaqMan<sup>®</sup> quantitative PCR (Perkin Elmer Applied Biosystems) in cDNA prepared from the following normal human tissues: heart, kidney, skeletal muscle, pancreas, skin, dorsal root ganglion,

- 106 -

breast, ovary, prostate, salivary glands, lung, colon, liver and lymph node. Figure 1 graphically represents the results of the TaqMan® expression study. The columns labelled A to V depict the expression level observed for OV88 in the following tissues:

- Column A: Heart, normal tissue
- 5 Column B: Heart, CHF tissue
- Column C: Kidney, normal tissue
- Column D: Skeletal muscle, normal tissue
- Column E: Pancreas, normal tissue
- Column F: Skin, normal tissue
- 10 Column G: Dorsal root, normal tissue
- Column H: Breast, normal tissue
- Column I: Breast, tumor tissue
- Column J: Ovary, normal tissue
- Column K: Ovary, tumor tissue
- 15 Column L: Prostate, normal tissue
- Column M: Prostate, tumor tissue
- Column N: Salivary glands, normal tissue
- Column O: Lung, normal tissue
- Column P: Lung, tumor tissue
- 20 Column Q: Lung, COPD tissue
- Column R: Colon, IBD tissue
- Column S: Liver, normal tissue
- Column T: Liver fibrosis
- Column U: Lymph node, normal tissue
- 25 Column V: Positive control

#### IX. Summary of the Data Provided in the Tables

- Tables 1-3 list the markers of the present invention. In the Tables the markers are identified with a name ("Marker"), the name the gene is commonly known
- 30 by, if applicable ("Gene Name"), the Sequence Listing identifier of the cDNA sequence of a nucleotide transcript encoded by or corresponding to the marker ("SEQ ID NO (nts)"), the Sequence Listing identifier of the amino acid sequence of a protein encoded

- 107 -

by the nucleotide transcript ("SEQ ID NO (AAs)"), and the location of the protein coding sequence within the cDNA sequence ("CDS").

Table 1 lists all of the markers of the invention, which are over-expressed in ovarian cancer cells compared to normal (*i.e.*, non-cancerous) ovarian cells and  
5 comprises markers listed in Tables 2 and 3. Table 2 lists newly-identified nucleotide and amino acid sequences useful as ovarian cancer markers. Table 3 lists newly-identified nucleotide sequences useful as ovarian cancer markers.

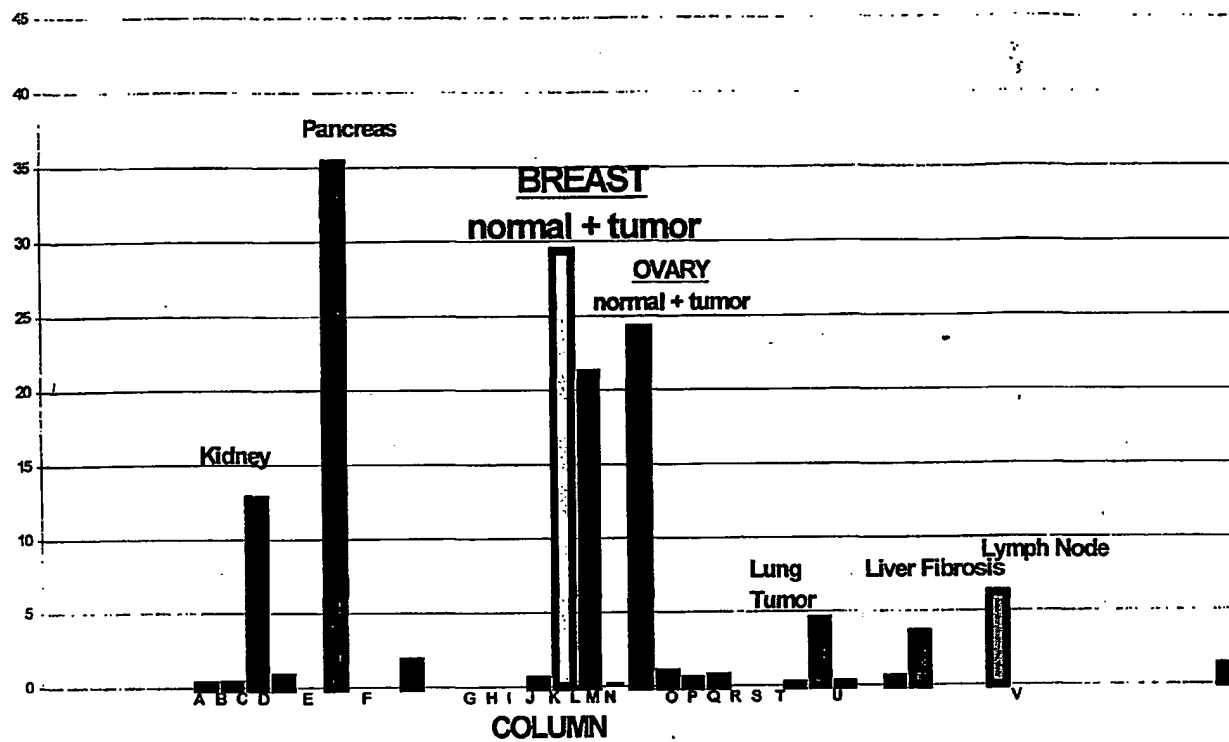
#### Other Embodiments

10 Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims:



What is claimed:

1. A method of assessing whether a patient is afflicted with ovarian cancer, the method comprising comparing:
  - 5 a) the level of expression of a marker in a patient sample, wherein the marker is selected from Table 1, and
  - b) the normal level of expression of the marker in a control non-ovarian cancer sample,wherein a significant increase in the level of expression of the marker in  
10 the patient sample and the normal level is an indication that the patient is afflicted with ovarian cancer.

Figure 1

## SEQUENCE LISTING

<110> Millennium Pharmaceuticals, Inc. et al.

<120> Nucleic Acid Molecules and Proteins For The Identification, Assessment, Prevention, and Therapy of Ovarian Cancer

<130> MRI-030PC

<150> 60/276,025

<151> 2001-03-14

<150> 60/325,149

<151> 2001-09-26

<150> 60/276,026

<151> 2001-03-14

<150> 60/324,967

<151> 2001/09/26

<150> 60/311,732

<151> 2001-08-10

<150> 60/325,102

<151> 2001-09-26

<150> 60/323,580

<151> 2001-09-19

<160> 363

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 4643

<212> DNA

<213> Homo sapiens

<400> 1

```

cctactctat tcagatattc tccagattcc taaagattag agatcatttc tcattctcct 60
aggagtactc acttcaggaa gcaaccagat aaaagagagg tgcaacggaa gccagaacat 120
tcctcctgga aattcaacct gtttcgcagt ttctcgagga atcagcattc agtcaatccg 180
ggccgggagc agtcatctgt ggtgaggctg attggctggg caggaacagc gccggggcgt 240
gggctgagca cagcgcttcg ctctctttgc cacaggaagc ctgagctcat tcgagtagcg 300
gctcttccaa gctcaaagaa gcagaggccg ctgttcgttt ccttttaggtc tttccactaa 360
agtcggagta tcttcttcca agatttcacg tcttggtggc cgttccaagg agcgcgaggt 420
cgggatggat cttgaagggg accgcaatgg aggagcaaag aagaagaact tttttaact 480
gaacaataaa agtgaaaaag ataagaagga aaagaaacca actgtcagtg tattttcaat 540
gtttcgctat tcaaattggc ttgacaagtt gtatatggtg gtgggaactt tggctgccat 600
catccatggg gctggacttc ctctcatgat gctggtgttt ggagaaatga cagatatctt 660
tgcaaatgca ggaaatttag aagatctgat gtcaaacatc actaatagaa gtgatataca 720
tgatacaggg ttcttcatga atctggagga agacatgacc aggtatgcct attattacag 780
tggaattggt gctgggggtgc tggttgctgc ttacattcag gtttcatttt ggtgcctggc 840
agctggaaga caaatcacaa aaattagaaa acagtttttt catgctataa tgcgacagga 900
gataggctgg tttgatgtgc acgatgttgg ggagcttaac acccgactta cagatgatgt 960
ctccaagatt aatgaaggaa ttggtgacaa aattggaatg ttctttcagt caatggcaac 1020

```

atctttcact	gggtttatag	taggattttac	acgtggttgg	aagctaacce	ttgtgatttt	1080
ggccatcagt	cctgttcttg	gactgtcagc	tgctgtctgg	gcaaagatac	tatcttcatt	1140
tactgataaa	gaactcttag	cgtatgcaaa	agctggagca	gtagctgaag	aggtccttggc	1200
agcaattaga	actgtgattg	catttgaggg	acaaaagaaa	gaacttgaaa	ggtacaacaa	1260
aaattttagaa	gaagctaaaa	gaattgggat	aaagaaagct	attacagcca	atatttctat	1320
aggtgctgct	ttcctgctga	tctatgcac	ttatgctctg	gccttctggt	atgggaccac	1380
cttggctctc	tcaggggaat	attctatttg	acaagtactc	actgtatttt	ctgtattaat	1440
tggggctttt	agtgttgga	agggatctcc	aagcattgaa	gcatttgcaa	atgcaagagg	1500
agcagcttat	gaaatcttca	agataattga	taataagcca	agtattgaca	gctattcgaa	1560
gagtgggcac	aaaccagata	atattaaggg	aaatttggaa	ttcagaaatg	ttcacttcag	1620
ttacccatct	cgaaaagaag	ttaagatctt	gaagggtctg	aacctgaagg	tgagagtggt	1680
gcagacggtg	gccctggttg	gaaacagtg	ctgtgggaag	agcacaacag	tccagctgat	1740
gcagaggctc	tatgacccca	cagaggggat	ggctagtggt	gatggacagg	atattaggac	1800
cataaatgta	aggtttctac	gggaaatcat	tggtgtggtg	agtcaggaa	ctgtattgtt	1860
tgcaccacg	atagctgaaa	acattcgcta	tggcgtgaa	aatgtcacca	tggtatgagat	1920
tgagaaagct	gtcaaggaa	ccaatgccta	tgactttatc	atgaaactgc	ctcataaatt	1980
tgacaccctg	gttgagaga	gaggggcccc	gttgagtgg	gggcagaagc	agaggatcgc	2040
cattgcacgt	gccctggttc	gcaaccccaa	gatcctcctg	ctggatgagg	ccacgtcagc	2100
cttgagacaca	gaaagcgaag	cagtgggtca	ggtggctctg	gataaggcca	gaaaaggctg	2160
gaccaccatt	gtgatgctc	atcgtttgc	tacagttcgt	aatgctgacg	tcatoctgg	2220
tttgcgatgat	ggagtcat	tgagaaaagg	aatcatgat	gaactcatga	aagagaaagg	2280
catttacttc	aaacttgtca	caatgcagac	agcaggaaat	gaagttgaat	tagaaaatgc	2340
agctgatgaa	tccaaaagt	aaattgatgc	cttggaaatg	tcttcaaag	attcaagatc	2400
cagtctaata	agaaaaagat	caactcgtag	gagtgtccgt	ggatcacaa	ccaagacag	2460
aaagcttagt	accaaagagg	ctctggatga	aagtatacct	ccagtttcct	tttggaggat	2520
tatgaagcta	aatttaactg	aatggcctta	ttttgttgtt	ggtgtatttt	gtgccattat	2580
aaatggaggc	ctgcaaccag	catttgcaat	aatattttca	aagattatag	gggtttttac	2640
aagaattgat	gatcctgaaa	caaaacgaca	gaatagtaac	ttgttttcac	tattgtttct	2700
agcccttga	attatttctt	ttattacatt	tttcttcag	ggtttcacat	ttggcaaagc	2760
tgagagatc	ctcaccaagc	ggctccgata	catggttttc	cgatccatgc	tcagacagga	2820
tgtgagttgg	tttgatgacc	ctaaaaacac	cactggagca	ttgactacca	ggctcgccaa	2880
tgatgctgct	caagttaaag	gggctatagg	ttccaggctt	gctgtaatta	cccagaatat	2940
agcaaatctt	gggacaggaa	taattatatt	cttcatctat	ggttggcaac	taacactgtt	3000
actcttagca	attgtaccca	tcattgcaat	agcaggagtt	gttgaatga	aatgttgtc	3060
tggaacaaga	ctgaaagata	agaaagaact	agaagggtct	gggaagatcg	ctactgaagc	3120
aatagaaaac	ttccgaaccg	ttgtttcttt	gactcaggag	cagaagtttg	aacatatgta	3180
tgctcagagt	ttgcaggtag	catacagaaa	ctctttgagg	aaagcacaca	tctttggaat	3240
tacattttcc	ttcaccagg	caatgatgta	tttttctat	gctggatgtt	tccggttttg	3300
agcctacttg	gtggcacata	aaactcatgag	ctttgaggat	gttctgttag	tattttcagc	3360
tgttgtcttt	ggtgccatgg	ccgtggggca	agtcagttca	tttgctcctg	actatgccaa	3420
agccaaaata	tcagcagccc	acatcatcat	gatcattgaa	aaaacccctt	tgattgacag	3480
ctacagcacg	gaaggcctaa	tgccgaacac	attggaagga	aatgtcacat	ttggtgaagt	3540
tgtattcaac	tatcccaccc	gaccggacat	cccagtgcct	cagggactga	gcctggagg	3600
gaagaagggc	cagacgctgg	ctctggtggg	cagcagtgcc	tgtgggaaga	gcacagtggt	3660
ccagctcctg	gagcggttct	acgacccctt	ggcagggaaa	gtgctgcttg	atggcaaaga	3720
aataaagcga	ctgaatgttc	agtggctccg	agcacacctg	ggcatcgtgt	cccaggagcc	3780
catcctgttt	gactgcagca	ttgctgagaa	cattgcctat	ggagacaaca	gccgggtggt	3840
gtcacaggaa	gagattgtga	gggcagcaaa	ggaggccaac	atacatgcct	tcacagagtc	3900
actgccta	aaatatagca	ctaaagtagg	agacaaagga	actcagctct	ctgggtggcca	3960
gaaacaacgc	attgccatag	ctcgtgccct	tgttagacag	cctcatattt	tgcttttggg	4020
tgaagccacg	tcagctctgg	atacagaaag	tgaaaagggt	gtccaagaag	ccctggacaa	4080
agccagagaa	ggccgcacct	gcattgtgat	tgctcaccgc	ctgtccacca	tccagaatgc	4140
agacttaata	gtggtgtttc	agaatggcag	agtcaggag	catggcacgc	atcagcagct	4200
gctggcacag	aaaggcatct	atctttcaat	ggtcagtgct	caggctggaa	caaagcgcca	4260
gtgaactctg	actgtatgag	atgttaaata	cttttttaata	tttgtttaga	tatgacattt	4320
attcaaagtt	aaaagcaaac	aottacagaa	ttatgaagag	gtatctgttt	aacatttcct	4380
cagtcaagtt	cagagctctc	agagacttcg	taattaaagg	aacagagtga	gagacatcat	4440
caagtggaga	gaaatcatag	tttaaactgc	attataaatt	ttataacaga	attaaagtag	4500

attttaaaag ataaaatgtg taattttgtt tatattttcc catttggact gtaactgact 4560  
gccttgctaa aagattatag aagtagcaaa aagtattgaa atgtttgcat aaagtgtcta 4620  
taataaaaact aaactttcat gtg 4643

<210> 2

<211> 1279

<212> PRT

<213> Homo sapiens

<400> 2

Met	Asp	Leu	Glu	Gly	Asp	Arg	Asn	Gly	Gly	Ala	Lys	Lys	Lys	Asn	Phe	1	5	10	15
Phe	Lys	Leu	Asn	Asn	Lys	Ser	Glu	Lys	Asp	Lys	Lys	Glu	Lys	Lys	Pro	20	25	30	
Thr	Val	Ser	Val	Phe	Ser	Met	Phe	Arg	Tyr	Ser	Asn	Trp	Leu	Asp	Lys	35	40	45	
Leu	Tyr	Met	Val	Val	Gly	Thr	Leu	Ala	Ala	Ile	Ile	His	Gly	Ala	Gly	50	55	60	
Leu	Pro	Leu	Met	Met	Leu	Val	Phe	Gly	Glu	Met	Thr	Asp	Ile	Phe	Ala	65	70	75	80
Asn	Ala	Gly	Asn	Leu	Glu	Asp	Leu	Met	Ser	Asn	Ile	Thr	Asn	Arg	Ser	85	90	95	
Asp	Ile	Asn	Asp	Thr	Gly	Phe	Phe	Met	Asn	Leu	Glu	Glu	Asp	Met	Thr	100	105	110	
Arg	Tyr	Ala	Tyr	Tyr	Tyr	Ser	Gly	Ile	Gly	Ala	Gly	Val	Leu	Val	Ala	115	120	125	
Ala	Tyr	Ile	Gln	Val	Ser	Phe	Trp	Cys	Leu	Ala	Ala	Gly	Arg	Gln	Ile	130	135	140	
His	Lys	Ile	Arg	Lys	Gln	Phe	Phe	His	Ala	Ile	Met	Arg	Gln	Glu	Ile	145	150	155	160
Gly	Trp	Phe	Asp	Val	His	Asp	Val	Gly	Glu	Leu	Asn	Thr	Arg	Leu	Thr	165	170	175	
Asp	Asp	Val	Ser	Lys	Ile	Asn	Glu	Gly	Ile	Gly	Asp	Lys	Ile	Gly	Met	180	185	190	
Phe	Phe	Gln	Ser	Met	Ala	Thr	Phe	Phe	Thr	Gly	Phe	Ile	Val	Gly	Phe	195	200	205	
Thr	Arg	Gly	Trp	Lys	Leu	Thr	Leu	Val	Ile	Leu	Ala	Ile	Ser	Pro	Val	210	215	220	
Leu	Gly	Leu	Ser	Ala	Ala	Val	Trp	Ala	Lys	Ile	Leu	Ser	Ser	Phe	Thr	225	230	235	240
Asp	Lys	Glu	Leu	Leu	Ala	Tyr	Ala	Lys	Ala	Gly	Ala	Val	Ala	Glu	Glu	245	250	255	
Val	Leu	Ala	Ala	Ile	Arg	Thr	Val	Ile	Ala	Phe	Gly	Gly	Gln	Lys	Lys	260	265	270	
Glu	Leu	Glu	Arg	Tyr	Asn	Lys	Asn	Leu	Glu	Glu	Ala	Lys	Arg	Ile	Gly	275	280	285	
Ile	Lys	Lys	Ala	Ile	Thr	Ala	Asn	Ile	Ser	Ile	Gly	Ala	Ala	Phe	Leu	290	295	300	
Leu	Ile	Tyr	Ala	Ser	Tyr	Ala	Leu	Ala	Phe	Trp	Tyr	Gly	Thr	Thr	Leu	305	310	315	320
Val	Leu	Ser	Gly	Glu	Tyr	Ser	Ile	Gly	Gln	Val	Leu	Thr	Val	Phe	Ser	325	330	335	
Val	Leu	Ile	Gly	Ala	Phe	Ser	Val	Gly	Gln	Ala	Ser	Pro	Ser	Ile	Glu	340	345	350	
Ala	Phe	Ala	Asn	Ala	Arg	Gly	Ala	Ala	Tyr	Glu	Ile	Phe	Lys	Ile	Ile	355	360	365	
Asp	Asn	Lys	Pro	Ser	Ile	Asp	Ser	Tyr	Ser	Lys	Ser	Gly	His	Lys	Pro	370	375	380	

Asp Asn Ile Lys Gly Asn Leu Glu Phe Arg Asn Val His Phe Ser Tyr  
 385 390 395 400  
 Pro Ser Arg Lys Glu Val Lys Ile Leu Lys Gly Leu Asn Leu Lys Val  
 405 410 415  
 Gln Ser Gly Gln Thr Val Ala Leu Val Gly Asn Ser Gly Cys Gly Lys  
 420 425 430  
 Ser Thr Thr Val Gln Leu Met Gln Arg Leu Tyr Asp Pro Thr Glu Gly  
 435 440 445  
 Met Val Ser Val Asp Gly Gln Asp Ile Arg Thr Ile Asn Val Arg Phe  
 450 455 460  
 Leu Arg Glu Ile Ile Gly Val Val Ser Gln Glu Pro Val Leu Phe Ala  
 465 470 475 480  
 Thr Thr Ile Ala Glu Asn Ile Arg Tyr Gly Arg Glu Asn Val Thr Met  
 485 490 495  
 Asp Glu Ile Glu Lys Ala Val Lys Glu Ala Asn Ala Tyr Asp Phe Ile  
 500 505 510  
 Met Lys Leu Pro His Lys Phe Asp Thr Leu Val Gly Glu Arg Gly Ala  
 515 520 525  
 Gln Leu Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu  
 530 535 540  
 Val Arg Asn Pro Lys Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu  
 545 550 555 560  
 Asp Thr Glu Ser Glu Ala Val Val Gln Val Ala Leu Asp Lys Ala Arg  
 565 570 575  
 Lys Gly Arg Thr Thr Ile Val Ile Ala His Arg Leu Ser Thr Val Arg  
 580 585 590  
 Asn Ala Asp Val Ile Ala Gly Phe Asp Asp Gly Val Ile Val Glu Lys  
 595 600 605  
 Gly Asn His Asp Glu Leu Met Lys Glu Lys Gly Ile Tyr Phe Lys Leu  
 610 615 620  
 Val Thr Met Gln Thr Ala Gly Asn Glu Val Glu Leu Glu Asn Ala Ala  
 625 630 635 640  
 Asp Glu Ser Lys Ser Glu Ile Asp Ala Leu Glu Met Ser Ser Asn Asp  
 645 650 655  
 Ser Arg Ser Ser Leu Ile Arg Lys Arg Ser Thr Arg Arg Ser Val Arg  
 660 665 670  
 Gly Ser Gln Ala Gln Asp Arg Lys Leu Ser Thr Lys Glu Ala Leu Asp  
 675 680 685  
 Glu Ser Ile Pro Pro Val Ser Phe Trp Arg Ile Met Lys Leu Asn Leu  
 690 695 700  
 Thr Glu Trp Pro Tyr Phe Val Val Gly Val Phe Cys Ala Ile Ile Asn  
 705 710 715 720  
 Gly Gly Leu Gln Pro Ala Phe Ala Ile Ile Phe Ser Lys Ile Ile Gly  
 725 730 735  
 Val Phe Thr Arg Ile Asp Asp Pro Glu Thr Lys Arg Gln Asn Ser Asn  
 740 745 750  
 Leu Phe Ser Leu Leu Phe Leu Ala Leu Gly Ile Ile Ser Phe Ile Thr  
 755 760 765  
 Phe Phe Leu Gln Gly Phe Thr Phe Gly Lys Ala Gly Glu Ile Leu Thr  
 770 775 780  
 Lys Arg Leu Arg Tyr Met Val Phe Arg Ser Met Leu Arg Gln Asp Val  
 785 790 795 800  
 Ser Trp Phe Asp Asp Pro Lys Asn Thr Thr Gly Ala Leu Thr Thr Arg  
 805 810 815  
 Leu Ala Asn Asp Ala Ala Gln Val Lys Gly Ala Ile Gly Ser Arg Leu  
 820 825 830  
 Ala Val Ile Thr Gln Asn Ile Ala Asn Leu Gly Thr Gly Ile Ile Ile  
 835 840 845

Ser Phe Ile Tyr Gly Trp Gln Leu Thr Leu Leu Leu Leu Ala Ile Val  
 850 855 860  
 Pro Ile Ile Ala Ile Ala Gly Val Val Glu Met Lys Met Leu Ser Gly  
 865 870 875 880  
 Gln Ala Leu Lys Asp Lys Lys Glu Leu Glu Gly Ala Gly Lys Ile Ala  
 885 890 895  
 Thr Glu Ala Ile Glu Asn Phe Arg Thr Val Val Ser Leu Thr Gln Glu  
 900 905 910  
 Gln Lys Phe Glu His Met Tyr Ala Gln Ser Leu Gln Val Pro Tyr Arg  
 915 920 925  
 Asn Ser Leu Arg Lys Ala His Ile Phe Gly Ile Thr Phe Ser Phe Thr  
 930 935 940  
 Gln Ala Met Met Tyr Phe Ser Tyr Ala Gly Cys Phe Arg Phe Gly Ala  
 945 950 955 960  
 Tyr Leu Val Ala His Lys Leu Met Ser Phe Glu Asp Val Leu Leu Val  
 965 970 975  
 Phe Ser Ala Val Val Phe Gly Ala Met Ala Val Gly Gln Val Ser Ser  
 980 985 990  
 Phe Ala Pro Asp Tyr Ala Lys Ala Lys Ile Ser Ala Ala His Ile Ile  
 995 1000 1005  
 Met Ile Ile Glu Lys Thr Pro Leu Ile Asp Ser Tyr Ser Thr Glu Gly  
 1010 1015 1020  
 Leu Met Pro Asn Thr Leu Glu Gly Asn Val Thr Phe Gly Glu Val Val  
 1025 1030 1035 1040  
 Phe Asn Tyr Pro Thr Arg Pro Asp Ile Pro Val Leu Gln Gly Leu Ser  
 1045 1050 1055  
 Leu Glu Val Lys Lys Gly Gln Thr Leu Ala Leu Val Gly Ser Ser Gly  
 1060 1065 1070  
 Cys Gly Lys Ser Thr Val Val Gln Leu Leu Glu Arg Phe Tyr Asp Pro  
 1075 1080 1085  
 Leu Ala Gly Lys Val Leu Leu Asp Gly Lys Glu Ile Lys Arg Leu Asn  
 1090 1095 1100  
 Val Gln Trp Leu Arg Ala His Leu Gly Ile Val Ser Gln Glu Pro Ile  
 1105 1110 1115 1120  
 Leu Phe Asp Cys Ser Ile Ala Glu Asn Ile Ala Tyr Gly Asp Asn Ser  
 1125 1130 1135  
 Arg Val Val Ser Gln Glu Glu Ile Val Arg Ala Ala Lys Glu Ala Asn  
 1140 1145 1150  
 Ile His Ala Phe Ile Glu Ser Leu Pro Asn Lys Tyr Ser Thr Lys Val  
 1155 1160 1165  
 Gly Asp Lys Gly Thr Gln Leu Ser Gly Gly Gln Lys Gln Arg Ile Ala  
 1170 1175 1180  
 Ile Ala Arg Ala Leu Val Arg Gln Pro His Ile Leu Leu Leu Asp Glu  
 1185 1190 1195 1200  
 Ala Thr Ser Ala Leu Asp Thr Glu Ser Glu Lys Val Val Gln Glu Ala  
 1205 1210 1215  
 Leu Asp Lys Ala Arg Glu Gly Arg Thr Cys Ile Val Ile Ala His Arg  
 1220 1225 1230  
 Leu Ser Thr Ile Gln Asn Ala Asp Leu Ile Val Val Phe Gln Asn Gly  
 1235 1240 1245  
 Arg Val Lys Glu His Gly Thr His Gln Gln Leu Leu Ala Gln Lys Gly  
 1250 1255 1260  
 Ile Tyr Phe Ser Met Val Ser Val Gln Ala Gly Thr Lys Arg Gln  
 1265 1270 1275

&lt;210&gt; 3

&lt;211&gt; 3859

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

```

aatctatcag ggaacggcgg tggccgggtgc ggcgtgttcg gtgcgctctg gccgctcagg 60
ccgtgcggtt gggtagcgcc acgcgaggcg gcgaggcgcc aagcgtgttt ctaggtcgtg 120
gcgtcggtt tccggagctt tggcggcagc taggggagga tggcggagtc ttcggataag 180
ctctatcag tcgagtacgc caagagcggg cgcgcctctt gcaagaaatg cagcgagagc 240
atccccaagg actcgctccg gatggccatc atggtgcagt cgcctatgtt tgatggaaaa 300
gtccacact ggtaccactt ctctgcttc tggaggttg gccactccat ccggcaccct 360
gacgttgagg tggatgggtt ctctgagctt cggtgggatg accagcagaa agtcaagaag 420
acagcggaag ctggaggagt gacaggcaaa ggccaggatg gaattggtag caaggcagag 480
aagactctgg gtgactttgc agcagagtat gccaaagcca acagaagtac gtgcaagggg 540
tgtatggaga agatagaaaa gggccagggt gcgctgtcca agaagatggt ggaccgggag 600
aagccacagc taggcatgat tgaccgctgg taccatccag gctgctttgt caagaacagg 660
gaggagctgg gtttccggcc cgagtacagt gcgagtcagc tcaagggtct cagcctcctt 720
gctacagagg ataaagaagc cctgaagaag cagctccag gagtcaagag tgaaggaaa 780
agaaaaggcg atgagtgga tggagtggat gaagtggcga agaagaaatc taaaaaagaa 840
aaagacaagg atagtaagct tgaaaaagcc ctaaaggctc agaacgacct gatctggaac 900
atcaaggacg agctaaagaa agtgtgttca actaatgacc tgaaggagct actcatcttc 960
aacaagcagc aagtgccttc tggggagtgc gcgatcttgg accgagtagc tgatggcatg 1020
gtgttcggtg cctccttcc ctgagaggaa tgctcggttc agctggtctt caagagcgat 1080
gcctattact gcactgggga cgtcactgcc tggaccaagt gtatggtcaa gacacagaca 1140
cccaaccgga aggagtgggt aaccccaaag gaattccgag aaatctctta cctcaagaaa 1200
ttgaaggtta aaaagcagga ccgtatatct cccccagaaa ccagcgctc cgtggcggcc 1260
acgcctccgc cctccacagc ctcggtcctt gctgctgtga actcctctgc ttcagcagat 1320
aagccattat ccaactgaa gatcctgact ctcggaagc tgtcccgaa caaggatgaa 1380
gtgaaggcca tgaatgaaa actcgggggg aagttgacgg ggacggccaa caaggcttcc 1440
ctgtgcatca gcaccaaaaa ggaggtggaa aagatgaata agaagatgga ggaagttaa 1500
gaagccaaca tccgagttgt gtctgaggac ttctccagg acgtctccgc ctccaccaag 1560
agccttcagg agttgttctt agcgcacatc ttgtcccctt ggggggcaga ggtgaaggca 1620
gagcctgttg aagttgtggc cccaagagg aagtcagggg ctgcgctctc caaaaaaagc 1680
aagggccagg tcaaggagga aggtatcaac aaatctgaaa agagaatgaa attaactctt 1740
aaaggaggag cagctgtgga tctgattct ggactggaac actctgcgca tgtcctggag 1800
aaagttggga aggtcttcag tgccaccctt ggctggttg acatcgtaa aggaaccaac 1860
tctactaca agctgcagct tctggaggac gacaagaaa acaggtattg gatattcagg 1920
tcttggggcc gtgtgggtac ggtgatcggt agcaacaaac tggaacagat gccgtccaag 1980
gaggatgcca ttgagcagtt catgaaatta tatgaagaaa aaaccgggaa cgcttggcac 2040
tccaaaaatt tcacgaagta tccaaaaag ttttaccctt tggagattga ctatggccag 2100
gatgaagagg cagtgaagaa gctcacagta aatcctggca ccaagtccaa gctcccaag 2160
ccagttcagg acctcatcaa gatgatctt gatgtgaaa gtatgaagaa agccatggtg 2220
gagtatgaga tgcacctca gaagatgccc ttggggaagc tgagcaaaag gcagatccag 2280
gccgcatact ccatcctcag tgaggtccag caggcgtgt ctcagggcag cagcgactct 2340
cagatcctgg atctctcaa tgccttttac accctgatcc ccacgactt tgggatgaag 2400
aagcctccgc tctgaacaa tgcagacagt gtgcaggcca aggtggaaat gcttgacaac 2460
ctgctggaca tgcaggtggc ctacagtctg ctacggggag ggtctgatga tagcagcaag 2520
gatcccatcg atgtcaacta tgagaagctc aaaactgaca ttaaggtggt tgacagagat 2580
tctgaagaag ccgagatcat caggaagtat gttaagaaca ctcatgcaac cacacacagt 2640
gcgtatgact tggaagtcac cgatatctt aagatagagc gtgaaggcga atgccagcgt 2700
tacaagccct ttaagcagct tcataaccga agattgctgt ggcacgggtc caggaccacc 2760
aactttgctg ggatcctgtc ccagggtctt cggtagccc cgcctgaagc gcccggtgca 2820
ggctacatgt ttggtaaaag gatctatttc gctgacatgg tctccaagag tgccaactac 2880
taccatacgt ctcagggaga cccaataggc ttaatcctgt tgggagaagt tgcccttggg 2940
aacatgtatg aactgaagca cgcttcacat atcagcaggt taccaaggg caagcacagt 3000
gtcaaaaggt tgggcaaaac taccctgat ccttcagcta acattagtct ggatggtgta 3060
gacgttcctc ttgggaccgg gatttcactt ggtgtgatag acacctctct actatataac 3120
gagtacattg tctatgatat tgctcaggta aatctgaagt atctgctgaa actgaaattc 3180
aattttaaga cctccctgtg gtaattggga gaggtagccg agtcacaccc ggtggctgtg 3240

```



```

gtatgaattc acccgaagcg cttctgcacc aactcacctg gccgctaagt tgctgatggg 3300
tagtacctgt actaaaccac ctcagaaaagg attttacaga aacgtgttaa aggttttctc 3360
taactttctca agtcccttgt tttgtgttgt gtctgtgggg aggggttgtt ttggggttgt 3420
ttttgttttt tcttgccagg tagataaaac tgacatagag aaaaggctgg agagagattc 3480
tgttgcatag actagtctta tggaaaaaac caaagcttcg ttagaatgtc tgccttactg 3540
gtttccccag ggaaggaaaa atacacttcc accctttttt ctaagtgttc gtcttttagt 3600
ttgatttttg aaagatgtta agcattttatt tttagttaaa ataaaaacta atttcatact 3660
atttagattt tcttttttat cttgcactta ttgtcccctt tttagttttt tttgtttgcc 3720
tcttgtggtg aggggtgtgg gaagaccaa ggaaggaacg ctaacaattt ctcatactta 3780
gaaacaaaa gagctttcct tctccaggaa tactgaacat gggagctctt gaaatatgta 3840
gtattaaaag ttgcatttg 3859

```

&lt;210&gt; 4

&lt;211&gt; 1014

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

```

Met Ala Glu Ser Ser Asp Lys Leu Tyr Arg Val Glu Tyr Ala Lys Ser
1          5          10          15
Gly Arg Ala Ser Cys Lys Lys Cys Ser Glu Ser Ile Pro Lys Asp Ser
20        25        30
Leu Arg Met Ala Ile Met Val Gln Ser Pro Met Phe Asp Gly Lys Val
35        40        45
Pro His Trp Tyr His Phe Ser Cys Phe Trp Lys Val Gly His Ser Ile
50        55        60
Arg His Pro Asp Val Glu Val Asp Gly Phe Ser Glu Leu Arg Trp Asp
65        70        75        80
Asp Gln Gln Lys Val Lys Lys Thr Ala Glu Ala Gly Gly Val Thr Gly
85        90        95
Lys Gly Gln Asp Gly Ile Gly Ser Lys Ala Glu Lys Thr Leu Gly Asp
100       105       110
Phe Ala Ala Glu Tyr Ala Lys Ser Asn Arg Ser Thr Cys Lys Gly Cys
115       120       125
Met Glu Lys Ile Glu Lys Gly Gln Val Arg Leu Ser Lys Lys Met Val
130       135       140
Asp Pro Glu Lys Pro Gln Leu Gly Met Ile Asp Arg Trp Tyr His Pro
145       150       155       160
Gly Cys Phe Val Lys Asn Arg Glu Glu Leu Gly Phe Arg Pro Glu Tyr
165       170       175
Ser Ala Ser Gln Leu Lys Gly Phe Ser Leu Leu Ala Thr Glu Asp Lys
180       185       190
Glu Ala Leu Lys Lys Gln Leu Pro Gly Val Lys Ser Glu Gly Lys Arg
195       200       205
Lys Gly Asp Glu Val Asp Gly Val Asp Glu Val Ala Lys Lys Lys Ser
210       215       220
Lys Lys Glu Lys Asp Lys Asp Ser Lys Leu Glu Lys Ala Leu Lys Ala
225       230       235       240
Gln Asn Asp Leu Ile Trp Asn Ile Lys Asp Glu Leu Lys Lys Val Cys
245       250       255
Ser Thr Asn Asp Leu Lys Glu Leu Leu Ile Phe Asn Lys Gln Gln Val
260       265       270
Pro Ser Gly Glu Ser Ala Ile Leu Asp Arg Val Ala Asp Gly Met Val
275       280       285
Phe Gly Ala Leu Leu Pro Cys Glu Glu Cys Ser Gly Gln Leu Val Phe
290       295       300
Lys Ser Asp Ala Tyr Tyr Cys Thr Gly Asp Val Thr Ala Trp Thr Lys
305       310       315       320

```

Cys Met Val Lys Thr Gln Thr Pro Asn Arg Lys Glu Trp Val Thr Pro  
 325 330 335  
 Lys Glu Phe Arg Glu Ile Ser Tyr Leu Lys Lys Leu Lys Val Lys Lys  
 340 345 350  
 Gln Asp Arg Ile Phe Pro Pro Glu Thr Ser Ala Ser Val Ala Ala Thr  
 355 360 365  
 Pro Pro Pro Ser Thr Ala Ser Ala Pro Ala Ala Val Asn Ser Ser Ala  
 370 375 380  
 Ser Ala Asp Lys Pro Leu Ser Asn Met Lys Ile Leu Thr Leu Gly Lys  
 385 390 395 400  
 Leu Ser Arg Asn Lys Asp Glu Val Lys Ala Met Ile Glu Lys Leu Gly  
 405 410 415  
 Gly Lys Leu Thr Gly Thr Ala Asn Lys Ala Ser Leu Cys Ile Ser Thr  
 420 425 430  
 Lys Lys Glu Val Glu Lys Met Asn Lys Lys Met Glu Glu Val Lys Glu  
 435 440 445  
 Ala Asn Ile Arg Val Val Ser Glu Asp Phe Leu Gln Asp Val Ser Ala  
 450 455 460  
 Ser Thr Lys Ser Leu Gln Glu Leu Phe Leu Ala His Ile Leu Ser Pro  
 465 470 475 480  
 Trp Gly Ala Glu Val Lys Ala Glu Pro Val Glu Val Val Ala Pro Arg  
 485 490 495  
 Gly Lys Ser Gly Ala Ala Leu Ser Lys Lys Ser Lys Gly Gln Val Lys  
 500 505 510  
 Glu Glu Gly Ile Asn Lys Ser Glu Lys Arg Met Lys Leu Thr Leu Lys  
 515 520 525  
 Gly Gly Ala Ala Val Asp Pro Asp Ser Gly Leu Glu His Ser Ala His  
 530 535 540  
 Val Leu Glu Lys Gly Gly Lys Val Phe Ser Ala Thr Leu Gly Leu Val  
 545 550 555 560  
 Asp Ile Val Lys Gly Thr Asn Ser Tyr Tyr Lys Leu Gln Leu Leu Glu  
 565 570 575  
 Asp Asp Lys Glu Asn Arg Tyr Trp Ile Phe Arg Ser Trp Gly Arg Val  
 580 585 590  
 Gly Thr Val Ile Gly Ser Asn Lys Leu Glu Gln Met Pro Ser Lys Glu  
 595 600 605  
 Asp Ala Ile Glu Gln Phe Met Lys Leu Tyr Glu Glu Lys Thr Gly Asn  
 610 615 620  
 Ala Trp His Ser Lys Asn Phe Thr Lys Tyr Pro Lys Lys Phe Tyr Pro  
 625 630 635 640  
 Leu Glu Ile Asp Tyr Gly Gln Asp Glu Glu Ala Val Lys Lys Leu Thr  
 645 650 655  
 Val Asn Pro Gly Thr Lys Ser Lys Leu Pro Lys Pro Val Gln Asp Leu  
 660 665 670  
 Ile Lys Met Ile Phe Asp Val Glu Ser Met Lys Lys Ala Met Val Glu  
 675 680 685  
 Tyr Glu Ile Asp Leu Gln Lys Met Pro Leu Gly Lys Leu Ser Lys Arg  
 690 695 700  
 Gln Ile Gln Ala Ala Tyr Ser Ile Leu Ser Glu Val Gln Gln Ala Val  
 705 710 715 720  
 Ser Gln Gly Ser Ser Asp Ser Gln Ile Leu Asp Leu Ser Asn Arg Phe  
 725 730 735  
 Tyr Thr Leu Ile Pro His Asp Phe Gly Met Lys Lys Pro Pro Leu Leu  
 740 745 750  
 Asn Asn Ala Asp Ser Val Gln Ala Lys Val Glu Met Leu Asp Asn Leu  
 755 760 765  
 Leu Asp Ile Glu Val Ala Tyr Ser Leu Leu Arg Gly Gly Ser Asp Asp  
 770 775 780

Ser Ser Lys Asp Pro Ile Asp Val Asn Tyr Glu Lys Leu Lys Thr Asp  
 785 790 795 800  
 Ile Lys Val Val Asp Arg Asp Ser Glu Glu Ala Glu Ile Ile Arg Lys  
 805 810 815  
 Tyr Val Lys Asn Thr His Ala Thr Thr His Ser Ala Tyr Asp Leu Glu  
 820 825 830  
 Val Ile Asp Ile Phe Lys Ile Glu Arg Glu Gly Glu Cys Gln Arg Tyr  
 835 840 845  
 Lys Pro Phe Lys Gln Leu His Asn Arg Arg Leu Leu Trp His Gly Ser  
 850 855 860  
 Arg Thr Thr Asn Phe Ala Gly Ile Leu Ser Gln Gly Leu Arg Ile Ala  
 865 870 875 880  
 Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly Ile Tyr  
 885 890 895  
 Phe Ala Asp Met Val Ser Lys Ser Ala Asn Tyr Tyr His Thr Ser Gln  
 900 905 910  
 Gly Asp Pro Ile Gly Leu Ile Leu Leu Gly Glu Val Ala Leu Gly Asn  
 915 920 925  
 Met Tyr Glu Leu Lys His Ala Ser His Ile Ser Arg Leu Pro Lys Gly  
 930 935 940  
 Lys His Ser Val Lys Gly Leu Gly Lys Thr Thr Pro Asp Pro Ser Ala  
 945 950 955 960  
 Asn Ile Ser Leu Asp Gly Val Asp Val Pro Leu Gly Thr Gly Ile Ser  
 965 970 975  
 Ser Gly Val Ile Asp Thr Ser Leu Leu Tyr Asn Glu Tyr Ile Val Tyr  
 980 985 990  
 Asp Ile Ala Gln Val Asn Leu Lys Tyr Leu Leu Lys Leu Lys Phe Asn  
 995 1000 1005  
 Phe Lys Thr Ser Leu Trp  
 1010

&lt;210&gt; 5

&lt;211&gt; 1465

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

ggcacgaggg ggaacgtctc agctctcggc gcacggccca gggttatcttg tagcatagca 60  
 acttcggatt tcaactctacc cggagagttt cccgcttggt tgaacacatt ggcctcagga 120  
 agcttccttc aaaatgtcta ctgttcacga aatcctgtgc aagctcagct tggagggtga 180  
 tcaacttaca cccccaagtg catatgggtc tgtcaaagcc tatactaact ttgatgctga 240  
 gcgggatgct ttgaacattg aaacagccat caagaccaaa ggtgtggatg aggtcaccat 300  
 tgtcaacatt ttgaccaacc gcagcaatgc acagagacag gatattgcct tcgcctacca 360  
 gagaaggacc aaaaaggaac ttgcatcagc actgaagtca gccttatctg gccacctgga 420  
 gacggtgatt ttgggcctat tgaagacacc tgctcagtat gacgcttctg agctaaaagc 480  
 ttccatgaag gggtctggga cgcagagga ctctctcatt gagatcatct gctccagaac 540  
 caaccaggag ctgcaggaaa ttaacagagt ctacaaggaa atgtacaaga ctgatctgga 600  
 gaaggacatt atttcggaca catctggtga cttccgcaag ctgatgggtg ccctggcaaa 660  
 gggtagaaga gcagaggatg gctctgtcat tgattatgaa ctgattgacc aagatgctcg 720  
 ggatctctat gacgctggag tgaagaggaa aggaactgat gttcccaagt ggatcagcat 780  
 catgaccgag cggagcgtgc cccacctcca gaaagtattt gataggtaca agagttacag 840  
 cccttatgac atgttggaag gcatcaggaa agaggttaaa ggagacctgg aaaatgcttt 900  
 cctgaacctg gttcagtgca ttcagaacaa gccctgtat tttgctgac ggctgtatga 960  
 ctccatgaag ggcaaggga cgcagataa ggtcctgatc agaatactgg tctcccgag 1020  
 tgaagtggac atgttgaaaa ttaggtctga attcaagaga aagtacggca agtccctgta 1080  
 ctattatata cagcaagaca ctaaggcgca ctaccagaaa gcgctgctgt acctgtgtgg 1140  
 tggagatgac tgaagcccga cacggcctga gcgtccagaa atgggtgctca ccatgcttcc 1200

```

agctaacagg tctagaaaac cagcttgcca ataacagtc ccgtggccat ccctgtgagg 1260
gtgacgtag cattaccccc aacctcatt tagttgccta agcattgcct ggccttcctg 1320
tctagtctct cctgtaagcc aaagaaatga acattccaag gagttggaag tgaagtctat 1380
gatgtgaaac actttgcctc ctgtgtactg tgtcataaac agatgaataa actgaatttg 1440
tactttaaaa aaaaaaaaaa aaaaaa                                1465

```

&lt;210&gt; 6

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

```

Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp
 1          5          10          15
His Ser Thr Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr Asn
 20          25          30
Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys Thr
 35          40          45
Lys Gly Val Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg Ser
 50          55          60
Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr Lys
 65          70          75          80
Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu Glu
 85          90          95
Thr Val Ile Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala Ser
100          105          110
Glu Leu Lys Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser Leu
115          120          125
Ile Glu Ile Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile Asn
130          135          140
Arg Val Tyr Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile Ile
145          150          155          160
Ser Asp Thr Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala Lys
165          170          175
Gly Arg Arg Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile Asp
180          185          190
Gln Asp Ala Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly Thr
195          200          205
Asp Val Pro Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Val Pro His
210          215          220
Leu Gln Lys Val Phe Asp Arg Tyr Lys Ser Tyr Ser Pro Tyr Asp Met
225          230          235          240
Leu Glu Ser Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn Ala Phe
245          250          255
Leu Asn Leu Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe Ala Asp
260          265          270
Arg Leu Tyr Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys Val Leu
275          280          285
Ile Arg Ile Met Val Ser Arg Ser Glu Val Asp Met Leu Lys Ile Arg
290          295          300
Ser Glu Phe Lys Arg Lys Tyr Gly Lys Ser Leu Tyr Tyr Tyr Ile Gln
305          310          315          320
Gln Asp Thr Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu Cys Gly
325          330          335
Gly Asp Asp

```

<210> 7  
 <211> 1362  
 <212> DNA  
 <213> Homo sapiens

<400> 7  
 catttgggga cgctctcagc tctcgggcgca cggcccagct tccttcaaaa tgtctactgt 60  
 tcacgaaatc ctgtgcaagc tcagcttgga gggatgatcac tctacacccc caagtgcata 120  
 tgggtctgtc aaagcctata ctaactttga tgctgagcgg gatgctttga acattgaaac 180  
 agccatcaag accaaaggtg tggatgaggt caccattgtc aacattttga ccaaccgcag 240  
 caatgcacag agacaggata ttgccttcgc ctaccagaga aggacaaaaa aggaacttgc 300  
 atcagcactg aagtcagcct tatctggcca cctggagacg gtgattttgg gcctattgaa 360  
 gacacctgct cagtatgacg cttctgagct aaaagcttcc atgaaggggc tgggaaccga 420  
 cgaggactct ctcatctgaga tcatctgctc cagaaccaac caggagctgc aggaaattaa 480  
 cagagtctac aaggaaatgt acaagactga tctggagaag gacattattt cggacacatc 540  
 tgggtgacttc cgcaagctga tgggtgccct ggcaaagggt agaagagcag aggatggctc 600  
 tgtcattgat tatgaactga ttgaccaaga tgctcgggat ctctatgacg ctggagtga 660  
 gaggaagga actgatgttc ccaagtggat cagcatcatg accgagcggg gcgtgccccca 720  
 cctccagaaa gtatttgata ggtacaagag ttacagccct tatgacatgt tggaaagcat 780  
 caggaaagag gttaaaggag acctggaaaa tgctttcctg aacctgggtc agtgattca 840  
 gaacaagccc ctgtattttg ctgatcggct gtatgactcc atgaaggga aggggacgcg 900  
 agataaggtc ctgatcagaa tcatgggtctc ccgcagtga gtggacatgt tgaaaattag 960  
 gtctgaattc aagagaaagt acggcaagtc cctgtactat tatatccagc aagacactaa 1020  
 gggcgactac cagaaagcgc tgctgtacct gtgtggtgga gatgactgaa gcccgcacag 1080  
 gcctgagcgt ccagaaatgg tgctcaccat gcttcacgct aacaggtcta gaaaaccagc 1140  
 ttgcgaataa cagtccccgt ggccatccct gtgaggggtga cgttagcatt accccaacc 1200  
 tcattttagt tgctaagca ttgcctggcc ttctgtctta gtctctcctg taagccaaag 1260  
 aatgaacat tccaaggagt tggaagtga gtctatgatg tgaaacactt tgcctcctgt 1320  
 gtactgtgtc ataaacagat gaataaactg aatttgtact tt 1362

<210> 8  
 <211> 339  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
 Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp  
 1 5 10 15  
 His Ser Thr Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr Asn  
 20 25 30  
 Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys Thr  
 35 40 45  
 Lys Gly Val Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg Ser  
 50 55 60  
 Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr Lys  
 65 70 75 80  
 Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu Glu  
 85 90 95  
 Thr Val Ile Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala Ser  
 100 105 110  
 Glu Leu Lys Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser Leu  
 115 120 125  
 Ile Glu Ile Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile Asn  
 130 135 140  
 Arg Val Tyr Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile Ile  
 145 150 155 160  
 Ser Asp Thr Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala Lys  
 165 170 175

Gly Arg Arg Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile Asp  
 180 185 190  
 Gln Asp Ala Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly Thr  
 195 200 205  
 Asp Val Pro Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Val Pro His  
 210 215 220  
 Leu Gln Lys Val Phe Asp Arg Tyr Lys Ser Tyr Ser Pro Tyr Asp Met  
 225 230 235 240  
 Leu Glu Ser Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn Ala Phe  
 245 250 255  
 Leu Asn Leu Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe Ala Asp  
 260 265 270  
 Arg Leu Tyr Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys Val Leu  
 275 280 285  
 Ile Arg Ile Met Val Ser Arg Ser Glu Val Asp Met Leu Lys Ile Arg  
 290 295 300  
 Ser Glu Phe Lys Arg Lys Tyr Gly Lys Ser Leu Tyr Tyr Tyr Ile Gln  
 305 310 315 320  
 Gln Asp Thr Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu Cys Gly  
 325 330 335  
 Gly Asp Asp

&lt;210&gt; 9

&lt;211&gt; 1982

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 9

gcagaggagg agcgacgccc ggcctcgaag aactttctgct tgggtggctg aactctgac 60  
 ttgacctaga gtcatggcca tggcaaccaa aggaggtact gtcaaagctg cttcaggatt 120  
 caatgccatg gaagatgccc agaccctgag gaaggccatg aaagggtctg gcaccgatga 180  
 agacgccatt attagcgctc ttgcctaccg caacaccgcc cagcgccagg agatcaggac 240  
 agcctacaag agcaccatcg gcagggaact gatagacgac ctgaagtcag aactgagtgg 300  
 caacttcgag caggtgattg tggggatgat gacgcccacg gtgctgtatg acgtgcaaga 360  
 gctgcgaagg gccatgaagg gagccggcac tgatgagggc tgcctaattg agatcctggc 420  
 ctcccggacc cctgaggaga tccggcgcat aagccaaacc taccagcagc aatatggacg 480  
 gagccttgaa gatgacattc gctctgacac atcgttcatg ttccagcgag tgctggtgtc 540  
 tctgtcagct ggtgggaggg atgaaggaaa ttatctggac gatgctctcg tgagacagga 600  
 tgcccaggac ctgtatgagg ctggagagaa gaaatggggg acagatgagg tgaaatttct 660  
 aactgtttct tgttcccggg accgaaatca cctgttgcac gtgtttgatg aatacaaaag 720  
 gatatcacag aaggatattg aacagagtat taaatctgaa acatctggta gctttgaaga 780  
 tgctctgctg gctatagtaa agtgcacgag gaacaaatct gcatattttg ctgaaaagct 840  
 ctataaatcg atgaagggtc tgggcaccga tgataacacc ctcatcagag tgatggtttc 900  
 tcgagcagaa attgacatgt tggatatccg ggcacacttc aagagactct atggaaaagtc 960  
 tctgtactcg ttcatacagg gtgacacatc tggagactac aggaaagtac tgcttgttct 1020  
 ctgtggagga gatgattaaa ataaaaatcc cagaaggaca ggaggattct caacactttg 1080  
 aattttttta acttcatttt tctacactgc tattatcatt atctcagaat gcttatttcc 1140  
 aattaaaacg cctacagctg cctcctagaa tatagactgt ctgtattatt attcacctat 1200  
 aattagtcac tatgatgctt taaagctgta cttgcatttc aaagcttata agatataaat 1260  
 ggagatttta aagtagaaat aaatatgtat tccatgtttt taaaagatta ctttctactt 1320  
 tgtgtttcac agacattgaa tatattaaat tattccatat tttcttttca gtgaaaaatt 1380  
 ttttaaatgg aagactgttc taaaatcact tttttcccta atccaatttt tagagtggct 1440  
 agtagtttct tcaattgaaa ttgtaagcat cgggtcagta agaagccca tccagtttcc 1500  
 tatatttcat agtcaaagcc ttgaaagcat ctacaaatct ctttttttag gttttgtcca 1560  
 tagcatcagt tgatccttac taagttttcc atgggagact tccttcatca catcttatgt 1620  
 tgaaatcact ttctgtagtc aaagtatacc aaaaccaatt tatctgaact aaattctaaa 1680

```

gtatgggttat acaaaccata tacatctggt taccaaacat aaatgctgaa cattccatat 1740
tattatagtt aatgtcttaa tccagcttgc aagtgaatgg aaaaaaaaaat aagctttcaaa 1800
ctaggatttc tgggaatgat gtaatgctct gaatttagta tgatataaag aaaacttttt 1860
tgtgctaaaa atacttttta aaatcaattt tggtgattgt agtaatttct atttgcaactg 1920
tgcctttcaa ctccagaaac attctaagat gtacttggat ttaattaaaa agttcacttt 1980
gt
1982

```

&lt;210&gt; 10

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 10

```

Met Ala Met Ala Thr Lys Gly Gly Thr Val Lys Ala Ala Ser Gly Phe
  1          5          10          15
Asn Ala Met Glu Asp Ala Gln Thr Leu Arg Lys Ala Met Lys Gly Leu
  20          25          30
Gly Thr Asp Glu Asp Ala Ile Ile Ser Val Leu Ala Tyr Arg Asn Thr
  35          40          45
Ala Gln Arg Gln Glu Ile Arg Thr Ala Tyr Lys Ser Thr Ile Gly Arg
  50          55          60
Asp Leu Ile Asp Asp Leu Lys Ser Glu Leu Ser Gly Asn Phe Glu Gln
  65          70          75          80
Val Ile Val Gly Met Met Thr Pro Thr Val Leu Tyr Asp Val Gln Glu
  85          90          95
Leu Arg Arg Ala Met Lys Gly Ala Gly Thr Asp Glu Gly Cys Leu Ile
  100         105         110
Glu Ile Leu Ala Ser Arg Thr Pro Glu Glu Ile Arg Arg Ile Ser Gln
  115         120         125
Thr Tyr Gln Gln Gln Tyr Gly Arg Ser Leu Glu Asp Asp Ile Arg Ser
  130         135         140
Asp Thr Ser Phe Met Phe Gln Arg Val Leu Val Ser Leu Ser Ala Gly
  145         150         155         160
Gly Arg Asp Glu Gly Asn Tyr Leu Asp Asp Ala Leu Val Arg Gln Asp
  165         170         175
Ala Gln Asp Leu Tyr Glu Ala Gly Glu Lys Lys Trp Gly Thr Asp Glu
  180         185         190
Val Lys Phe Leu Thr Val Leu Cys Ser Arg Asn Arg Asn His Leu Leu
  195         200         205
His Val Phe Asp Glu Tyr Lys Arg Ile Ser Gln Lys Asp Ile Glu Gln
  210         215         220
Ser Ile Lys Ser Glu Thr Ser Gly Ser Phe Glu Asp Ala Leu Leu Ala
  225         230         235         240
Ile Val Lys Cys Met Arg Asn Lys Ser Ala Tyr Phe Ala Glu Lys Leu
  245         250         255
Tyr Lys Ser Met Lys Gly Leu Gly Thr Asp Asp Asn Thr Leu Ile Arg
  260         265         270
Val Met Val Ser Arg Ala Glu Ile Asp Met Leu Asp Ile Arg Ala His
  275         280         285
Phe Lys Arg Leu Tyr Gly Lys Ser Leu Tyr Ser Phe Ile Lys Gly Asp
  290         295         300
Thr Ser Gly Asp Tyr Arg Lys Val Leu Leu Val Leu Cys Gly Gly Asp
  305         310         315         320
Asp

```

&lt;210&gt; 11

<211> 1316  
 <212> DNA  
 <213> Homo sapiens

<400> 11

```

agctagacgc cccgaggtcg gagtgaagcg ccgggaccga gccccgtctc ccagggagtc 60
cggggagcac ggcaccgagg agagcgcggg agccaacctg ggcgcatcat gcgcagggcc 120
cgggagcgtg ggccggtcta caccgcccgc tgggtcacgt ggcccggaag ggccggcggc 180
tgccccggcc ggggggcggg ggtcgcgcgc gggttgcgct ggacgacgga gagcggcggg 240
cccgcagcgg cctggagcct cccaaccgcg gccgcgctgg ccctcgagcg taggagccgc 300
ccctgcccc cccgcgcggg cccgcgcgcc ggccgcccgc ccctatata gcgcgcccc 360
gcagggcccg cgccaggccg ccagcctcgg agtgggcgcg ggacagtgcg cggcgccccg 420
cagccaggcc cccgcccccg ccgcatccac ctccctcgcc gcctgcgacc caacgggcgc 480
ccccgcggc cagctcgcgc cgggcccccg cgccaccat gaagaaggag gtgtgctccg 540
tggccttcct caaggccgtg ttgcagagt tcttgccac cctcatcttc gtcttctttg 600
gcctgggctc ggccctcaag tggccgtcgg cgctgcctac catcctgcag atcgcgctgg 660
cgtttgccct ggccatagga acgctggccc agggccctgg acccgtgagc ggcgccaca 720
tcaacccgc catcaccctg gccctcttgg tgggcaacca gatctcgctg ctccgggctt 780
tctctacgt ggcgcccag ctggtggcg ccattgcgg ggctggcatc ctctacggtg 840
tggcaccgct caatgcccgg ggcaatctgg ccgtcaacgc gctcaacaac aacacaacgc 900
agggccaggc catggtggtg gagctgattc tgacctcca gctggcactc tgcattctcg 960
cctccactga ctcccgccgc accagccctg tgggctcccc agccctgtcc attggcctgt 1020
ctgtcaccct gggccacctt gtcggaatct acttactg ctgctccatg aaccagccc 1080
gctcttttgg cctgcggtg gtcatgaatc ggttcagccc cgctcactgg gttttctggg 1140
tagggcccat cgtggggcg gtcctggctg ccatacctta ctctacctg ctcttccca 1200
actccctgag cctgagtgcg cgtgtggcca tcatcaaagg cacgtatgag cctgacgagg 1260
actgggagga gcagcgggaa gagcggaaga agaccatgga gctgaccacc cgctga 1316

```

<210> 12  
 <211> 265  
 <212> PRT  
 <213> Homo sapiens

<400> 12

```

Met Lys Lys Glu Val Cys Ser Val Ala Phe Leu Lys Ala Val Phe Ala
 1          5          10          15
Glu Phe Leu Ala Thr Leu Ile Phe Val Phe Phe Gly Leu Gly Ser Ala
 20          25          30
Leu Lys Trp Pro Ser Ala Leu Pro Thr Ile Leu Gln Ile Ala Leu Ala
 35          40          45
Phe Gly Leu Ala Ile Gly Thr Leu Ala Gln Ala Leu Gly Pro Val Ser
 50          55          60
Gly Gly His Ile Asn Pro Ala Ile Thr Leu Ala Leu Leu Val Gly Asn
 65          70          75          80
Gln Ile Ser Leu Leu Arg Ala Phe Phe Tyr Val Ala Ala Gln Leu Val
 85          90          95
Gly Ala Ile Ala Gly Ala Gly Ile Leu Tyr Gly Val Ala Pro Leu Asn
100          105          110
Ala Arg Gly Asn Leu Ala Val Asn Ala Leu Asn Asn Asn Thr Thr Gln
115          120          125
Gly Gln Ala Met Val Val Glu Leu Ile Leu Thr Phe Gln Leu Ala Leu
130          135          140
Cys Ile Phe Ala Ser Thr Asp Ser Arg Arg Thr Ser Pro Val Gly Ser
145          150          155          160
Pro Ala Leu Ser Ile Gly Leu Ser Val Thr Leu Gly His Leu Val Gly
165          170          175
Ile Tyr Phe Thr Gly Cys Ser Met Asn Pro Ala Arg Ser Phe Gly Pro
180          185          190

```



Ala Val Val Met Asn Arg Phe Ser Pro Ala His Trp Val Phe Trp Val  
 195 200 205  
 Gly Pro Ile Val Gly Ala Val Leu Ala Ala Ile Leu Tyr Phe Tyr Leu  
 210 215 220  
 Leu Phe Pro Asn Ser Leu Ser Leu Ser Glu Arg Val Ala Ile Ile Lys  
 225 230 235 240  
 Gly Thr Tyr Glu Pro Asp Glu Asp Trp Glu Glu Gln Arg Glu Glu Arg  
 245 250 255  
 Lys Lys Thr Met Glu Leu Thr Thr Arg  
 260 265

<210> 13  
 <211> 1653  
 <212> DNA  
 <213> Homo sapiens

<400> 13  
 acgtccgggg aggggccagg tgagcggcag acccggcacg caggtggggg ccggcgggggt 60  
 ccgtggccag agctgcagag agacaaggcg gcggcggctg ctgtgctggg tgcagtgagg 120  
 aagaggccct cggtgggtgcc catggctggc caggatcctg cgctgagcac gagtaccccg 180  
 ttctacgacg tggccagaca tggcattctg caggtggcag gggatgaccg ctttggaga 240  
 cgtgttgta cgttcagctg ctgccggatg ccgccctccc acgagctgga ccaccagcgg 300  
 ctgctggagt atttgaagta cactctggac caatacgttg agaacgatta taccatcgtc 360  
 tatttccact acgggctgaa cagccggaac aagccttccc tgggctggct ccagagcgca 420  
 tacaaggagt tcgataggaa agacggggat ctactatgt ggcccagggt ggtctcgaac 480  
 tccaagctca agcgtacctc ccacctcagc ctcccaaagt actgggatta caggtacaag 540  
 aagaacttga aggccttcta cgtggtgcac cccaccagct tcatcaagggt cctgtggaac 600  
 atcttgaagc ccctcatcag tcacaagttt gggaagaaag tcatctattt caactacctg 660  
 agtgagctcc acgaacacct taaatacgac cagctgggtca tccctcccga agttttgcgg 720  
 tacgatgaga agctccagag cctgcacgag ggccggacgc cgctcctac caagacacca 780  
 ccgcccgggc ccccgctgcc cacacagcag tttggcgtca gtctgcaata cctcaaagac 840  
 aaaaatcaag gcgaactcat cccccctgtg ctgaggttca cagtgcgta cctgagagag 900  
 aaaggcctgc gcaccgaggg cctgttccgg agatccgcca gcgtgcagac cgtccgcgag 960  
 atccagaggc tctacaacca agggaagccc gtgaactttg acgactacgg ggacattcac 1020  
 atccctgccg tgatcctgaa gaccttctct cgagagctgc cccagccgct tctgaccttc 1080  
 caggccctacg agcagattct cgggatcacc tgtgtggaga gcagcctgcg tgtcactggc 1140  
 tgccgccaga tcttacggag cctcccagag cacaactacg tcgtctcccg ctacctatg 1200  
 ggctttctgc atgcggtgtc ccgggagagc atcttcaaca aaatgaacag ctctaacctg 1260  
 gcctgtgtct tcgggctgaa tttgatctgg ccatcccagg gggctctctc cctgagtggc 1320  
 cttgtgcccc tgaacatgtt cactgaactg ctgatcgagt actatgaaaa gatcttcagc 1380  
 accccggagg cacctgggga gcacggcctg gcaccatggg aacaggggag cagggcagcc 1440  
 cctttgcagg aggtgtgcc acggacacaa gccacgggcc tcaccaagcc taccctacct 1500  
 ccgagtcctc tgatggcagc cagaagacgt ctctagtgtt gcgaacactc tgtatgtttc 1560  
 gagctacctc ccacacctgt ctgtgcactt gtatgttttg taaacttggc atctgtaaaa 1620  
 ataaccagcc attagatgaa ttcagaacct tct 1653

<210> 14  
 <211> 464  
 <212> PRT  
 <213> Homo sapiens

<400> 14  
 Met Ala Gly Gln Asp Pro Ala Leu Ser Thr Ser His Pro Phe Tyr Asp  
 1 5 10 15  
 Val Ala Arg His Gly Ile Leu Gln Val Ala Gly Asp Asp Arg Phe Gly  
 20 25 30

Arg	Arg	Val	Val	Thr	Phe	Ser	Cys	Cys	Arg	Met	Pro	Pro	Ser	His	Glu
		35					40					45			
Leu	Asp	His	Gln	Arg	Leu	Leu	Glu	Tyr	Leu	Lys	Tyr	Thr	Leu	Asp	Gln
	50					55					60				
Tyr	Val	Glu	Asn	Asp	Tyr	Thr	Ile	Val	Tyr	Phe	His	Tyr	Gly	Leu	Asn
65					70					75					80
Ser	Arg	Asn	Lys	Pro	Ser	Leu	Gly	Trp	Leu	Gln	Ser	Ala	Tyr	Lys	Glu
			85						90					95	
Phe	Asp	Arg	Lys	Asp	Gly	Asp	Leu	Thr	Met	Trp	Pro	Arg	Leu	Val	Ser
			100					105						110	
Asn	Ser	Lys	Leu	Lys	Arg	Ser	Ser	His	Leu	Ser	Leu	Pro	Lys	Tyr	Trp
		115					120					125			
Asp	Tyr	Arg	Tyr	Lys	Lys	Asn	Leu	Lys	Ala	Leu	Tyr	Val	Val	His	Pro
	130					135					140				
Thr	Ser	Phe	Ile	Lys	Val	Leu	Trp	Asn	Ile	Leu	Lys	Pro	Leu	Ile	Ser
145					150					155					160
His	Lys	Phe	Gly	Lys	Lys	Val	Ile	Tyr	Phe	Asn	Tyr	Leu	Ser	Glu	Leu
			165						170					175	
His	Glu	His	Leu	Lys	Tyr	Asp	Gln	Leu	Val	Ile	Pro	Pro	Glu	Val	Leu
			180					185						190	
Arg	Tyr	Asp	Glu	Lys	Leu	Gln	Ser	Leu	His	Glu	Gly	Arg	Thr	Pro	Pro
		195					200					205			
Pro	Thr	Lys	Thr	Pro	Pro	Pro	Arg	Pro	Pro	Leu	Pro	Thr	Gln	Gln	Phe
	210					215					220				
Gly	Val	Ser	Leu	Gln	Tyr	Leu	Lys	Asp	Lys	Asn	Gln	Gly	Glu	Leu	Ile
225					230					235					240
Pro	Pro	Val	Leu	Arg	Phe	Thr	Val	Thr	Tyr	Leu	Arg	Glu	Lys	Gly	Leu
			245						250					255	
Arg	Thr	Glu	Gly	Leu	Phe	Arg	Arg	Ser	Ala	Ser	Val	Gln	Thr	Val	Arg
		260						265					270		
Glu	Ile	Gln	Arg	Leu	Tyr	Asn	Gln	Gly	Lys	Pro	Val	Asn	Phe	Asp	Asp
		275				280						285			
Tyr	Gly	Asp	Ile	His	Ile	Pro	Ala	Val	Ile	Leu	Lys	Thr	Phe	Leu	Arg
	290					295					300				
Glu	Leu	Pro	Gln	Pro	Leu	Leu	Thr	Phe	Gln	Ala	Tyr	Glu	Gln	Ile	Leu
305					310					315					320
Gly	Ile	Thr	Cys	Val	Glu	Ser	Ser	Leu	Arg	Val	Thr	Gly	Cys	Arg	Gln
			325						330					335	
Ile	Leu	Arg	Ser	Leu	Pro	Glu	His	Asn	Tyr	Val	Val	Leu	Arg	Tyr	Leu
		340						345					350		
Met	Gly	Phe	Leu	His	Ala	Val	Ser	Arg	Glu	Ser	Ile	Phe	Asn	Lys	Met
		355					360					365			
Asn	Ser	Ser	Asn	Leu	Ala	Cys	Val	Phe	Gly	Leu	Asn	Leu	Ile	Trp	Pro
	370					375					380				
Ser	Gln	Gly	Val	Ser	Ser	Leu	Ser	Ala	Leu	Val	Pro	Leu	Asn	Met	Phe
385					390					395					400
Thr	Glu	Leu	Leu	Ile	Glu	Tyr	Tyr	Glu	Lys	Ile	Phe	Ser	Thr	Pro	Glu
			405						410					415	
Ala	Pro	Gly	Glu	His	Gly	Leu	Ala	Pro	Trp	Glu	Gln	Gly	Ser	Arg	Ala
		420						425					430		
Ala	Pro	Leu	Gln	Glu	Ala	Val	Pro	Arg	Thr	Gln	Ala	Thr	Gly	Leu	Thr
	435						440					445			
Lys	Pro	Thr	Leu	Pro	Pro	Ser	Pro	Leu	Met	Ala	Ala	Arg	Arg	Arg	Leu
	450					455					460				

&lt;210&gt; 15

&lt;211&gt; 2043

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 15

```

atgaggactc tccgcaggtt gaagttcatg agttcgccca gcctcagtga cctgggcaag 60
agagagccgg ccgcccgcgc ggacgagcgg ggcacgcagc agcgccgggc ctgcgccaac 120
gccacctgga acagcatcca caacggggtg atcgccgtct tccagcgcaa ggggctgccc 180
gaccaggagc tcttcagcct caacgagggc gtccggcagc tgttgaagac agagctgggg 240
tccttcttca cggagtacct gcagaaccag ctgctgacaa aaggcatggt gatccttcgg 300
gacaagattc gcttctatga gggacagaag ctgctggact cactggcaga gacctgggac 360
ttcttcttca gtgacgtgct gcccatgctg caggccatct tctaccgggt gcagggcaag 420
gagccatcgg tgcgcagct ggccctgctg cacttccgga atgccatcac cctcagtgtg 480
aagctagagg atgcgtggc ccgggcccac gccctgtgtc cccctgccat cgtgcagatg 540
ctgctggtgc tgcagggggt acatgagtcc aggggctgga ctgaggacta cctgcgcctg 600
gagacgctgg tccagaaggt ggtgtcgcca tacctgggca cctacggcct ccactccagc 660
gagggggcct tcaccattc ctgcatcctg gagctgcaga gagacaaggc ggcggcggt 720
gctgtgctgg gtgcagttag gaagaggccc tcggtggtgc ccatggctgg ccaggatcct 780
gcgctgagca cgagtcaccc gttctacgac gtggccagac atggcattct gcagggtggca 840
ggggatgacc gctttggaag acgtgtgtc acgttcagct gctgccggat gccaccctcc 900
cacgagctgg accaccagcg gctgctggag tacaagaaga acttgaaggc cctctacgtg 960
gtgcacccca ccagcttcat caaggtcctg tggaaacatct tgaagcccct catcagtcac 1020
aagtttgagg agaaagtcac ctatttcaac tacctgagtg agctccacga acaccttaaa 1080
tacgaccagc tggatcatcc tcccgaagtt ttgcggtacg atgagaagct ccagagcctg 1140
cacgagggcc ggacgcccgc tcccaccaag acaccaccgc cgcgccccc gctgccca 1200
cagcagtttg gcgtcagtct gcaatacctc aaagacaaaa atcaaggcga actcatcccc 1260
cctgtgctga ggttcacagt gacgtacctg agagagaaaag gcctgcgcac cgagggcctg 1320
ttccggagat ccgccagcgt gcagaccgtc cgcgagatcc agaggctcta caaccaaggg 1380
aagcccgtga actttgacga ctacggggac attcacatcc ctgccgtgat cctgaagacc 1440
ttcctgcgag agctgccccca gccgcttctg accttccagg cctacgagca gattctcggg 1500
atcacctgtg tggagagcag cctgcgtgtc actggctgcc gccagatctt acggagcctc 1560
ccagagcaca actacgtcgt cctccgctac ctcatgggct tcctgcatgc ggtgtcccgg 1620
gagagcatct tcaacaaaat gaacagctct aacctggcct gtgtcttcgg gctgaatttg 1680
atctggccat ccaggggggt ctccctcctg agtgcccttg tgcccctgaa catgttcaact 1740
gaactgctga tcgagtacta tgaagagatc ttcagcacc cggaggcacc tggggagcac 1800
ggcctggcac catgggaaca ggggagcagg gcagcccctt tgaggaggc tgtgccacgg 1860
acacaagcca cgggcctcac caagcctacc ctacctcga gtcccctgat ggcagccaga 1920
agacgtctct agtgttgcca acactctgta tatttcgagc tacctcccac acctgtctgt 1980
gcacttgtat gttttgtaaa cttggcatct gtaaaaaataa ccagccatta gatgaattca 2040
gaa
2043

```

&lt;210&gt; 16

&lt;211&gt; 643

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

```

Met Arg Thr Leu Arg Arg Leu Lys Phe Met Ser Ser Pro Ser Leu Ser
1           5           10           15
Asp Leu Gly Lys Arg Glu Pro Ala Ala Ala Asp Glu Arg Gly Thr
20           25           30
Gln Gln Arg Arg Ala Cys Ala Asn Ala Thr Trp Asn Ser Ile His Asn
35           40           45
Gly Val Ile Ala Val Phe Gln Arg Lys Gly Leu Pro Asp Gln Glu Leu
50           55           60
Phe Ser Leu Asn Glu Gly Val Arg Gln Leu Leu Lys Thr Glu Leu Gly
65           70           75           80
Ser Phe Phe Thr Glu Tyr Leu Gln Asn Gln Leu Leu Thr Lys Gly Met
85           90           95

```

Val Ile Leu Arg Asp Lys Ile Arg Phe Tyr Glu Gly Gln Lys Leu Leu  
 100 105 110  
 Asp Ser Leu Ala Glu Thr Trp Asp Phe Phe Phe Ser Asp Val Leu Pro  
 115 120 125  
 Met Leu Gln Ala Ile Phe Tyr Pro Val Gln Gly Lys Glu Pro Ser Val  
 130 135 140  
 Arg Gln Leu Ala Leu Leu His Phe Arg Asn Ala Ile Thr Leu Ser Val  
 145 150 155 160  
 Lys Leu Glu Asp Ala Leu Ala Arg Ala His Ala Arg Val Pro Pro Ala  
 165 170 175  
 Ile Val Gln Met Leu Leu Val Leu Gln Gly Val His Glu Ser Arg Gly  
 180 185 190  
 Val Thr Glu Asp Tyr Leu Arg Leu Glu Thr Leu Val Gln Lys Val Val  
 195 200 205  
 Ser Pro Tyr Leu Gly Thr Tyr Gly Leu His Ser Ser Glu Gly Pro Phe  
 210 215 220  
 Thr His Ser Cys Ile Leu Glu Leu Gln Arg Asp Lys Ala Ala Ala Ala  
 225 230 235 240  
 Ala Val Leu Gly Ala Val Arg Lys Arg Pro Ser Val Val Pro Met Ala  
 245 250 255  
 Gly Gln Asp Pro Ala Leu Ser Thr Ser His Pro Phe Tyr Asp Val Ala  
 260 265 270  
 Arg His Gly Ile Leu Gln Val Ala Gly Asp Asp Arg Phe Gly Arg Arg  
 275 280 285  
 Val Val Thr Phe Ser Cys Cys Arg Met Pro Pro Ser His Glu Leu Asp  
 290 295 300  
 His Gln Arg Leu Leu Glu Tyr Lys Lys Asn Leu Lys Ala Leu Tyr Val  
 305 310 315 320  
 Val His Pro Thr Ser Phe Ile Lys Val Leu Trp Asn Ile Leu Lys Pro  
 325 330 335  
 Leu Ile Ser His Lys Phe Gly Lys Lys Val Ile Tyr Phe Asn Tyr Leu  
 340 345 350  
 Ser Glu Leu His Glu His Leu Lys Tyr Asp Gln Leu Val Ile Pro Pro  
 355 360 365  
 Glu Val Leu Arg Tyr Asp Glu Lys Leu Gln Ser Leu His Glu Gly Arg  
 370 375 380  
 Thr Pro Pro Pro Thr Lys Thr Pro Pro Pro Arg Pro Pro Leu Pro Thr  
 385 390 395 400  
 Gln Gln Phe Gly Val Ser Leu Gln Tyr Leu Lys Asp Lys Asn Gln Gly  
 405 410 415  
 Glu Leu Ile Pro Pro Val Leu Arg Phe Thr Val Thr Tyr Leu Arg Glu  
 420 425 430  
 Lys Gly Leu Arg Thr Glu Gly Leu Phe Arg Arg Ser Ala Ser Val Gln  
 435 440 445  
 Thr Val Arg Glu Ile Gln Arg Leu Tyr Asn Gln Gly Lys Pro Val Asn  
 450 455 460  
 Phe Asp Asp Tyr Gly Asp Ile His Ile Pro Ala Val Ile Leu Lys Thr  
 465 470 475 480  
 Phe Leu Arg Glu Leu Pro Gln Pro Leu Leu Thr Phe Gln Ala Tyr Glu  
 485 490 495  
 Gln Ile Leu Gly Ile Thr Cys Val Glu Ser Ser Leu Arg Val Thr Gly  
 500 505 510  
 Cys Arg Gln Ile Leu Arg Ser Leu Pro Glu His Asn Tyr Val Val Leu  
 515 520 525  
 Arg Tyr Leu Met Gly Phe Leu His Ala Val Ser Arg Glu Ser Ile Phe  
 530 535 540  
 Asn Lys Met Asn Ser Ser Asn Leu Ala Cys Val Phe Gly Leu Asn Leu  
 545 550 555 560

Ile Trp Pro Ser Gln Gly Val Ser Ser Leu Ser Ala Leu Val Pro Leu  
 565 570 575  
 Asn Met Phe Thr Glu Leu Leu Ile Glu Tyr Tyr Glu Lys Ile Phe Ser  
 580 585 590  
 Thr Pro Glu Ala Pro Gly Glu His Gly Leu Ala Pro Trp Glu Gln Gly  
 595 600 605  
 Ser Arg Ala Ala Pro Leu Gln Glu Ala Val Pro Arg Thr Gln Ala Thr  
 610 615 620  
 Gly Leu Thr Lys Pro Thr Leu Pro Pro Ser Pro Leu Met Ala Ala Arg  
 625 630 635 640  
 Arg Arg Leu

&lt;210&gt; 17

&lt;211&gt; 2274

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

atgaggactc tccgcaggtt gaagttcatg agttcgccca gcctcagtga cctgggcaag 60  
 agagagccgg ccgcccgc ggacgagcgg ggcaegcagc agcgccgggc ctgcgccaac 120  
 gccacctgga acagcatcca caacggggtg atcgccgtct tccagcgcaa ggggctgccc 180  
 gaccaggagc tcttcagcct caacgagggc gtccggcagc tgttgaagac agagctgggg 240  
 tccttcttca cggagtacct gcagaaccag ctgctgacaa aaggcatggt gatccttcgg 300  
 gacaagattc gtttctatga gggacagaag ctgctggact cactggcaga gacctgggac 360  
 ttcttcttca gtgacgtgct gcccattgctg caggccatct tctaccgggt gcagggcaag 420  
 gagccatcgg tgcgccagct ggccctgctg cacttccgga atgccatcac cctcagtgtg 480  
 aagctagagg atgcgctggc ccgggcccac gcccggtgac cccctgccat cgtgcagatg 540  
 ctgctggtgc tgcagggggg acatgagtcc aggggctgta ctgaggacta cctgcgcctg 600  
 gagacgtggt tccagaaggt ggtgtcgcca tacctgggca cctacggcct cactccagc 660  
 gagggggcct tcacccattc ctgcatcctg gagctgcaga gagacaaggc ggccggcggt 720  
 gctgtgctgg gtgcagtggg gaagaggccc tcgggtggtg ccatggctgg ccaggatcct 780  
 gcgctgagca cgagtcaccc gttctacgac gtggccagac atggcattct gcaggtggca 840  
 ggggatgacc gctttggaag acgtgttgc acgttcagct gctgccggat gccaccctcc 900  
 cagcagctgg accaccagcg gctgctggag tatttgaagt acacactgga ccaatacgtt 960  
 gagaacgatt ataccatcgt ctatttccac tacgggctga acagccgga caagccttcc 1020  
 ctgggctggc tccagagcgc atacaaggag ttogatagga aagacgggga tctcactatg 1080  
 tggcccaggc tgggtctgaa ctccaagctc aagcgatcct cccacctcag cctcccaaag 1140  
 tactgggatt acaggtacaa gaagaacttg aaggccctct acgtggtgca cccaccagc 1200  
 ttcattcaagg tcctgtggaa catcttgaag cccctcatca gtcacaagtt tgggaagaaa 1260  
 gtcattctatt tcaactacct gagtgagctc caccgaacac ttaaatacga ccagctggtc 1320  
 atccctcccc aagttttgcg gtacgatgag aagctccaga gcctgcacga gggccggacg 1380  
 ccgctcccca ccaagacacc accgcccggg ccccgctgc ccacacagca gtttgccgtc 1440  
 agtctgcaat acctcaaaga caaaaatcaa ggccgaactca tccccctgt gctgaggttc 1500  
 acagtgcagt acctgagaga gaaaggcctg gcacccgagg gcctgtccg gagatccgcc 1560  
 agcgtgcaga ccgtccgcca gatccagagg ctctacaacc aagggaagcc cgtgaacttt 1620  
 gacgactacg gggacattca catccctgcc gtgatcctga agaccttct gcgagagctg 1680  
 cccagccgc ttctgacctt ccaggcctac gagcagattc tcgggatcac ctgtgtggag 1740  
 agcagcctgc gtgtcactgg ctgccgccag atcttacgga gcctcccaga gcacaactac 1800  
 gtcgtcctcc gctacctcat gggcttcctg catgcggtgt cccgggagag catcttcaac 1860  
 aaaatgaaca gctctaacct ggctgtgtc ttccgggctga atttgatctg gccatcccag 1920  
 ggggtctcct ccctgagtg ccttgtgccc ctgaacatgt tcaactgaact gctgatcgag 1980  
 tactatgaaa agatcttcag caccocggag gcacctggg agcacggcct ggcaccatgg 2040  
 gaacagggga gcagggcag ccctttgcag gaggtgtgc caccgacaca agccacgggc 2100  
 ctaccaagc ctacctacc tccgagtccc ctgatggcag ccagaagacg tctctagtgt 2160  
 tgcgaacact ctgtatatct cgagctacct cccacacctg tctgtgcact tgtatgtttt 2220  
 gtaaacttgg catctgtaaa aataaccagc cattagatga attcagaacc ttct 2274

<210> 18  
 <211> 751  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(751)  
 <223> Xaa = Any Amino Acid

<400> 18

Met	Arg	Thr	Leu	Arg	Arg	Leu	Lys	Phe	Met	Ser	Ser	Pro	Ser	Leu	Ser
1				5				10						15	
Asp	Leu	Gly	Lys	Arg	Glu	Pro	Ala	Ala	Ala	Ala	Asp	Glu	Arg	Gly	Thr
		20					25					30			
Gln	Gln	Arg	Arg	Ala	Cys	Ala	Asn	Ala	Thr	Trp	Asn	Ser	Ile	His	Asn
		35					40					45			
Gly	Val	Ile	Ala	Val	Phe	Gln	Arg	Lys	Gly	Leu	Pro	Asp	Gln	Glu	Leu
	50					55					60				
Phe	Ser	Leu	Asn	Glu	Gly	Val	Arg	Gln	Leu	Leu	Lys	Thr	Glu	Leu	Gly
65				70					75					80	
Ser	Phe	Phe	Thr	Glu	Tyr	Leu	Gln	Asn	Gln	Leu	Leu	Thr	Lys	Gly	Met
			85					90						95	
Val	Ile	Leu	Arg	Asp	Lys	Ile	Arg	Phe	Tyr	Glu	Gly	Gln	Lys	Leu	Leu
		100						105					110		
Asp	Ser	Leu	Ala	Glu	Thr	Trp	Asp	Phe	Phe	Phe	Ser	Asp	Val	Leu	Pro
		115					120					125			
Met	Leu	Gln	Ala	Ile	Phe	Tyr	Pro	Val	Gln	Gly	Lys	Glu	Pro	Ser	Val
	130					135					140				
Arg	Gln	Leu	Ala	Leu	Leu	His	Phe	Arg	Asn	Ala	Ile	Thr	Leu	Ser	Val
145				150						155				160	
Lys	Leu	Glu	Asp	Ala	Leu	Ala	Arg	Ala	His	Ala	Arg	Val	Pro	Pro	Ala
			165					170						175	
Ile	Val	Gln	Met	Leu	Leu	Val	Leu	Gln	Gly	Val	His	Glu	Ser	Arg	Gly
		180						185					190		
Val	Thr	Glu	Asp	Tyr	Leu	Arg	Leu	Glu	Thr	Leu	Val	Gln	Lys	Val	Val
	195						200					205			
Ser	Pro	Tyr	Leu	Gly	Thr	Tyr	Gly	Leu	His	Ser	Ser	Glu	Gly	Pro	Phe
	210				215						220				
Thr	His	Ser	Cys	Ile	Leu	Glu	Leu	Gln	Arg	Asp	Lys	Ala	Ala	Ala	Ala
225				230						235				240	
Ala	Val	Leu	Gly	Ala	Val	Arg	Lys	Arg	Pro	Ser	Val	Val	Pro	Met	Ala
			245						250					255	
Gly	Gln	Asp	Pro	Ala	Leu	Ser	Thr	Ser	His	Pro	Phe	Tyr	Asp	Val	Ala
		260						265					270		
Arg	His	Gly	Ile	Leu	Gln	Val	Ala	Gly	Asp	Asp	Arg	Phe	Gly	Arg	Arg
	275					280						285			
Val	Val	Thr	Phe	Ser	Cys	Cys	Arg	Met	Pro	Pro	Ser	His	Glu	Leu	Asp
	290					295					300				
His	Gln	Arg	Leu	Leu	Glu	Tyr	Leu	Lys	Tyr	Thr	Leu	Asp	Gln	Tyr	Val
305				310						315				320	
Glu	Asn	Asp	Tyr	Thr	Ile	Val	Tyr	Phe	His	Tyr	Gly	Leu	Asn	Ser	Arg
			325						330					335	
Asn	Lys	Pro	Ser	Leu	Gly	Trp	Leu	Gln	Ser	Ala	Tyr	Lys	Glu	Phe	Asp
		340						345					350		
Arg	Lys	Asp	Gly	Asp	Leu	Thr	Met	Trp	Pro	Arg	Leu	Val	Ser	Asn	Ser
		355					360					365			

Lys Leu Lys Arg Ser Ser His Leu Ser Leu Pro Lys Tyr Trp Asp Tyr  
 370 375 380  
 Arg Tyr Lys Lys Asn Leu Lys Ala Leu Tyr Val Val His Pro Thr Ser  
 385 390 395 400  
 Phe Ile Lys Val Leu Trp Asn Ile Leu Lys Pro Leu Ile Ser His Lys  
 405 410 415  
 Phe Gly Lys Lys Val Ile Tyr Phe Asn Tyr Leu Ser Glu Leu His Glu  
 420 425 430  
 His Leu Lys Tyr Asp Gln Leu Val Ile Pro Pro Glu Val Leu Arg Tyr  
 435 440 445  
 Asp Glu Lys Leu Gln Ser Leu His Glu Gly Arg Thr Pro Pro Pro Thr  
 450 455 460  
 Lys Thr Pro Pro Pro Arg Pro Pro Leu Pro Thr Gln Gln Phe Gly Val  
 465 470 475 480  
 Ser Leu Gln Tyr Leu Lys Asp Lys Asn Gln Gly Glu Leu Ile Pro Pro  
 485 490 495  
 Val Leu Arg Phe Thr Val Thr Tyr Leu Arg Glu Lys Gly Leu Arg Thr  
 500 505 510  
 Glu Gly Leu Phe Arg Arg Ser Ala Ser Val Gln Thr Val Arg Glu Ile  
 515 520 525  
 Gln Arg Leu Tyr Asn Gln Gly Lys Pro Val Asn Phe Asp Asp Tyr Gly  
 530 535 540  
 Asp Ile His Ile Pro Ala Val Ile Leu Lys Thr Phe Leu Arg Glu Leu  
 545 550 555 560  
 Pro Gln Pro Leu Leu Thr Phe Gln Ala Tyr Glu Gln Ile Leu Gly Ile  
 565 570 575  
 Thr Cys Val Glu Ser Ser Leu Arg Val Thr Gly Cys Arg Gln Ile Leu  
 580 585 590  
 Arg Ser Leu Pro Glu His Asn Tyr Val Val Leu Arg Tyr Leu Met Gly  
 595 600 605  
 Phe Leu His Ala Val Ser Arg Glu Ser Ile Phe Asn Lys Met Asn Ser  
 610 615 620  
 Ser Asn Leu Ala Cys Val Phe Gly Leu Asn Leu Ile Trp Pro Ser Gln  
 625 630 635 640  
 Gly Val Ser Ser Leu Ser Ala Leu Val Pro Leu Asn Met Phe Thr Glu  
 645 650 655  
 Leu Leu Ile Glu Tyr Tyr Glu Lys Ile Phe Ser Thr Pro Glu Ala Pro  
 660 665 670  
 Gly Glu His Gly Leu Ala Pro Trp Glu Gln Gly Ser Arg Ala Ala Pro  
 675 680 685  
 Leu Gln Glu Ala Val Pro Arg Thr Gln Ala Thr Gly Leu Thr Lys Pro  
 690 695 700  
 Thr Leu Pro Pro Ser Pro Leu Met Ala Ala Arg Arg Arg Leu Xaa Cys  
 705 710 715 720  
 Cys Glu His Ser Val Tyr Phe Glu Leu Pro Pro Thr Pro Val Cys Ala  
 725 730 735  
 Leu Val Cys Phe Val Asn Leu Ala Ser Val Lys Ile Thr Ser His  
 740 745 750

&lt;210&gt; 19

&lt;211&gt; 718

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

Met Arg Thr Leu Arg Arg Leu Lys Phe Met Ser Ser Pro Ser Leu Ser  
 1 5 10 15

Asp Leu Gly Lys Arg Glu Pro Ala Ala Ala Asp Glu Arg Gly Thr  
 20 25 30  
 Gln Gln Arg Arg Ala Cys Ala Asn Ala Thr Trp Asn Ser Ile His Asn  
 35 40 45  
 Gly Val Ile Ala Val Phe Gln Arg Lys Gly Leu Pro Asp Gln Glu Leu  
 50 55 60  
 Phe Ser Leu Asn Glu Gly Val Arg Gln Leu Leu Lys Thr Glu Leu Gly  
 65 70 75 80  
 Ser Phe Phe Thr Glu Tyr Leu Gln Asn Gln Leu Leu Thr Lys Gly Met  
 85 90 95  
 Val Ile Leu Arg Asp Lys Ile Arg Phe Tyr Glu Gly Gln Lys Leu Leu  
 100 105 110  
 Asp Ser Leu Ala Glu Thr Trp Asp Phe Phe Phe Ser Asp Val Leu Pro  
 115 120 125  
 Met Leu Gln Ala Ile Phe Tyr Pro Val Gln Gly Lys Glu Pro Ser Val  
 130 135 140  
 Arg Gln Leu Ala Leu Leu His Phe Arg Asn Ala Ile Thr Leu Ser Val  
 145 150 155 160  
 Lys Leu Glu Asp Ala Leu Ala Arg Ala His Ala Arg Val Pro Pro Ala  
 165 170 175  
 Ile Val Gln Met Leu Leu Val Leu Gln Gly Val His Glu Ser Arg Gly  
 180 185 190  
 Val Thr Glu Asp Tyr Leu Arg Leu Glu Thr Leu Val Gln Lys Val Val  
 195 200 205  
 Ser Pro Tyr Leu Gly Thr Tyr Gly Leu His Ser Ser Glu Gly Pro Phe  
 210 215 220  
 Thr His Ser Cys Ile Leu Glu Leu Gln Arg Asp Lys Ala Ala Ala Ala  
 225 230 235 240  
 Ala Val Leu Gly Ala Val Arg Lys Arg Pro Ser Val Val Pro Met Ala  
 245 250 255  
 Gly Gln Asp Pro Ala Leu Ser Thr Ser His Pro Phe Tyr Asp Val Ala  
 260 265 270  
 Arg His Gly Ile Leu Gln Val Ala Gly Asp Asp Arg Phe Gly Arg Arg  
 275 280 285  
 Val Val Thr Phe Ser Cys Cys Arg Met Pro Pro Ser His Glu Leu Asp  
 290 295 300  
 His Gln Arg Leu Leu Glu Tyr Leu Lys Tyr Thr Leu Asp Gln Tyr Val  
 305 310 315 320  
 Glu Asn Asp Tyr Thr Ile Val Tyr Phe His Tyr Gly Leu Asn Ser Arg  
 325 330 335  
 Asn Lys Pro Ser Leu Gly Trp Leu Gln Ser Ala Tyr Lys Glu Phe Asp  
 340 345 350  
 Arg Lys Asp Gly Asp Leu Thr Met Trp Pro Arg Leu Val Ser Asn Ser  
 355 360 365  
 Lys Leu Lys Arg Ser Ser His Leu Ser Leu Pro Lys Tyr Trp Asp Tyr  
 370 375 380  
 Arg Tyr Lys Lys Asn Leu Lys Ala Leu Tyr Val Val His Pro Thr Ser  
 385 390 395 400  
 Phe Ile Lys Val Leu Trp Asn Ile Leu Lys Pro Leu Ile Ser His Lys  
 405 410 415  
 Phe Gly Lys Lys Val Ile Tyr Phe Asn Tyr Leu Ser Glu Leu His Glu  
 420 425 430  
 His Leu Lys Tyr Asp Gln Leu Val Ile Pro Pro Glu Val Leu Arg Tyr  
 435 440 445  
 Asp Glu Lys Leu Gln Ser Leu His Glu Gly Arg Thr Pro Pro Pro Thr  
 450 455 460  
 Lys Thr Pro Pro Pro Arg Pro Pro Leu Pro Thr Gln Gln Phe Gly Val  
 465 470 475 480



Ser Leu Gln Tyr Leu Lys Asp Lys Asn Gln Gly Glu Leu Ile Pro Pro  
 485 490 495  
 Val Leu Arg Phe Thr Val Thr Tyr Leu Arg Glu Lys Gly Leu Arg Thr  
 500 505 510  
 Glu Gly Leu Phe Arg Arg Ser Ala Ser Val Gln Thr Val Arg Glu Ile  
 515 520 525  
 Gln Arg Leu Tyr Asn Gln Gly Lys Pro Val Asn Phe Asp Asp Tyr Gly  
 530 535 540  
 Asp Ile His Ile Pro Ala Val Ile Leu Lys Thr Phe Leu Arg Glu Leu  
 545 550 555 560  
 Pro Gln Pro Leu Leu Thr Phe Gln Ala Tyr Glu Gln Ile Leu Gly Ile  
 565 570 575  
 Thr Cys Val Glu Ser Ser Leu Arg Val Thr Gly Cys Arg Gln Ile Leu  
 580 585 590  
 Arg Ser Leu Pro Glu His Asn Tyr Val Val Leu Arg Tyr Leu Met Gly  
 595 600 605  
 Phe Leu His Ala Val Ser Arg Glu Ser Ile Phe Asn Lys Met Asn Ser  
 610 615 620  
 Ser Asn Leu Ala Cys Val Phe Gly Leu Asn Leu Ile Trp Pro Ser Gln  
 625 630 635 640  
 Gly Val Ser Ser Leu Ser Ala Leu Val Pro Leu Asn Met Phe Thr Glu  
 645 650 655  
 Leu Leu Ile Glu Tyr Tyr Glu Lys Ile Phe Ser Thr Pro Glu Ala Pro  
 660 665 670  
 Gly Glu His Gly Leu Ala Pro Trp Glu Gln Gly Ser Arg Ala Ala Pro  
 675 680 685  
 Leu Gln Glu Ala Val Pro Arg Thr Gln Ala Thr Gly Leu Thr Lys Pro  
 690 695 700  
 Thr Leu Pro Pro Ser Pro Leu Met Ala Ala Arg Arg Arg Leu  
 705 710 715

&lt;210&gt; 20

&lt;211&gt; 1431

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 20

acgtccgggg aggggccagg tgagcggcag acccggcagc cagggtggggg ccggcgggggt 60  
 ccgtggccag agctgcagag agacaaggcg gcggcggctg ctgtgctggg tgcagtgagg 120  
 aagaggccct cgggtggtgcc catggctggc caggatcctg cgctgagcac gattcaccgc 180  
 ttctacgacg tggccagaca tggcattctg cagggtggcag gggatgaccg ctttggaga 240  
 cgtgttgta cgttcagctg ctgccggatg ccaccctccc acgagctgga ccaccagcgg 300  
 ctgctggaca ggtacaagaa gaacttgaag gccctctacg tgggtgcaccc caccagcttc 360  
 atcaaggtcc tgtggaacat ctgaagccc ctcatcagtc acaagtttg gaagaaagtc 420  
 atctatttca actacctgag tgagctccac gaacacctta aatacgacca gctggtcattc 480  
 cctcccgaag ttttgcggtg cgatgagaag ctccagagcc tgcacgaggg ccggacgccg 540  
 cctcccacca agacaccacc gccgcggccc ccgctgccc caacagcagtt tggcgtcagt 600  
 ctgcaatacc tcaaagacaa aaatcaaggc gaactcatcc cccctgtgct gaggttcaca 660  
 gtgacgtacc tgagagagaa aggcctgcgc accgagggcc tgttccggag atccgccagc 720  
 gtgcagaccg tccgcgagat ccagaggctc tacaaccaag ggaagcccgt gaactttgac 780  
 gactacgggg acattcacat ccctgccgtg atcctgaaga ccttcctgcg agagctgccc 840  
 cagccgcttc tgaccttcca ggctacgag cagattctcg ggatcacctg tgtggagagc 900  
 agcctgcgtg tcaactggctg ccgccagatc ttacggagcc tcccagagca caactacgtc 960  
 gtcctccgct acctcatggg ctctctgcat gcgctgtccc gggagagcat cttcaacaaa 1020  
 atgaacagct ctaacctggc ctgtgtcttc gggctgaatt tgatctggcc atcccagggg 1080  
 gtctcctccc tgagtgcctt tgtgcccctg aacatgttca ctgaactgct gatcgagtac 1140  
 tatgaaaaga tcttcagcac cccggaggga cctggggagc acggcctggc accatgggaa 1200

caggggagca gggcagcccc ttgagcaggag gctgtgtccac ggacacaagc cacgggacctc 1260  
 accaagccta ccctacctcc gaggccccctg atggcagcca gaagacgtct ctagtggttc 1320  
 gaacactctg tatatttcga gctacctccc acacctgtct gtgcacttgt atgttttcta 1380  
 aacttgcat ctgtaaaaat aaccagccat tagatgaatt cagaaccttc t 1431

<210> 21

<211> 390

<212> PRT

<213> Homo sapiens

<400> 21

Met	Ala	Gly	Gln	Asp	Pro	Ala	Leu	Ser	Thr	Ser	His	Pro	Phe	Tyr	Asp
1				5					10					15	
Val	Ala	Arg	His	Gly	Ile	Leu	Gln	Val	Ala	Gly	Asp	Asp	Arg	Phe	Gly
			20					25					30		
Arg	Arg	Val	Val	Thr	Phe	Ser	Cys	Cys	Arg	Met	Pro	Pro	Ser	His	Glu
		35					40					45			
Leu	Asp	His	Gln	Arg	Leu	Leu	Asp	Arg	Tyr	Lys	Lys	Asn	Leu	Lys	Ala
	50					55					60				
Leu	Tyr	Val	Val	His	Pro	Thr	Ser	Phe	Ile	Lys	Val	Leu	Trp	Asn	Ile
65					70				75					80	
Leu	Lys	Pro	Leu	Ile	Ser	His	Lys	Phe	Gly	Lys	Lys	Val	Ile	Tyr	Phe
				85					90					95	
Asn	Tyr	Leu	Ser	Glu	Leu	His	Glu	His	Leu	Lys	Tyr	Asp	Gln	Leu	Val
		100						105					110		
Ile	Pro	Pro	Glu	Val	Leu	Arg	Tyr	Asp	Glu	Lys	Leu	Gln	Ser	Leu	His
	115						120					125			
Glu	Gly	Arg	Thr	Pro	Pro	Pro	Thr	Lys	Thr	Pro	Pro	Pro	Arg	Pro	Pro
	130					135					140				
Leu	Pro	Thr	Gln	Gln	Phe	Gly	Val	Ser	Leu	Gln	Tyr	Leu	Lys	Asp	Lys
145					150				155					160	
Asn	Gln	Gly	Glu	Leu	Ile	Pro	Pro	Val	Leu	Arg	Phe	Thr	Val	Thr	Tyr
				165					170					175	
Leu	Arg	Glu	Lys	Gly	Leu	Arg	Thr	Glu	Gly	Leu	Phe	Arg	Arg	Ser	Ala
		180					185						190		
Ser	Val	Gln	Thr	Val	Arg	Glu	Ile	Gln	Arg	Leu	Tyr	Asn	Gln	Gly	Lys
	195						200					205			
Pro	Val	Asn	Phe	Asp	Asp	Tyr	Gly	Asp	Ile	His	Ile	Pro	Ala	Val	Ile
	210					215					220				
Leu	Lys	Thr	Phe	Leu	Arg	Glu	Leu	Pro	Gln	Pro	Leu	Leu	Thr	Phe	Gln
225					230				235					240	
Ala	Tyr	Glu	Gln	Ile	Leu	Gly	Ile	Thr	Cys	Val	Glu	Ser	Ser	Leu	Arg
				245					250					255	
Val	Thr	Gly	Cys	Arg	Gln	Ile	Leu	Arg	Ser	Leu	Pro	Glu	His	Asn	Tyr
			260					265						270	
Val	Val	Leu	Arg	Tyr	Leu	Met	Gly	Phe	Leu	His	Ala	Val	Ser	Arg	Glu
		275					280					285			
Ser	Ile	Phe	Asn	Lys	Met	Asn	Ser	Ser	Asn	Leu	Ala	Cys	Val	Phe	Gly
	290					295					300				
Leu	Asn	Leu	Ile	Trp	Pro	Ser	Gln	Gly	Val	Ser	Ser	Leu	Ser	Ala	Leu
305					310				315					320	
Val	Pro	Leu	Asn	Met	Phe	Thr	Glu	Leu	Leu	Ile	Glu	Tyr	Tyr	Glu	Lys
				325					330					335	
Ile	Phe	Ser	Thr	Pro	Glu	Ala	Pro	Gly	Glu	His	Gly	Leu	Ala	Pro	Trp
			340					345						350	
Glu	Gln	Gly	Ser	Arg	Ala	Ala	Pro	Leu	Gln	Glu	Ala	Val	Pro	Arg	Thr
			355				360					365			
Gln	Ala	Thr	Gly	Leu	Thr	Lys	Pro	Thr	Leu	Pro	Pro	Ser	Pro	Leu	Met

370  
Ala Ala Arg Arg Arg Leu  
385 390

380

<210> 22  
<211> 2019  
<212> DNA  
<213> Homo sapiens

&lt;400&gt; 22

```

atgaggactc tccgcaggtt gaagttcatg agttcgccca gcctcagtga cctgggcaag 60
agagagccgg ccgccgccgc ggacgagcgg ggacgcagc agcgccgggc ctgcgccaac 120
gccacctgga acagcatcca caacggggtg atcgccgtct tccagcgcaa ggggctgccc 180
gaccaggagc tcttcagcct caacgagggc gtccggcagc tgttgaagac agagctgggg 240
tccttcttca cggagtacct gcagaaccag ctgctgacaa aaggcatggt gatccttcgg 300
gacaagattc gcttctatga gggacagaag ctgctggact cactggcaga gacctgggac 360
ttcttcttca gtgacgtgct gcccatgctg caggccatct tctaccgggt gcagggcaag 420
gagccatcgg tgcgccagct ggccctgctg cacttcggga atgccatcac cctcagtgtg 480
aagctagagg atgcgtggc ccggggcccat gcccggtgtc ccctgccat cgtgcagatg 540
ctgctgggtg tgcagggggt acatgagtc aggggctga ctgaggacta cctgcgcctg 600
gagacgctgg tccagaagggt ggtgtcgcca tacctgggca cctacggcct ccactccagc 660
gaggggccct tcacccattc ctgcatcctg gagctgcaga gagacaaggc ggcggcgggt 720
gctgtgctgg gtgacgtgag gaagaggccc tcggtggtgc ccatggctgg ccaggatcct 780
gcgctgagca cgagtcaccc gttctacgac gtggccagac atggcattct gcagggtggca 840
ggggatgacc gctttggaag acgtgtgtgc acgttcagct gctgccggat gccaccctcc 900
cacgagctgg accaccagcg gctgctggag tatttgaagt acacactgga ccaatacgtt 960
gagaacgatt ataccatcgt ctatttccac tacgggctga acagccggaa caagccttcc 1020
ctgggctggc tccagagcgc atacaaggag ttcgatagga aagacgggga tctcactatg 1080
tggcccaggc tggctctgaa ctccaagctc aagcgatcct cccacctcag cctcccaaag 1140
tactgggatt acaggtacaa gaagaacttg aaggccctct acgtggtgca cccaccagc 1200
ttcatcaagg tcctgtggaa catcttgaag cccctcatca gtcacaagtt tgggaagaaa 1260
gtcatctatt tcaactacct gagtgagctc caagaacacc ttaaatacga ccagctggtc 1320
atccctcccg aagttttgcg gtacgatgag aagctccaga gcctgcacga gggccggacg 1380
ccgctccca ccaagacacc accgccgcgg ccccgctgc ccacacagca gtttggcgctc 1440
agtctgcaat acctcaaaga caaaaatcaa gggaactca tccccctgt gctgaggttc 1500
acagtacgt acctgagaga gaaaggcctc ccagagcaca actacgtcgt cctccgctac 1560
ctcatgggtc tctgcatgc ggtgtcccgg gatagcatct tcaacaaaat gaacagctct 1620
aacctggcct gtgtcttcgg gctgaatttg atctggccat cccagggggt ctctccctg 1680
agtgcccttg tgccctgaa catgttact gaactgctga tcgagtacta tgaaaagatc 1740
ttcagcacc cggaggcacc tggggagcac ggctggcac catgggaaca ggggagcagg 1800
gcagcccctt tgcaggaggc tgtgccacgg acacaagcca cgggcctcac caagcctacc 1860
ctacctccga gtcccctgat ggcagccaga agacgtctct agtgttgca acactctgta 1920
tatttcgagc tacctccac acctgtctgt gcacttgat gttttgtaaa cttggcatct 1980
gtaaaaataa ccagccatta gatgaattca gaaccttct 2019

```

<210> 23  
<211> 633  
<212> PRT  
<213> Homo sapiens

&lt;400&gt; 23

```

Met Arg Thr Leu Arg Arg Leu Lys Phe Met Ser Ser Pro Ser Leu Ser
1           5           10          15
Asp Leu Gly Lys Arg Glu Pro Ala Ala Ala Asp Glu Arg Gly Thr
20          25          30
Gln Gln Arg Arg Ala Cys Ala Asn Ala Thr Trp Asn Ser Ile His Asn
35          40          45

```

Gly	Val	Ile	Ala	Val	Phe	Gln	Arg	Lys	Gly	Leu	Pro	Asp	Gln	Glu	Leu	50	55	60
Phe	Ser	Leu	Asn	Glu	Gly	Val	Arg	Gln	Leu	Leu	Lys	Thr	Glu	Leu	Gly	65	70	75
Ser	Phe	Phe	Thr	Glu	Tyr	Leu	Gln	Asn	Gln	Leu	Leu	Thr	Lys	Gly	Met	85	90	95
Val	Ile	Leu	Arg	Asp	Lys	Ile	Arg	Phe	Tyr	Glu	Gly	Gln	Lys	Leu	Leu	100	105	110
Asp	Ser	Leu	Ala	Glu	Thr	Trp	Asp	Phe	Phe	Phe	Ser	Asp	Val	Leu	Pro	115	120	125
Met	Leu	Gln	Ala	Ile	Phe	Tyr	Pro	Val	Gln	Gly	Lys	Glu	Pro	Ser	Val	130	135	140
Arg	Gln	Leu	Ala	Leu	Leu	His	Phe	Arg	Asn	Ala	Ile	Thr	Leu	Ser	Val	145	150	155
Lys	Leu	Glu	Asp	Ala	Leu	Ala	Arg	Ala	His	Ala	Arg	Val	Pro	Pro	Ala	165	170	175
Ile	Val	Gln	Met	Leu	Leu	Val	Leu	Gln	Gly	Val	His	Glu	Ser	Arg	Gly	180	185	190
Val	Thr	Glu	Asp	Tyr	Leu	Arg	Leu	Glu	Thr	Leu	Val	Gln	Lys	Val	Val	195	200	205
Ser	Pro	Tyr	Leu	Gly	Thr	Tyr	Gly	Leu	His	Ser	Ser	Glu	Gly	Pro	Phe	210	215	220
Thr	His	Ser	Cys	Ile	Leu	Glu	Leu	Gln	Arg	Asp	Lys	Ala	Ala	Ala	Ala	225	230	235
Ala	Val	Leu	Gly	Ala	Val	Arg	Lys	Arg	Pro	Ser	Val	Val	Pro	Met	Ala	245	250	255
Gly	Gln	Asp	Pro	Ala	Leu	Ser	Thr	Ser	His	Pro	Phe	Tyr	Asp	Val	Ala	260	265	270
Arg	His	Gly	Ile	Leu	Gln	Val	Ala	Gly	Asp	Asp	Arg	Phe	Gly	Arg	Arg	275	280	285
Val	Val	Thr	Phe	Ser	Cys	Cys	Arg	Met	Pro	Pro	Ser	His	Glu	Leu	Asp	290	295	300
His	Gln	Arg	Leu	Leu	Glu	Tyr	Leu	Lys	Tyr	Thr	Leu	Asp	Gln	Tyr	Val	305	310	315
Glu	Asn	Asp	Tyr	Thr	Ile	Val	Tyr	Phe	His	Tyr	Gly	Leu	Asn	Ser	Arg	325	330	335
Asn	Lys	Pro	Ser	Leu	Gly	Trp	Leu	Gln	Ser	Ala	Tyr	Lys	Glu	Phe	Asp	340	345	350
Arg	Lys	Asp	Gly	Asp	Leu	Thr	Met	Trp	Pro	Arg	Leu	Val	Ser	Asn	Ser	355	360	365
Lys	Leu	Lys	Arg	Ser	Ser	His	Leu	Ser	Leu	Pro	Lys	Tyr	Trp	Asp	Tyr	370	375	380
Arg	Tyr	Lys	Lys	Asn	Leu	Lys	Ala	Leu	Tyr	Val	Val	His	Pro	Thr	Ser	385	390	395
Phe	Ile	Lys	Val	Leu	Trp	Asn	Ile	Leu	Lys	Pro	Leu	Ile	Ser	His	Lys	405	410	415
Phe	Gly	Lys	Lys	Val	Ile	Tyr	Phe	Asn	Tyr	Leu	Ser	Glu	Leu	His	Glu	420	425	430
His	Leu	Lys	Tyr	Asp	Gln	Leu	Val	Ile	Pro	Pro	Glu	Val	Leu	Arg	Tyr	435	440	445
Asp	Glu	Lys	Leu	Gln	Ser	Leu	His	Glu	Gly	Arg	Thr	Pro	Pro	Pro	Thr	450	455	460
Lys	Thr	Pro	Pro	Pro	Arg	Pro	Pro	Leu	Pro	Thr	Gln	Gln	Phe	Gly	Val	465	470	475
Ser	Leu	Gln	Tyr	Leu	Lys	Asp	Lys	Asn	Gln	Gly	Glu	Leu	Ile	Pro	Pro	485	490	495
Val	Leu	Arg	Phe	Thr	Val	Thr	Tyr	Leu	Arg	Glu	Lys	Gly	Leu	Pro	Glu	500	505	510

His Asn Tyr Val Val Leu Arg Tyr Leu Met Gly Phe Leu His Ala Val  
 515 520 525  
 Ser Arg Glu Ser Ile Phe Asn Lys Met Asn Ser Ser Asn Leu Ala Cys  
 530 535 540  
 Val Phe Gly Leu Asn Leu Ile Trp Pro Ser Gln Gly Val Ser Ser Leu  
 545 550 555 560  
 Ser Ala Leu Val Pro Leu Asn Met Phe Thr Glu Leu Leu Ile Glu Tyr  
 565 570 575  
 Tyr Glu Lys Ile Phe Ser Thr Pro Glu Ala Pro Gly Glu His Gly Leu  
 580 585 590  
 Ala Pro Trp Glu Gln Gly Ser Arg Ala Ala Pro Leu Gln Glu Ala Val  
 595 600 605  
 Pro Arg Thr Gln Ala Thr Gly Leu Thr Lys Pro Thr Leu Pro Pro Ser  
 610 615 620  
 Pro Leu Met Ala Ala Arg Arg Arg Leu  
 625 630

<210> 24  
 <211> 1398  
 <212> DNA  
 <213> Homo sapiens

<400> 24  
 acgtccgggg aggggccagg tgagcggcag acccggcag caggtggggg ccggcggggg 60  
 cagtggccag agctgcagag agacaaggcg gcggcggctg ctgtgctggg tgcagtgagg 120  
 aagaggccct cgggtgtgcc catggctggc caggatcctg cgctgagcac gagtcacccg 180  
 ttctacgacg tggccagaca tggcattctg caggtggcag gggatgaccg ctttgggaaga 240  
 cgtgtttgtca cgttcagctg ctgccggatg ccaccctccc acgagctgga ccaccagcgg 300  
 ctgctggagt atttgaagta cacactggac caatacgttg agaacgatta taccatcgtc 360  
 tatttccact acgggctgaa cagccggaac aagccttccc tgggctggct ccagagcgca 420  
 tacaaggagt tcgataggaa agacggggat ctactatgt ggcccaggct ggtctcgaac 480  
 tccaagctca agcgatcctc ccacctcagc ctcccaaagt actgggatta caggtacaag 540  
 aagaacttga aggcctcta cgtggtgcac ccaccagct tcatcaaggc cctgtggaac 600  
 atcttgaagc ccctcatcag tcacaagttt gggaagaaag tcatctatct caactacctg 660  
 agtgagctcc acgaacacct taaatacgac cagctgggtc tccctccga agttttgcgg 720  
 tacgatgaga agctccagag cctgcacgag ggccggacgc cgcctccac caagacacca 780  
 ccgccgcggc ccccgctgcc cacacagcag tttggcgtca gtctgcaata cctcaaagac 840  
 aaaaatcaag gcgaactcat cccctctgtg ctgaggttca cagtgcgta cctgagagag 900  
 aaaggcctcc cagagcacia ctacgtcgtc ctccgctacc tcatgggctt cctgcatgcg 960  
 gtgtcccgga agagcatctt caacaaaatg aacagctcta acctggcctg tgtcttcggg 1020  
 ctgaatttga tctggccatc ccagggggtc tctccctga gtgccctgt gcccctgaac 1080  
 atgttactg aactgctgat cgagtactat gaaaagatct tcagcacccc ggaggcacct 1140  
 ggggagcacg gcctggcacc atgggaacag gggagcaggg cagcccttt gcaggaggct 1200  
 gtgccacgga cacaagccac gggcctcacc aagcctaccc tacctccgag tcccctgatg 1260  
 gcagccagaa gacgtctcta gtgttgca cactctgtat atttcgagct acctcccaca 1320  
 cctgtctgtg cacttgtatg ttttgtaaac ttggcatctg taaaaataac cagccattag 1380  
 atgaattcag aaccttct

<210> 25  
 <211> 379  
 <212> PRT  
 <213> Homo sapiens

<400> 25  
 Met Ala Gly Gln Asp Pro Ala Leu Ser Thr Ser His Pro Phe Tyr Asp  
 1 5 10 15  
 Val Ala Arg His Gly Ile Leu Gln Val Ala Gly Asp Asp Arg Phe Gly

		20					25			30			
Arg	Arg	Val	Val	Thr	Phe	Ser	Cys	Cys	Arg	Met	Pro	Pro	Ser
		35					40				45		
Leu	Asp	His	Gln	Arg	Leu	Leu	Glu	Tyr	Leu	Lys	Tyr	Thr	Leu
	50					55					60		
Tyr	Val	Glu	Asn	Asp	Tyr	Thr	Ile	Val	Tyr	Phe	His	Tyr	Gly
	65				70					75			80
Ser	Arg	Asn	Lys	Pro	Ser	Leu	Gly	Trp	Leu	Gln	Ser	Ala	Tyr
			85					90					95
Phe	Asp	Arg	Lys	Asp	Gly	Asp	Leu	Thr	Met	Trp	Pro	Arg	Leu
		100					105						110
Asn	Ser	Lys	Leu	Lys	Arg	Ser	Ser	His	Leu	Ser	Leu	Pro	Lys
	115						120					125	
Asp	Tyr	Arg	Tyr	Lys	Lys	Asn	Leu	Lys	Ala	Leu	Tyr	Val	Val
	130					135					140		
Thr	Ser	Phe	Ile	Lys	Val	Leu	Trp	Asn	Ile	Leu	Lys	Pro	Leu
	145			150					155				160
His	Lys	Phe	Gly	Lys	Lys	Val	Ile	Tyr	Phe	Asn	Tyr	Leu	Ser
			165					170					175
His	Glu	His	Leu	Lys	Tyr	Asp	Gln	Leu	Val	Ile	Pro	Pro	Glu
		180					185						190
Arg	Tyr	Asp	Glu	Lys	Leu	Gln	Ser	Leu	His	Glu	Gly	Arg	Thr
	195					200					205		
Pro	Thr	Lys	Thr	Pro	Pro	Pro	Arg	Pro	Pro	Leu	Pro	Thr	Gln
	210					215					220		
Gly	Val	Ser	Leu	Gln	Tyr	Leu	Lys	Asp	Lys	Asn	Gln	Gly	Glu
	225				230				235				240
Pro	Pro	Val	Leu	Arg	Phe	Thr	Val	Thr	Tyr	Leu	Arg	Glu	Lys
			245					250					255
Pro	Glu	His	Asn	Tyr	Val	Val	Leu	Arg	Tyr	Leu	Met	Gly	Phe
		260					265					270	
Ala	Val	Ser	Arg	Glu	Ser	Ile	Phe	Asn	Lys	Met	Asn	Ser	Ser
	275						280				285		
Ala	Cys	Val	Phe	Gly	Leu	Asn	Leu	Ile	Trp	Pro	Ser	Gln	Gly
	290					295				300			
Ser	Leu	Ser	Ala	Leu	Val	Pro	Leu	Asn	Met	Phe	Thr	Glu	Leu
	305				310					315			320
Glu	Tyr	Tyr	Glu	Lys	Ile	Phe	Ser	Thr	Pro	Glu	Ala	Pro	Gly
			325					330					335
Gly	Leu	Ala	Pro	Trp	Glu	Gln	Gly	Ser	Arg	Ala	Ala	Pro	Leu
		340					345					350	
Ala	Val	Pro	Arg	Thr	Gln	Ala	Thr	Gly	Leu	Thr	Lys	Pro	Thr
	355						360					365	
Pro	Ser	Pro	Leu	Met	Ala	Ala	Arg	Arg	Arg	Leu			
	370					375							

&lt;210&gt; 26

&lt;211&gt; 1787

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 26

```

atgaggactc tccgcagggt gaagttcatg agttcgccca gcctcagtga cctgggcaag 60
agagagccgg ccgccgccgc ggacgagcgg ggcacgcagc agcgccgggc ctgcgccaac 120
gccacctgga acagcatcca caacgggggtg atcgccgtct tccagcgcaa ggggctgccc 180
gaccaggagc tcttcagcct caacgagggc gtccggcagc tggtgaagac agagctgggg 240
tccttcttca cggagtacct gcagaaccag ctgctgacaa aaggcatggt gatccttcgg 300

```

```

gacaagattc gcttctatga gggacagaag ctgctggact cactggcaga gacctgggac 360
ttcttcttca gtgacgtgct gcccatgctg caggccatct tctaccoggt gcagggcaag 420
gagccatcgg tgcgccagct ggccctgctg cacttccgga atgccatcac cctcagtgtg 480
aagctagagg atgcgctggc ccgggcccat gcccggtgtc cccctgccat cgtgcagatg 540
ctgctgggtgc tgcagggggg acatgagtcc agggggcgtga ctgaggacta cctgcgcctg 600
gagacgctgg tccagaaggt ggtgtcgcca tacctgggca cctacggcct ccactccagc 660
gagggggcct tcacccattc ctgcatcctg gagctgcaga gagacaaggc ggcggcggct 720
gctgtgctgg gtgcagttag gaagaggccc tcgggtggtg ccatggctgg ccaggatcct 780
gcgctgagca cgagtcaccc gttctacgac gtggccagac atggcattct gcagggtggca 840
ggggatgacc gctttggaag acgtgttgct acgttcagct gctgccggat gccacctctc 900
cacgagctgg accaccagcg gctgctggag tacaagaaga acttgaaggc cctctacgtg 960
gtgcacccca ccagcttcat caaggtcctg tgaacatct tgaagcccct catcagtcac 1020
aagtttggga agaaagtcac ctatttcaac tacctgagtg agctccacga acaccttaaa 1080
tacgaccagc tgggtcatccc tcccgaagtt ttgcggtagc atgagaagct ccagagcctg 1140
cacgagggcc ggacgccgcc tcccaccaag acaccaccgc cgcgggcccc gctgcccaca 1200
cagcagtttg gcgtcagtct gcaatacctc aaagacaaaa atcaaggcga actcatcccc 1260
cctgtgctga ggttcacagt gacgtacctg agagagaaa cctcccagag cacaactacg 1320
tcgtcctccg ctacctcatg ggcttcctgc atgcggtgtc ccgggagagc atcttcaaca 1380
aaatgaacag ctctaacctg gcctgtgtct tcgggctgaa tttgatctgg ccatcccagg 1440
gggtctctct cctgagtgcc ctgtgcccc tgaacatggt cactgaactg ctgatcgagt 1500
actatgaaaa gatcttcagc accccggagg cacctgggga gcacggcctg gcaccatggg 1560
aacaggggag cagggcgagc cctttgcagg aggtctgtgc acggacacaa gccacgggcc 1620
tcaccaagcc taccctacct ccgagtcccc tgatggcagc cagaagacgt ctctagtgtt 1680
gcgaacactc tgtatatattc gagctacctc ccacacctgt ctgtgcactt gtatgttttg 1740
taaacttggc atctgtaaaa ataaccagcc attagatgaa ttcagaa 1787

```

&lt;210&gt; 27

&lt;211&gt; 461

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 27

```

Met Arg Thr Leu Arg Arg Leu Lys Phe Met Ser Ser Pro Ser Leu Ser
1          5          10          15
Asp Leu Gly Lys Arg Glu Pro Ala Ala Ala Asp Glu Arg Gly Thr
20          25          30
Gln Gln Arg Arg Ala Cys Ala Asn Ala Thr Trp Asn Ser Ile His Asn
35          40          45
Gly Val Ile Ala Val Phe Gln Arg Lys Gly Leu Pro Asp Gln Glu Leu
50          55          60
Phe Ser Leu Asn Glu Gly Val Arg Gln Leu Leu Lys Thr Glu Leu Gly
65          70          75          80
Ser Phe Phe Thr Glu Tyr Leu Gln Asn Gln Leu Leu Thr Lys Gly Met
85          90          95
Val Ile Leu Arg Asp Lys Ile Arg Phe Tyr Glu Gly Gln Lys Leu Leu
100          105          110
Asp Ser Leu Ala Glu Thr Trp Asp Phe Phe Phe Ser Asp Val Leu Pro
115          120          125
Met Leu Gln Ala Ile Phe Tyr Pro Val Gln Gly Lys Glu Pro Ser Val
130          135          140
Arg Gln Leu Ala Leu Leu His Phe Arg Asn Ala Ile Thr Leu Ser Val
145          150          155          160
Lys Leu Glu Asp Ala Leu Ala Arg Ala His Ala Arg Val Pro Pro Ala
165          170          175
Ile Val Gln Met Leu Leu Val Leu Gln Gly Val His Glu Ser Arg Gly
180          185          190
Val Thr Glu Asp Tyr Leu Arg Leu Glu Thr Leu Val Gln Lys Val Val
195          200          205

```

Ser Pro Tyr Leu Gly Thr Tyr Gly Leu His Ser Ser Glu Gly Pro Phe  
 210 215 220  
 Thr His Ser Cys Ile Leu Glu Leu Gln Arg Asp Lys Ala Ala Ala Ala  
 225 230 235 240  
 Ala Val Leu Gly Ala Val Arg Lys Arg Pro Ser Val Val Pro Met Ala  
 245 250 255  
 Gly Gln Asp Pro Ala Leu Ser Thr Ser His Pro Phe Tyr Asp Val Ala  
 260 265 270  
 Arg His Gly Ile Leu Gln Val Ala Gly Asp Asp Arg Phe Gly Arg Arg  
 275 280 285  
 Val Val Thr Phe Ser Cys Cys Arg Met Pro Pro Ser His Glu Leu Asp  
 290 295 300  
 His Gln Arg Leu Leu Glu Tyr Lys Lys Asn Leu Lys Ala Leu Tyr Val  
 305 310 315 320  
 Val His Pro Thr Ser Phe Ile Lys Val Leu Trp Asn Ile Leu Lys Pro  
 325 330 335  
 Leu Ile Ser His Lys Phe Gly Lys Lys Val Ile Tyr Phe Asn Tyr Leu  
 340 345 350  
 Ser Glu Leu His Glu His Leu Lys Tyr Asp Gln Leu Val Ile Pro Pro  
 355 360 365  
 Glu Val Leu Arg Tyr Asp Glu Lys Leu Gln Ser Leu His Glu Gly Arg  
 370 375 380  
 Thr Pro Pro Pro Thr Lys Thr Pro Pro Pro Arg Pro Pro Leu Pro Thr  
 385 390 395 400  
 Gln Gln Phe Gly Val Ser Leu Gln Tyr Leu Lys Asp Lys Asn Gln Gly  
 405 410 415  
 Glu Leu Ile Pro Pro Val Leu Arg Phe Thr Val Thr Tyr Leu Arg Glu  
 420 425 430  
 Lys Ala Ser Gln Ser Thr Thr Thr Ser Ser Ser Ala Thr Ser Trp Ala  
 435 440 445  
 Ser Cys Met Arg Cys Pro Gly Arg Ala Ser Ser Thr Lys  
 450 455 460

&lt;210&gt; 28

&lt;211&gt; 1176

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 28

acgtccgggg aggggccagg tgagcggcag acccggcacg cagggtggggg ccggcggggg 60  
 ccgtggccag agctgcagag agacaaggcg gcggcggctg ctgtgctggg tgcagtgagg 120  
 aagaggccct cgggtggtgcc catggctggc caggatcctg cgctgagcac gagtcacccg 180  
 ttctacgacg tggccagaca tggcattctg cagggtggcag gggatgaccg ctttgggaaga 240  
 cgtgttgtca cgttcagctg ctgccggatg ccaccctccc acgagctgga ccaccagcgg 300  
 ctgctggaca ggtacaagaa gaacttgaag gccctctacg tgggtgcaccc caccagcttc 360  
 atcaaggctc tgtggaacat cttgaagccc ctcatcagtc acaagtttgg gaagaaagtc 420  
 atctatttca actacctgag tgagctccac gaacacctta aatacgacca gctggtcatc 480  
 cctcccgaag ttttgcggtg cgatgagaag ctccagagcc tgcacgaggg ccggacgccc 540  
 cctcccacca agacaccacc gccgcggccc ccgctgccc aacagcagtt tggcgtcagt 600  
 ctgcaatacc tcaaagacaa aaatcaaggc gaactcatcc cccctgtgct gaggttcaca 660  
 gtgacgtacc tgagagagaa aggcctccca gagcacaact acgtcgtcct ccgctacctc 720  
 atgggcttcc tgcattgcgg gtcccgagg agcatcttca acaaaatgaa cagctctaac 780  
 ctggcctgtg tcttcgggct gaatttgatc tggccatccc aggggggtctc ctccctgagt 840  
 gccctgtgct cctgaacat gttcactgaa ctgctgatcg agtactatga aaagatcttc 900  
 agcaccccg aggcacctgg ggagcacggc ctggcaccat gggaacaggg gagcagggca 960  
 gcccttttgc agggaggtgt gccacggaca caagccacgg gcctcaccaa gcctacccta 1020  
 cctccgagtc ccctgatggc agccagaaga cgtctctagt gttgcgaaca ctctgtatat 1080



ttcgagctac ctccacacacc tgtctgtgca cttgtatggt ttgtaaactt ggcatctgta 1140  
 aaaataacca gccattagat gaattcagaa ctttct 1176

<210> 29  
 <211> 305  
 <212> PRT  
 <213> Homo sapiens

<400> 29  
 Met Ala Gly Gln Asp Pro Ala Leu Ser Thr Ser His Pro Phe Tyr Asp  
 1 5 10 15  
 Val Ala Arg His Gly Ile Leu Gln Val Ala Gly Asp Asp Arg Phe Gly  
 20 25 30  
 Arg Arg Val Val Thr Phe Ser Cys Cys Arg Met Pro Pro Ser His Glu  
 35 40 45  
 Leu Asp His Gln Arg Leu Leu Asp Arg Tyr Lys Lys Asn Leu Lys Ala  
 50 55 60  
 Leu Tyr Val Val His Pro Thr Ser Phe Ile Lys Val Leu Trp Asn Ile  
 65 70 75 80  
 Leu Lys Pro Leu Ile Ser His Lys Phe Gly Lys Lys Val Ile Tyr Phe  
 85 90 95  
 Asn Tyr Leu Ser Glu Leu His Glu His Leu Lys Tyr Asp Gln Leu Val  
 100 105 110  
 Ile Pro Pro Glu Val Leu Arg Tyr Asp Glu Lys Leu Gln Ser Leu His  
 115 120 125  
 Glu Gly Arg Thr Pro Pro Pro Thr Lys Thr Pro Pro Pro Arg Pro Pro  
 130 135 140  
 Leu Pro Thr Gln Gln Phe Gly Val Ser Leu Gln Tyr Leu Lys Asp Lys  
 145 150 155 160  
 Asn Gln Gly Glu Leu Ile Pro Pro Val Leu Arg Phe Thr Val Thr Tyr  
 165 170 175  
 Leu Arg Glu Lys Gly Leu Pro Glu His Asn Tyr Val Val Leu Arg Tyr  
 180 185 190  
 Leu Met Gly Phe Leu His Ala Val Ser Arg Glu Ser Ile Phe Asn Lys  
 195 200 205  
 Met Asn Ser Ser Asn Leu Ala Cys Val Phe Gly Leu Asn Leu Ile Trp  
 210 215 220  
 Pro Ser Gln Gly Val Ser Ser Leu Ser Ala Leu Val Pro Leu Asn Met  
 225 230 235 240  
 Phe Thr Glu Leu Leu Ile Glu Tyr Tyr Glu Lys Ile Phe Ser Thr Pro  
 245 250 255  
 Glu Ala Pro Gly Glu His Gly Leu Ala Pro Trp Glu Gln Gly Ser Arg  
 260 265 270  
 Ala Ala Pro Leu Gln Glu Ala Val Pro Arg Thr Gln Ala Thr Gly Leu  
 275 280 285  
 Thr Lys Pro Thr Leu Pro Pro Ser Pro Leu Met Ala Ala Arg Arg Arg  
 290 295 300  
 Leu  
 305

<210> 30  
 <211> 3257  
 <212> DNA  
 <213> Homo sapiens

<400> 30  
 atttccttct cccctttccc gccagcttcg catccatctc cccaccccg taacccctc 60

ctgcctccat	ccaccggggc	tatggccgca	gaagaggat	tgcagacggt	ggaccattat	120
aagactgaga	tagagaggct	aaccaaggag	ctcacggaga	ccaccacga	gaagatccag	180
gctgccgagt	acgggctggt	ggtgctggag	gagaagctga	ccctcaaaca	gcagtatgat	240
gaactggagg	ctgagtacga	cagcctcaaa	caggagctgg	agcagctcaa	agaggcattt	300
gggcagtcct	tctccatcca	ccggaagggt	gctgaagatg	gagagactcg	ggaggaaacg	360
cttctgcagg	agtcagcatc	gaaggaggct	tactatctgg	ggaagatctt	ggagatgcag	420
aacgagctga	aacagagccg	ggctgtggtc	actaatgtac	aggcagaaaa	cgagaggctc	480
accgcagtcg	tgcaggatct	gaaggagaac	aatgagatgg	tggagctaca	gagaatacgg	540
atgaaggatg	aaatccgaga	atataagttc	cgggaggcac	ggctccttca	ggactatact	600
gaattggaag	aagaaaaatat	cacattgcag	aaactagtgt	ccacgttgaa	gcagaaccag	660
gttgaatacg	aaggcttaaa	gcatgagatt	aagcgatttg	aggaggagac	ggtactgctg	720
aacagccagc	tggaagatgc	catccgattg	aaagagattg	ctgagcacca	actggaagaa	780
gccctcgaga	ctttaaaaa	tgaagagag	caaaagaaca	acctgcggaa	ggagctctcc	840
cagtatatca	gcctcaatga	taaccatac	agcatctcag	tagatggact	caaatttgcc	900
gaggatggga	gtgaaccaa	caatgatgac	aaaatgaacg	gtcatatcca	tgggcctctt	960
gtgaaactga	atggagacta	tccgactccc	accttaagga	aaggagagtc	tctgaaccct	1020
gtctctgact	tattcagtga	gctgaacatt	tcagaaatac	agaagttgaa	gcagcagctt	1080
atgcaggtag	agcgggaaaa	ggccattctt	ttggccaacc	tacaggagtc	acagacacag	1140
ctggaacaca	ccaagggggc	actgcaggag	cagcatgagc	gggtgcaccg	gctcacagag	1200
cacgtcaatg	ccatgagggg	cctgcaaagc	agcaaggagc	tcaaggctga	gctggacggg	1260
gagaagggcc	gggactcagg	ggaggaggcc	catgactatg	aggtggacat	caatggttta	1320
gagatccttg	aatgcaaata	caggggtggca	gtaactgagg	tgattgatct	gaaagctgaa	1380
attaaggcct	taaaggagaa	atataataaa	tctgtagaaa	actacactga	tgagaaggcc	1440
aagtatgaga	gtaaaaacca	gatgtatgat	gagcagggtga	caagccttga	gaagaccacc	1500
aaggagagtg	gtgagaagat	ggcccacatg	gagaaggagt	tgcaaaaagat	gaccagcata	1560
gccaacgaaa	atcacagtac	ccttaatacg	gccaggatg	agttagtgc	attcagtgcg	1620
gagttagctc	agctttacca	ccatgtgtgt	ctatgttaata	atgaaactcc	caacagggtc	1680
atgctggatt	actataggca	gagcagagtc	accgcagtg	gcagcctgaa	agggcccgat	1740
gatcccagag	gacttttgtc	cccacgatta	gccaggcggg	gtgtgtcatc	cccggtagaa	1800
acaaggacct	catctgaacc	agttgcaaaa	gaaagcacag	agcccagcaa	agaaccaagt	1860
ccaactaaga	ccccacaaat	ctctcctgtt	attactgccc	caccgtcatc	tccagtattg	1920
gatacaagtg	acatccgcaa	agagccaatg	aatatctaca	accttaatgc	cataatccgg	1980
gaccaaataca	agcatctgca	gaaagctgtg	gaccggctcct	tgcaactgtc	tcgtaaaaga	2040
gcagcagctc	gggagctagc	ccccatgatt	gataaagaca	aggaagcctt	aatggaagag	2100
atcctcaagc	taaagtccct	gctgagcacc	aaacgggagc	agatcgccac	attgagggcg	2160
gtgttgaaaag	ccaacaagca	gacagctgag	gtggcgctag	ctaactctca	gaacaaatat	2220
gaaaatgaaa	aagcaatggg	gactgaaacc	atgacgaagc	ttagaaatga	actgaaggct	2280
ttgaaagaag	atgctgcaac	cttctcatcc	ctgagaacaa	tgtttgcaac	aagatgtgat	2340
gaatatgtca	ccagtttgga	tgagatgcag	agacagttag	cagctgcaga	ggatgagaag	2400
aagactctga	acactttgtt	acgaatggct	atccagcaaa	aactcgccct	gaccagagg	2460
ctggaggact	tagagtttga	ccatgagcag	tcccgacgca	gcaaaggcaa	acttggaag	2520
agcaagatcg	gcagccctaa	agtaagtggg	gagycatcag	tcaccgtgcc	caccatagac	2580
acttacctcc	tgcatagtca	gggcccacag	acaccaaca	ttcgggtcag	cagtggcact	2640
cagaggaaaa	gacaattttc	accttccctt	tgtgatcaga	gccgtcccag	gacttcaggg	2700
gcttcctacc	tacagaattt	attaagagtt	ccccctgac	ccacctccac	agaatcattt	2760
cttctgaagg	gcccccttc	catgagtga	ttcatccaag	ggcaccggct	cagcaaggaa	2820
aaaagggttaa	ccgtggctcc	accagattgt	cagcagcctg	ctgcctccgt	accgccacag	2880
tgctcacaac	tagccgggag	gcaagactgc	ccaactgtca	gtcctgacac	agctctccct	2940
gaggagcagc	cacattccag	ctccagtg	gcccctctcc	actgtctctc	caagcctcct	3000
caccctagt	cttcatctcc	tgtggacgaa	catctgggg	ggaagttttg	tagccacaca	3060
caggatactg	cccaagatcc	agcgggtgtt	ttcttctcgg	ttgttagatg	tacaatttga	3120
ttaatgtcca	tcgtttttga	agacgagaaa	gttgagaaga	acacgaagca	cagaccctga	3180
tgtgataaaa	cattttgtgg	tttctctgag	tcacagataa	acttctgcca	tcaaatggct	3240
acagttcatt	taaattt					3257

&lt;210&gt; 31

&lt;211&gt; 975

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 31.

```

Met Ala Ala Glu Glu Val Leu Gln Thr Val Asp His Tyr Lys Thr Glu
 1          5          10          15
Ile Glu Arg Leu Thr Lys Glu Leu Thr Glu Thr Thr His Glu Lys Ile
 20          25          30
Gln Ala Ala Glu Tyr Gly Leu Val Val Leu Glu Glu Lys Leu Thr Leu
 35          40          45
Lys Gln Gln Tyr Asp Glu Leu Glu Ala Glu Tyr Asp Ser Leu Lys Gln
 50          55          60
Glu Leu Glu Gln Leu Lys Glu Ala Phe Gly Gln Ser Phe Ser Ile His
65          70          75          80
Arg Lys Val Ala Glu Asp Gly Glu Thr Arg Glu Glu Thr Leu Leu Gln
 85          90          95
Glu Ser Ala Ser Lys Glu Ala Tyr Tyr Leu Gly Lys Ile Leu Glu Met
100          105          110
Gln Asn Glu Leu Lys Gln Ser Arg Ala Val Val Thr Asn Val Gln Ala
115          120          125
Glu Asn Glu Arg Leu Thr Ala Val Val Gln Asp Leu Lys Glu Asn Asn
130          135          140
Glu Met Val Glu Leu Gln Arg Ile Arg Met Lys Asp Glu Ile Arg Glu
145          150          155          160
Tyr Lys Phe Arg Glu Ala Arg Leu Leu Gln Asp Tyr Thr Glu Leu Glu
165          170          175
Glu Glu Asn Ile Thr Leu Gln Lys Leu Val Ser Thr Leu Lys Gln Asn
180          185          190
Gln Val Glu Tyr Glu Gly Leu Lys His Glu Ile Lys Arg Phe Glu Glu
195          200          205
Glu Thr Val Leu Leu Asn Ser Gln Leu Glu Asp Ala Ile Arg Leu Lys
210          215          220
Glu Ile Ala Glu His Gln Leu Glu Glu Ala Leu Glu Thr Leu Lys Asn
225          230          235          240
Glu Arg Glu Gln Lys Asn Asn Leu Arg Lys Glu Leu Ser Gln Tyr Ile
245          250          255
Ser Leu Asn Asp Asn His Ile Ser Ile Ser Val Asp Gly Leu Lys Phe
260          265          270
Ala Glu Asp Gly Ser Glu Pro Asn Asn Asp Asp Lys Met Asn Gly His
275          280          285
Ile His Gly Pro Leu Val Lys Leu Asn Gly Asp Tyr Arg Thr Pro Thr
290          295          300
Leu Arg Lys Gly Glu Ser Leu Asn Pro Val Ser Asp Leu Phe Ser Glu
305          310          315          320
Leu Asn Ile Ser Glu Ile Gln Lys Leu Lys Gln Gln Leu Met Gln Val
325          330          335
Glu Arg Glu Lys Ala Ile Leu Leu Ala Asn Leu Gln Glu Ser Gln Thr
340          345          350
Gln Leu Glu His Thr Lys Gly Ala Leu Thr Glu Gln His Glu Arg Val
355          360          365
His Arg Leu Thr Glu His Val Asn Ala Met Arg Gly Leu Gln Ser Ser
370          375          380
Lys Glu Leu Lys Ala Glu Leu Asp Gly Glu Lys Gly Arg Asp Ser Gly
385          390          395          400
Glu Glu Ala His Asp Tyr Glu Val Asp Ile Asn Gly Leu Glu Ile Leu
405          410          415
Glu Cys Lys Tyr Arg Val Ala Val Thr Glu Val Ile Asp Leu Lys Ala
420          425          430
Glu Ile Lys Ala Leu Lys Glu Lys Tyr Asn Lys Ser Val Glu Asn Tyr

```

		435					440					445				
Thr	Asp	Glu	Lys	Ala	Lys	Tyr	Glu	Ser	Lys	Ile	Gln	Met	Tyr	Asp	Glu	
	450					455					460					
Gln	Val	Thr	Ser	Leu	Glu	Lys	Thr	Thr	Lys	Glu	Ser	Gly	Glu	Lys	Met	
465					470					475					480	
Ala	His	Met	Glu	Lys	Glu	Leu	Gln	Lys	Met	Thr	Ser	Ile	Ala	Asn	Glu	
				485					490					495		
Asn	His	Ser	Thr	Leu	Asn	Thr	Ala	Gln	Asp	Glu	Leu	Val	Thr	Phe	Ser	
			500				505					510				
Glu	Glu	Leu	Ala	Gln	Leu	Tyr	His	His	Val	Cys	Leu	Cys	Asn	Asn	Glu	
		515				520					525					
Thr	Pro	Asn	Arg	Val	Met	Leu	Asp	Tyr	Tyr	Arg	Gln	Ser	Arg	Val	Thr	
	530				535						540					
Arg	Ser	Gly	Ser	Leu	Lys	Gly	Pro	Asp	Asp	Pro	Arg	Gly	Leu	Leu	Ser	
545					550					555					560	
Pro	Arg	Leu	Ala	Arg	Arg	Gly	Val	Ser	Ser	Pro	Val	Glu	Thr	Arg	Thr	
				565					570					575		
Ser	Ser	Glu	Pro	Val	Ala	Lys	Glu	Ser	Thr	Glu	Pro	Ser	Lys	Glu	Pro	
			580				585					590				
Ser	Pro	Thr	Lys	Thr	Pro	Thr	Ile	Ser	Pro	Val	Ile	Thr	Ala	Pro	Pro	
		595				600						605				
Ser	Ser	Pro	Val	Leu	Asp	Thr	Ser	Asp	Ile	Arg	Lys	Glu	Pro	Met	Asn	
	610				615					620						
Ile	Tyr	Asn	Leu	Asn	Ala	Ile	Ile	Arg	Asp	Gln	Ile	Lys	His	Leu	Gln	
625				630						635					640	
Lys	Ala	Val	Asp	Arg	Ser	Leu	Gln	Leu	Ser	Arg	Gln	Arg	Ala	Ala	Ala	
				645					650					655		
Arg	Glu	Leu	Ala	Pro	Met	Ile	Asp	Lys	Asp	Lys	Glu	Ala	Leu	Met	Glu	
			660				665						670			
Glu	Ile	Leu	Lys	Leu	Lys	Ser	Leu	Leu	Ser	Thr	Lys	Arg	Glu	Gln	Ile	
		675				680						685				
Ala	Thr	Leu	Arg	Ala	Val	Leu	Lys	Ala	Asn	Lys	Gln	Thr	Ala	Glu	Val	
	690				695						700					
Ala	Leu	Ala	Asn	Leu	Lys	Asn	Lys	Tyr	Glu	Asn	Glu	Lys	Ala	Met	Val	
705				710						715					720	
Thr	Glu	Thr	Met	Thr	Lys	Leu	Arg	Asn	Glu	Leu	Lys	Ala	Leu	Lys	Glu	
				725					730					735		
Asp	Ala	Ala	Thr	Phe	Ser	Ser	Leu	Arg	Thr	Met	Phe	Ala	Thr	Arg	Cys	
			740					745					750			
Asp	Glu	Tyr	Val	Thr	Gln	Leu	Asp	Glu	Met	Gln	Arg	Gln	Leu	Ala	Ala	
		755				760						765				
Ala	Glu	Asp	Glu	Lys	Lys	Thr	Leu	Asn	Thr	Leu	Leu	Arg	Met	Ala	Ile	
	770				775							780				
Gln	Gln	Lys	Leu	Ala	Leu	Thr	Gln	Arg	Leu	Glu	Asp	Leu	Glu	Phe	Asp	
785				790												

	900		905		910
Glu Lys Arg	Leu Thr Val Ala Pro	Pro Asp Cys	Gln Gln Pro	Ala Ala	
	915	920	925		
Ser Val Pro	Pro Gln Cys Ser Gln	Leu Ala Gly	Arg Gln Asp	Cys Pro	
	930	935	940		
Thr Val Ser	Pro Asp Thr Ala Leu	Pro Glu Glu	Gln Pro His	Ser Ser	
	945	950	955	960	
Ser Gln Cys	Ala Pro Leu His Cys	Leu Ser Lys	Pro Pro His	Pro	
	965	970	975		

<210> 32  
 <211> 2717  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
 cagggttaacg ctgtcttgtg gacccgcact tcccacccga gacctctcac tgagcccgag 60  
 ccgcgcgcga catgagccac gggaagggaa ccgacatgct cccggagatc gccgcgcgcg 120  
 tgggcttcct ctccagcctc ctgaggaccc ggggctgcgt gagcgagcag aggccttaagg 180  
 tcttcagcgg ggcgctccag gaggcactca cagagcacta caaacaccac tggtttcccg 240  
 aaaagccgtc caagggctcc ggctaccgct gcattcgcat caaccacaag atggacccca 300  
 tcatcagcag ggtggccagc cagatcggac tcagccagcc ccagctgcac cagctgctgc 360  
 ccagcgagct gaccctgtgg gtggaccctc atgaggtgtc ctaccgcatt ggggaggacg 420  
 gctccatctg cgtcttgtac gaggaggccc cactggccgc ctctgtggg ctctcacct 480  
 gcaagaacca agtgctgctg ggccggagca gccctccaa gaactacgtg atggcagctc 540  
 ccagctaggc ccttccgccc ccgccctggg cgccgcctg ctcatgctgc cgtgacaaca 600  
 ggccaccaca tacctcaacc tggggaactg tattttttaa tgaagagcta tttatatata 660  
 ttattttttt ttaagaaagg aggaaaagaa accaaaagtt ttttttaaga aaaaaaatcc 720  
 ttcaagggag ctgcttgga gtggcctccc caggtgcctt tggagagaac tgttgctgc 780  
 ttgagtctgt gagccagtgt ctgcctatag gagggggagc tgttaggggg tagacctagc 840  
 caaggagaag tgggagacgt ttggctagca cccaggaag atgtgagagg gagcaagcaa 900  
 ggtagcaac tgtgaacaga gaggtcggga tttgccctgg gggaggaaga gaggccaagt 960  
 tcagagctct ctgtctcccc cagccagaca cctgcacccc tggctcctct attactcagg 1020  
 ggcattcatg cctggactta aacaatacta tgttatcttt tcttttattt ttctaattag 1080  
 gtcctgggca gagagtgaag aggcctctcc tgattcctac tgtcctaagc tgcttttctt 1140  
 gaaatcatga cttgtttcta attctaccct caggggcctg tagatgttgc tttccagcca 1200  
 ggaatctaa gctttgggtt ttctgagggg gggaggaggg aactggagggt tattgggggt 1260  
 aggatggaa ggaactctgc acaaaacctt tgctttgcta gtgctgcttt gtgtgtatgt 1320  
 gtggcaata atttgggggt gatttgcaat gaaatttttg gacccaaaga gtatccactg 1380  
 gggatgtttt ttggccaaaa ctcttctttt tggaaaccaca tgaaagtctt gatgtgctg 1440  
 ccatgatccc tttgagaggt ggctcaaaag ctacagggaa ctccaggtcc tttattactg 1500  
 ccttcttttc aaaagcaca ctctcctcta accctcccct ccccttccc ttctggtcgg 1560  
 gtcataagagc taccgatttt tctaggacaa gagttctcag tcaactgtgca atatgcccc 1620  
 tgggtcccag gagggtctgg aggaaaactg gctatcagaa cctcctgatg ccctgggtgg 1680  
 cttagggaac catctctcct gctctccttg ggatgatggc tggtagtgca gccttgcatg 1740  
 tattccttgg ctgaatggga gagtgcctcc tgttctgcaa gactacttgg tattcttgta 1800  
 gggccgacac taaataaaag ccaaaccttg ggcactgttt tttctccctg gtgctcagag 1860  
 cacctgtggg aaaggttgct gtctgtctca gtacaatcca aatttgtcgt agacttgtgc 1920  
 aatatatact gttgtgggtt ggagaaaagt ggaaagctac actgggaaga aactcccttc 1980  
 cttcaatttc tcagtacat tgatgagggg tcctcaaaag acctcgagtt tcccaaaccc 2040  
 aatcacctta agaaggacag ggctagggca tttggccagg atggccaccc tcctgctgtt 2100  
 gcccttagt gaggaatctt caccacactt cctctacccc caggttctcc tccccacagc 2160  
 cagtcccctt tcttgattt ctaaactgct caattttgac tcaaagggtgc tatttaccaa 2220  
 aactctccc taccattcc tgccagctct gcctccttt caactctcca cattttgtat 2280  
 tgccttccca gacctgttc cagcttttat tgcttttaag ttcaacttgg gccacagac 2340  
 ccaagagcta atttctggt ttgtgggttg aaacaaagct gtgaatcact gcaggctgtg 2400  
 ttcttgcac ttgtctgcaa acaggtccct gcctttttag aagcagcctc atgggtctcat 2460

```

gcttaatctt gtctctcttc tcttctttat gatgttcact ttaaaaaaca caaaaccct 2520
gagctggact gttgagcagg cctgtctctc ctattaagta aaaataaata gtagtagtat 2580
gtttgtaagc tattctgaca gaaaagacaa aggttactaa ttgtatgata gtgtttttat 2640
atggaagaat gtacagctta tggacaaatg tacacctttt tgttacttta ataaaaatgt 2700
agtaggataa aaaaaaa 2717

```

&lt;210&gt; 33

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 33

```

Met Ser His Gly Lys Gly Thr Asp Met Leu Pro Glu Ile Ala Ala Ala
 1          5          10          15
Val Gly Phe Leu Ser Ser Leu Leu Arg Thr Arg Gly Cys Val Ser Glu
      20          25          30
Gln Arg Leu Lys Val Phe Ser Gly Ala Leu Gln Glu Ala Leu Thr Glu
      35          40          45
His Tyr Lys His His Trp Phe Pro Glu Lys Pro Ser Lys Gly Ser Gly
      50          55          60
Tyr Arg Cys Ile Arg Ile Asn His Lys Met Asp Pro Ile Ile Ser Arg
      65          70          75          80
Val Ala Ser Gln Ile Gly Leu Ser Gln Pro Gln Leu His Gln Leu Leu
      85          90          95
Pro Ser Glu Leu Thr Leu Trp Val Asp Pro Tyr Glu Val Ser Tyr Arg
      100          105          110
Ile Gly Glu Asp Gly Ser Ile Cys Val Leu Tyr Glu Glu Ala Pro Leu
      115          120          125
Ala Ala Ser Cys Gly Leu Leu Thr Cys Lys Asn Gln Val Leu Leu Gly
      130          135          140
Arg Ser Ser Pro Ser Lys Asn Tyr Val Met Ala Val Ser Ser
      145          150          155

```

&lt;210&gt; 34

&lt;211&gt; 5471

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 34

```

acagcttgca aactcggca tcttttctgg aggcgcctcc ttcagcagcc gcagatggca 60
tcgggtgctg ggctcggggc tcgcaattga ttctccccct tgcccacctc gattccaagg 120
acgcacctct ccttccccct cctcccttgc cgttctctgg tctgagccca gctcgcgacc 180
gccgggcaga ggatcagtcg cggcgccgca ggctgagcag cagcgctctc gctccctgac 240
ctggggagaa gcgcccaccc gggagagctg atccccggct gcctccagcg cccccacact 300
tttgacttcc aagccggggg ctccagagac cccgctcccc aggcgcact atgctggacc 360
cttcgtccag cgaagaagaa tcggatgaga tcgtggagga ggagagcggc aaggaggtgc 420
tcggctcggc ccgctccggc gcgcgcctgt ctcccagccg taccagcgag ggctcggccg 480
gcagcgccgg gctggggggc ggcggcgccg gcgcccggag cggggtgggt gcaggcggcg 540
gcgggggcaag cggcgcgagc agcggcgccg gggccggggg gctgcaaccc agcagcccg 600
ctggcgccgg ccggccctcc agccccagcc cgtcgggtgt gagcgagaag gagaaggaag 660
agtggagcgg gctgcagaaa gaggaggagg agaggaagaa gaggctgcag ctgtatgtgt 720
tcgtgatgct ctgcatcgcc taccctttta atgccaagca gccaccgac atggctcgcc 780
ggcagcagaa gatcagcaaa cagcagctgc agacagtcaa ggaccgggtt caggctttcc 840
tcaattggga aaccagatc atggctgacg aagccttcat gaacgctgtg cagagttact 900
atgaggtggt cctgaagagc gaccgtgtgg cccgcatggt tcagagtggg ggctgttccg 960
ccaacgactc ccgggaggtc ttcaagaagc acattgagaa gagagtgcgc agcctgcctg 1020
agattgacgg cctcagcaag gagactgtgc tgagctcctg gatggccaaa tttgatgcc 1080

```

tctaccgtgg	agaagaggac	ccgcggaagc	agcaggcccg	gatgacagcc	agcgagcct	1140
ccgagctgat	tctgagcaag	gagcaactct	atgagatggt	ccagaacatt	cttgggatca	1200
agaagttcga	acatcagctc	ctttacaatg	cctgccagct	ggacaatcca	gatgagcaag	1260
cagcccagat	cagacgagag	ctggatggac	gtctacaaat	ggcagaccaa	atagccaggg	1320
aacgcaaatt	tcccaagttt	gtatccaaag	aaatggaaaa	catgtacatt	gaggagctga	1380
agtcattctgt	caacctgctc	atggccaact	tggagagcat	gccggtatcc	aaaggcgggg	1440
agttcaagct	ccagaaaactc	aaacgcagcc	acaatgcttc	catcatcgac	atgggcgagg	1500
agagtggaa	ccagctctcc	aagtcagatg	tcgtgctgtc	tttctcattg	gaggtggtaa	1560
ttatggaagt	ccaaggcctc	aaatctttgg	ctccaaatcg	catcgtatat	tgcacaatgg	1620
aggtggaagg	aggagagaaa	ctacagactg	atcaggccga	ggcttctaaa	ccaacctggg	1680
gcacccaggg	tgacttctcc	acaacccatg	cactgccagc	tgtgaagggtg	aagctgttca	1740
cagagagcac	aggcgtcctg	gcgttggagg	acaaggagct	tgggcggggtt	attctccatc	1800
ccaccccgaa	cagccccaaa	cagtcagagt	ggcacaaaat	gacagtctcc	aaaaactgcc	1860
ccgaccaaga	tctcaaaatc	aaacttgctg	tccgaatgga	taagcctcaa	aacatgaagc	1920
attctgggta	tttatgggcc	atcggttaaga	atgtctggaa	gagatggaag	aaaaggtttt	1980
ttgtattggt	gcaggtcagt	cagtacacgt	ttgccatgtg	cagttatcgg	gagaagaaaag	2040
cggagcctca	ggaacttcta	caattggatg	gctacactgt	ggattacacc	gacccccagc	2100
caggtttgga	gggtggccga	gccttcttca	atgctgtcaa	ggaggagagc	accgtgatat	2160
ttgccagtga	cgatgaacaa	gaccgcaccc	tgtgggtcca	ggccatgtat	cggggccacgg	2220
ggcagctaca	caagcctgtg	ccccgacccc	aagtcacaga	actcaacgcc	aaggagggaa	2280
atgtacctca	gctggatgcc	cctatctctc	aattttacgc	agatagagct	caaaaacatg	2340
gcatggatga	atttatctct	tccaaccctc	gtaactttga	ccacgcttcc	ctctttgaga	2400
tggtacaacg	ccttactttg	gatacagac	ttaatgattc	ctattcttgc	ctgggctggg	2460
tcagtcctgg	ccaggtgttt	gtactagacg	agtattgcgc	ccgaaatgga	gtccgggggt	2520
gtcacccgaca	tctctgctac	ctcagagact	tgcttgaacg	ggcagaaaat	ggcgccatga	2580
tcgacccccac	ccttcttcac	tacagctttg	ccttctgtgc	atcccatgtc	catgggaaca	2640
ggcctgatgg	aattggaact	gtgactgttg	aagaaaagga	acgttttgaa	gaaatcaaag	2700
agaggtcccg	agttctgcta	gaaaatcaga	ttacacattt	taggtattgc	tttccatttg	2760
gtcgacctga	aggtgcclttg	aaagctactc	tctcactctt	ggaaagggtt	ttgatgaaag	2820
atattgttac	cccagtgcca	caagaggagg	taaaaacagt	tatccgtaaa	tgtctggaac	2880
aggctgcgtt	agtcaactat	tctcggtctc	cagagtatgc	caaaatcgaa	gagaatcaaa	2940
aggatgcaga	aaatgtaggc	cggttaatca	ctcctgccaa	aaagcttgaa	gatacaatac	3000
gtcttgctga	actagtcatt	gaagttcttc	agcaaaatga	ggagcaccac	gcagagccac	3060
atgttgataa	aggagaagcc	tttgcggtgt	ggtcagattt	aatggtggag	catgcggaga	3120
cgttcctgtc	actctttgca	gtagacatgg	atgcagcctt	agaggtgcaa	cctccagaca	3180
catgggacag	ttttccacta	tttcagctgc	tgaatgattt	tctccgtact	gactataatt	3240
tgtgcaattg	aaaatttcac	aaacacctgc	aagacctgtt	tgccccactt	gttggttagat	3300
atgtggtatc	gatggagtc	tcaattgcac	aatccattca	caggggcttt	gagcgggagt	3360
catgggaacc	agtcaagagt	ttaaccagta	acctacccaa	tgtgaacctc	cccaatgtga	3420
accttcccaa	agtaccaa	ctaccagtta	acatccctct	aggcatccca	caaatgccta	3480
ctttttcggc	accgtcatgg	atggctgcta	tatatgatgc	ggataatggg	tcaggcacct	3540
cagaagatct	gttttggaag	cttgacgccc	ttcagacctt	cattcgggac	ctgactggc	3600
ctgaagaaga	gttttggaag	cacctggaac	aacggctgaa	gttgatggca	agtgacatga	3660
tcgaatcttg	tgtcaaaaga	accaggattg	catttgaaagt	taagctgcaa	aaaaccagtc	3720
gatcaacaga	ttttcgagtc	ccacagtcaa	tatgcaccat	gtttaatggt	atggttgatg	3780
ccaaagctca	atcaacaaaa	ctttgcagca	tggaaatggg	ccaagagcat	caataccatt	3840
caaaaataga	cgaactaatt	gaagaaactg	ttaaagaaat	gataaacactc	ttggttgcaa	3900
agttcggttac	tatcttgga	ggagtgcgtg	caaaattatc	cagatatgac	gaagggactt	3960
tgttttcttc	ttttctgtca	tttaccgtga	aggcagcttc	caaatatgtg	gatgtacctc	4020
aacccgggat	ggacgtggcc	gacgcctacg	tgaacttctg	ccgccattct	caggatgtcc	4080
tgcgtgataa	ggtcaatgag	gagatgtaca	tagaaagggt	atttgatcaa	tggtacaaca	4140
gctccatgaa	cgtgatctgc	acctggttga	cggaccggat	ggacttacag	cttcatattt	4200
atcagttgaa	aacactaatt	agggtggtaa	agaaaacctc	cagagatttc	cgattgcaag	4260
gggtcctgga	ctccacctta	aacagcaaga	cctatgaaac	gatccggaac	cgtctcactg	4320
tggaggaagc	cacagcatca	gtgagtgaag	gtgggggact	gcagggcac	agcatgaagg	4380
acagcgcgaa	ggaagacgaa	gaagacgatt	agaccatttg	gtcctagagt	ctgctgggac	4440
agagtcctgt	aatcagtgca	tgtccttagt	ctgttagtta	aaccatttag	gaattttctg	4500
tcaactacca	tgcccatgag	atgtttatca	atacaactgc	catttttagct	atgtggtacc	4560

```

aagattagca aatgaccttc atatccactg atttcctgat gtccatgtct atatgtttac 4620
aagcaatatg gagcaccatt ctttaataac tgttcacatga gaatacatag tctaaccact 4680
aggcgtgtcc ctgttatcag caaagatcaa tgatgcttca ttcacgtact atgtatgcat 4740
tggtggtaaa tggatgtgag ggcaagtaca tcaagtacat tcactctgtt tcacgtatgt 4800
ggatgccagt taattaaatg agtacgtaaa taaattaatt aaaacacata gatctgcttt 4860
gtgtttttat ttttattttt tgaaaaacaa aaggcaagtc tccaacaatt aacttttgat 4920
gctttctgtt cccctaaaac caaaaaatga accccttggt tcgttggtta cccatccttt 4980
catttactca tataattagc caaaaaaaaa aggatggcta cataccaatg gattgattct 5040
cttaattgcc acggcaaggg ggcgatccta tcatgactta acatcaagcg cgcagttcaa 5100
aactactgtc ttctgtcaaa gttttctcct cttaaagtgt attttgcttt tacgtctcaa 5160
ctgtgtatgt aaaaaaaacg aatattttaa ttacaaccct agactaaaaa tgtgtttata 5220
ataagatgtg gatatttcct tcagtagatt gtaaccataa tttaaattat tttgttccac 5280
actgtttttt atatctgtca tgtacattgc attttgatct gtaactgcac aaccctgggg 5340
tttgctgcag agctattttt ttccatgtaa agtagtggat ccatcttgct tttgccttat 5400
ataaagccta cagttatgga agtgtggaaa actgtggctt ctcaataaat attcagatgt 5460
cctaagaata t                                     5471

```

&lt;210&gt; 35

&lt;211&gt; 1390

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 35

```

Pro Gly Glu Lys Arg Pro Pro Gly Arg Ala Asp Pro Arg Leu Pro Pro
1          5          10          15
Ala Pro Pro Thr Phe Cys Thr Pro Ser Arg Gly Leu Gln Arg Pro Arg
20          25          30
Ser Pro Gly Ala Thr Met Leu Asp Pro Ser Ser Ser Glu Glu Glu Ser
35          40          45
Asp Glu Ile Val Glu Glu Glu Ser Gly Lys Glu Val Leu Gly Ser Ala
50          55          60
Pro Ser Gly Ala Arg Leu Ser Pro Ser Arg Thr Ser Glu Gly Ser Ala
65          70          75          80
Gly Ser Ala Gly Leu Gly Gly Gly Gly Ala Gly Ala Gly Ala Gly Val
85          90          95
Gly Ala Gly Gly Gly Gly Gly Ser Gly Ala Ser Ser Gly Gly Gly Ala
100         105         110
Gly Gly Leu Gln Pro Ser Ser Arg Ala Gly Gly Gly Arg Pro Ser Ser
115         120         125
Pro Ser Pro Ser Val Val Ser Glu Lys Glu Lys Glu Glu Leu Glu Arg
130         135         140
Leu Gln Lys Glu Glu Glu Glu Arg Lys Lys Arg Leu Gln Leu Tyr Val
145         150         155         160
Phe Val Met Arg Cys Ile Ala Tyr Pro Phe Asn Ala Lys Gln Pro Thr
165         170         175
Asp Met Ala Arg Arg Gln Gln Lys Ile Ser Lys Gln Gln Leu Gln Thr
180         185         190
Val Lys Asp Arg Phe Gln Ala Phe Leu Asn Gly Glu Thr Gln Ile Met
195         200         205
Ala Asp Glu Ala Phe Met Asn Ala Val Gln Ser Tyr Tyr Glu Val Phe
210         215         220
Leu Lys Ser Asp Arg Val Ala Arg Met Val Gln Ser Gly Gly Cys Ser
225         230         235
Ala Asn Asp Ser Arg Glu Val Phe Lys Lys His Ile Glu Lys Arg Val
245         250         255
Arg Ser Leu Pro Glu Ile Asp Gly Leu Ser Lys Glu Thr Val Leu Ser
260         265         270
Ser Trp Met Ala Lys Phe Asp Ala Ile Tyr Arg Gly Glu Glu Asp Pro

```



275	280	285
Arg Lys Gln Gln Ala Arg Met Thr Ala Ser Ala Ala Ser Glu Leu Ile		
290	295	300
Leu Ser Lys Glu Gln Leu Tyr Glu Met Phe Gln Asn Ile Leu Gly Ile		
305	310	315
Lys Lys Phe Glu His Gln Leu Leu Tyr Asn Ala Cys Gln Leu Asp Asn		
	325	330
Pro Asp Glu Gln Ala Ala Gln Ile Arg Arg Glu Leu Asp Gly Arg Leu		
	340	345
Gln Met Ala Asp Gln Ile Ala Arg Glu Arg Lys Phe Pro Lys Phe Val		
	355	360
Ser Lys Glu Met Glu Asn Met Tyr Ile Glu Glu Leu Lys Ser Ser Val		
	370	375
Asn Leu Leu Met Ala Asn Leu Glu Ser Met Pro Val Ser Lys Gly Gly		
	385	390
Glu Phe Lys Leu Gln Lys Leu Lys Arg Ser His Asn Ala Ser Ile Ile		
	405	410
Asp Met Gly Glu Glu Ser Glu Asn Gln Leu Ser Lys Ser Asp Val Val		
	420	425
Leu Ser Phe Ser Leu Glu Val Val Ile Met Glu Val Gln Gly Leu Lys		
	435	440
Ser Leu Ala Pro Asn Arg Ile Val Tyr Cys Thr Met Glu Val Glu Gly		
	450	455
Gly Glu Lys Leu Gln Thr Asp Gln Ala Glu Ala Ser Lys Pro Thr Trp		
	465	470
Gly Thr Gln Gly Asp Phe Ser Thr Thr His Ala Leu Pro Ala Val Lys		
	485	490
Val Lys Leu Phe Thr Glu Ser Thr Gly Val Leu Ala Leu Glu Asp Lys		
	500	505
Glu Leu Gly Arg Val Ile Leu His Pro Thr Pro Asn Ser Pro Lys Gln		
	515	520
Ser Glu Trp His Lys Met Thr Val Ser Lys Asn Cys Pro Asp Gln Asp		
	530	535
Leu Lys Ile Lys Leu Ala Val Arg Met Asp Lys Pro Gln Asn Met Lys		
	545	550
His Ser Gly Tyr Leu Trp Ala Ile Gly Lys Asn Val Trp Lys Arg Trp		
	565	570
Lys Lys Arg Phe Phe Val Leu Val Gln Val Ser Gln Tyr Thr Phe Ala		
	580	585
Met Cys Ser Tyr Arg Glu Lys Lys Ala Glu Pro Gln Glu Leu Leu Gln		
	595	600
Leu Asp Gly Tyr Thr Val Asp Tyr Thr Asp Pro Gln Pro Gly Leu Glu		
	610	615
Gly Gly Arg Ala Phe Phe Asn Ala Val Lys Glu Gly Asp Thr Val Ile		
	625	630
Phe Ala Ser Asp Asp Glu Gln Asp Arg Ile Leu Trp Val Gln Ala Met		
	645	650
Tyr Arg Ala Thr Gly Gln Ser His Lys Pro Val Pro Pro Thr Gln Val		
	660	665
Gln Lys Leu Asn Ala Lys Gly Gly Asn Val Pro Gln Leu Asp Ala Pro		
	675	680
Ile Ser Gln Phe Tyr Ala Asp Arg Ala Gln Lys His Gly Met Asp Glu		
	690	695
Phe Ile Ser Ser Asn Pro Cys Asn Phe Asp His Ala Ser Leu Phe Glu		
	705	710
Met Val Gln Arg Leu Thr Leu Asp His Arg Leu Asn Asp Ser Tyr Ser		
	725	730
Cys Leu Gly Trp Phe Ser Pro Gly Gln Val Phe Val Leu Asp Glu Tyr		
	735	



	1205	1210	1215
Leu Leu Val	Ala Lys Phe Val Thr	Ile Leu Glu Gly Val	Leu Ala Lys
	1220	1225	1230
Leu Ser Arg	Tyr Asp Glu Gly Thr	Leu Phe Ser Ser Phe	Leu Ser Phe
	1235	1240	1245
Thr Val Lys	Ala Ala Ser Lys Tyr Val	Asp Val Pro Lys	Pro Gly Met
	1250	1255	1260
Asp Val Ala	Asp Ala Tyr Val Thr	Phe Val Arg His Ser	Gln Asp Val
	1265	1270	1275
Leu Arg Asp	Lys Val Asn Glu Glu Met	Tyr Ile Glu Arg	Leu Phe Asp
	1285	1290	1295
Gln Trp Tyr	Asn Ser Ser Met Asn Val	Ile Cys Thr Trp	Leu Thr Asp
	1300	1305	1310
Arg Met Asp	Leu Gln Leu His Ile Tyr	Gln Leu Lys Thr	Leu Ile Arg
	1315	1320	1325
Val Val Lys	Lys Thr Tyr Arg Asp	Phe Arg Leu Gln	Gly Val Leu Asp
	1330	1335	1340
Ser Thr Leu	Asn Ser Lys Thr Tyr Glu	Thr Ile Arg Asn	Arg Leu Thr
	1345	1350	1355
Val Glu Glu	Ala Thr Ala Ser Val Ser	Glu Gly Gly Gly	Leu Gln Gly
	1365	1370	1375
Ile Ser Met	Lys Asp Ser Asp Glu	Glu Asp Glu Glu	Asp Asp
	1380	1385	1390

&lt;210&gt; 36

&lt;211&gt; 4828

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

```

agtggcgctcg gaactgcaaa gcacctgtga gcttgcgga gtcagttcag actccagccc 60
gctccagccc ggcccgaacc gaccgcaccc ggcgcctgcc ctgcctcggc gtcccgggcc 120
agccatgggc ccttgagacc gcagcctctc ggcgctgctg ctgctgctgc aggtctcctc 180
ttggctctgc caggagccgg agccctgcca ccctggcttt gacgccgaga gctacacgtt 240
cacggtgccc cggcgccacc tggagagagg ccgcgtcctg ggcagagtga attttgaaga 300
ttgcaccggt cgacaaagga cagcctattt ttccctcgac acccgattca aagtgggcac 360
agatgggtgtg attacagtca aaaggcctct acggtttcat aaccacaga tccatttctt 420
gggtctacgcc tgggactcca cctacagaaa gttttccacc aaagtcacgc tgaatacagt 480
ggggcaccac caccgcccc cgccccatca ggctcctgtt tctggaatcc aagcagaatt 540
gctcacattt cccaactcct ctcttgccct cagaagacag aagagagact gggttattcc 600
tcccatcagc tgcccagaaa atgaaaaagg cccatttcct aaaaacctgg ttcagatcaa 660
atccaacaaa gacaaagaag gcaaggtttt ctacagcatc actggccaag gagctgacac 720
acccctgtt ggtgtcttta ttattgaaag agaaacagga tggctgaagg tgacagagcc 780
tctggataga gaacgcattg ccacatacac tctcttctct cagctgtgt catccaacgg 840
gaatgcagtt gaggatccaa tggagatttt gatcacggt accgatcaga atgacaacaa 900
gccgaattc acccaggagg tctttaaggg gtctgtcatg gaaggtgctc ttccaggaac 960
ctctgtgatg gaggtcacag ccacagacgc ggacgatgat gtgaacacct acaatgccgc 1020
catcgcttac accatcctca gccaatcc tgagctccct gacaaaaata tgttcaccat 1080
taacaggaac acaggagtca tcagtgtggt caccactggg ctggaccgag agagtttccc 1140
tacgtatacc ctggtggttc aagctgctga ccttcaagg gaggggttaa gcacaacagc 1200
aacagctgtg atcacagtca ctgacaccaa cgataatcct ccgatcttca atcccaccac 1260
gtacaagggt caggtgcctg agaacgaggc taacgtcgta atcaccacac tgaaagtgac 1320
tgatgctgat gcccacaata cccagcgtg ggaggctgta tacaccatat tgaatgatga 1380
tggtggacaa ttgtctgca ccacaaatcc agtgaacaac gatggcattt tgaaaacagc 1440
aaagggcttg gattttgagg ccaagcagca gtacattcta cacagccacc gtcaccgtgg 1500
ggtacctttt gaggtctctc tcaccacctc cacagccacc gtcaccgtgg atgtgctgga 1560
tgtgaatgaa gcccacatct ttgtgcctcc tgaaaagaga gtggaagtgt ccgaggactt 1620

```

tgccgtgggc	caggaaatca	catcctacac	tgcccaggag	ccagacacat	ttatggaaca	1680
gaaaataaca	tatcggattt	ggagagacac	tgccaactgg	ctggagatta	atccggacac	1740
tggtgccatt	tccactcggg	ctgagctgga	cagggaggat	tttgagcacg	tgaagaacag	1800
cacgtacaca	gccctaata	tagctacaga	caatggttct	ccagttgcta	ctggaacagg	1860
gacacttctg	ctgatcctgt	ctgatgtgaa	tgacaacgcc	cccataccag	aacctcgaac	1920
tatattcttc	tgtgagagga	atccaaagcc	tcaggtcata	aacatcattg	atgcagacct	1980
tcctcccaat	acatctccct	tcacagcaga	actaacacac	ggggcgagtg	ccaactggac	2040
cattcagtac	aacgacccaa	cccaagaatc	tatcattttg	aagccaaaga	tggccttaga	2100
ggtgggtgac	tacaaaatca	atctcaagct	catggataac	cagaataaag	accaagtga	2160
caccttagag	gtcagcgtgt	gtgactgtga	aggggcccgc	ggcgtctgta	ggaaggcaca	2220
gcctgtcgaa	gcaggattgc	aaattcctgc	cattctgggg	attcttggag	gaattcttgc	2280
tttgctaatt	ctgattctgc	tgctcttgct	gtttcttcgg	aggagagcgg	tggcctaaag	2340
gcccttactg	ccccagagg	atgacacccg	ggacaacgtt	tattactatg	atgaagaagg	2400
aggcgagaa	gaggaccagg	actttgactt	gagccagctg	cacaggggcc	tggacgctcg	2460
gcctgaagtg	actcgtaacg	acgttgcacc	aacctcatg	agtgtcccc	ggtatcttcc	2520
ccgccctgcc	aatcccgatg	aaattggaaa	ttttattgat	gaaaatctga	aagcggctga	2580
tactgacccc	acagccccgc	cttatgatcc	tctgctcgtg	tttgactatg	aaggaagcgg	2640
ttccgaagct	gctagtctga	gctccctgaa	ctcctcagag	tcagacaaag	accaggacta	2700
tgactacttg	aacgaatggg	gcaatcgctt	caagaagctg	gctgacatgt	acggaggcgg	2760
cgaggacgac	taggggactc	gagagaggcg	ggccccagac	ccatgtgctg	ggaaatgcag	2820
aaatcacgtt	gctgggtggt	tttcagctcc	cttcccttga	gatgagtttc	tggggaaaaa	2880
aaagagactg	gttagtgatg	cagttagtag	agctttatac	tctctccact	ttatagctct	2940
aataagtttg	tgttagaaaa	gtttcgactt	atcttctaaa	gctttttttt	ttttcccatc	3000
actctttaca	tgggtggtgat	gtccaaaaga	tacccaaatt	ttaatatatt	agaagaacaa	3060
ctttagcatc	agaaggttca	cccagcacct	tgcagatttt	cttaaggaat	tttgtctcac	3120
ttttaaaaaa	aaggggagaa	gtcagctact	ctagttctgt	tgttttgtgt	atataatttt	3180
ttaaaaaaaa	tttgtgtgct	tctgctcatt	actacactgg	tgtgtccctc	tgcccttttt	3240
ttttttttta	agacagggtc	tcattctatc	ggccaggctg	gagtgcagtg	gtgcaatcac	3300
agctcactgc	agccttgctc	tcccaggctc	aagctatcct	tgacacctag	cctcccaagt	3360
agctgggacc	acaggcatgc	accactacgc	atgactaatt	ttttaaatat	ttgagacggg	3420
gtctccctgt	gttaccacag	ctgggtctca	actcctgggc	tcaagtgatc	ctcccatctt	3480
ggcctcccag	agtattggga	ttacagacat	gagccactgc	acctgccag	ctccccaact	3540
ccctgccatt	ttttaagaga	cagtttctgt	ccatcgccca	ggcctgggat	gcagtgatgt	3600
gatcatagct	cactgtaacc	tcaaactctg	gggtctcaag	agttctccca	ccagcctcct	3660
ttttattttt	ttgtacagat	gggtcttgc	tatgttgccc	aagctggtct	taaactcctg	3720
gctcaagca	atccttctgc	cttggccccc	caaagtgtcg	ggattgtggg	catgagctgc	3780
tgtgccagc	ctccatgttt	taatatcaac	tctcactcct	gaattcagtt	gctttgcccc	3840
agataggagt	tctctgatgc	agaaattatt	gggtcttttt	agggtaagaa	gtttgtgtct	3900
ttgtctggcc	acatcttgac	taggtattgt	ctactctgaa	gacctttaat	ggcttccctc	3960
tttcatctcc	tgagtatgta	acttgcaatg	ggcagctatc	cagtgacttg	ttctgagtaa	4020
gtgtgttcat	taatgtttat	ttagctctga	agcaagagtg	atatactcca	ggacttagaa	4080
tagtgccata	agtgtctcag	ccaaagacag	agcggaacta	tgaaaagtgg	gcttggagat	4140
ggcaggagag	cttgtcattg	agcctggcaa	tttagcaaac	tgatgctgag	gatgattgag	4200
gtgggtctac	ctcatctctg	aaaattctgg	aaggaatgga	ggagtctcaa	catgtgtttc	4260
tgacacaaga	tccgtggttt	gtactcaaag	cccagaatcc	ccaagtgcct	gcttttgatg	4320
atgtctacag	aaaatgcttg	ctgagctgaa	cacatttgcc	caattccagg	tgtgcacaga	4380
aaaccgagaa	tattcaaaat	tccaaatttt	ttcttaggag	caagaagaaa	atgtggccct	4440
aaagggggtt	agttgagggg	tagggggtag	tgaggatctt	gatttggaac	tctttttatt	4500
taaatgtgaa	tttcaacttt	tgacaatcaa	agaaaagact	tttgttgaaa	tagctttact	4560
gtttctcaag	tgttttggag	aaaaaaatca	acctgtcaat	cacttttttg	aattgtcttg	4620
atttttcggc	agttcaagct	atatcgaata	tagttctgtg	tagagaatgt	cactgtagtt	4680
ttgagtgtat	acatgtgtgg	gtgctgataa	ttgtgtattt	tctttggggg	tggaaaagga	4740
aaacaattca	agctgagaaa	agtattctca	aagatgcatt	tttataaatt	ttattaaaca	4800
attttgttaa	accataaaaa	aaaaaaaaa				4828

&lt;210&gt; 37

&lt;211&gt; 882

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 37

```

Met Gly Pro Trp Ser Arg Ser Leu Ser Ala Leu Leu Leu Leu Leu Gln
 1      5      10      15
Val Ser Ser Trp Leu Cys Gln Glu Pro Glu Pro Cys His Pro Gly Phe
 20      25      30
Asp Ala Glu Ser Tyr Thr Phe Thr Val Pro Arg Arg His Leu Glu Arg
 35      40      45
Gly Arg Val Leu Gly Arg Val Asn Phe Glu Asp Cys Thr Gly Arg Gln
 50      55      60
Arg Thr Ala Tyr Phe Ser Leu Asp Thr Arg Phe Lys Val Gly Thr Asp
 65      70      75      80
Gly Val Ile Thr Val Lys Arg Pro Leu Arg Phe His Asn Pro Gln Ile
 85      90      95
His Phe Leu Val Tyr Ala Trp Asp Ser Thr Tyr Arg Lys Phe Ser Thr
 100     105     110
Lys Val Thr Leu Asn Thr Val Gly His His His Arg Pro Pro Pro His
 115     120     125
Gln Ala Ser Val Ser Gly Ile Gln Ala Glu Leu Leu Thr Phe Pro Asn
 130     135     140
Ser Ser Pro Gly Leu Arg Arg Gln Lys Arg Asp Trp Val Ile Pro Pro
 145     150     155     160
Ile Ser Cys Pro Glu Asn Glu Lys Gly Pro Phe Pro Lys Asn Leu Val
 165     170     175
Gln Ile Lys Ser Asn Lys Asp Lys Glu Gly Lys Val Phe Tyr Ser Ile
 180     185     190
Thr Gly Gln Gly Ala Asp Thr Pro Pro Val Gly Val Phe Ile Ile Glu
 195     200     205
Arg Glu Thr Gly Trp Leu Lys Val Thr Glu Pro Leu Asp Arg Glu Arg
 210     215     220
Ile Ala Thr Tyr Thr Leu Phe Ser His Ala Val Ser Ser Asn Gly Asn
 225     230     235     240
Ala Val Glu Asp Pro Met Glu Ile Leu Ile Thr Val Thr Asp Gln Asn
 245     250     255
Asp Asn Lys Pro Glu Phe Thr Gln Glu Val Phe Lys Gly Ser Val Met
 260     265     270
Glu Gly Ala Leu Pro Gly Thr Ser Val Met Glu Val Thr Ala Thr Asp
 275     280     285
Ala Asp Asp Asp Val Asn Thr Tyr Asn Ala Ala Ile Ala Tyr Thr Ile
 290     295     300
Leu Ser Gln Asp Pro Glu Leu Pro Asp Lys Asn Met Phe Thr Ile Asn
 305     310     315     320
Arg Asn Thr Gly Val Ile Ser Val Val Thr Thr Gly Leu Asp Arg Glu
 325     330     335
Ser Phe Pro Thr Tyr Thr Leu Val Val Gln Ala Ala Asp Leu Gln Gly
 340     345     350
Glu Gly Leu Ser Thr Thr Ala Thr Ala Val Ile Thr Val Thr Asp Thr
 355     360     365
Asn Asp Asn Pro Pro Ile Phe Asn Pro Thr Thr Tyr Lys Gly Gln Val
 370     375     380
Pro Glu Asn Glu Ala Asn Val Val Ile Thr Thr Leu Lys Val Thr Asp
 385     390     395     400
Ala Asp Ala Pro Asn Thr Pro Ala Trp Glu Ala Val Tyr Thr Ile Leu
 405     410     415
Asn Asp Asp Gly Gln Phe Val Val Thr Thr Asn Pro Val Asn Asn
 420     425     430
Asp Gly Ile Leu Lys Thr Ala Lys Gly Leu Asp Phe Glu Ala Lys Gln

```

										435					440					445											
Gln	Tyr	Ile	Leu	His	Val	Ala	Val	Thr	Asn	Val	Val	Pro	Phe	Glu	Val	Gln	Tyr	Ile	Leu	His	Val	Ala	Val	Thr	Asn	Val	Val	Pro	Phe	Glu	Val
	450					455					460										465					470					
Ser	Leu	Thr	Thr	Ser	Thr	Ala	Thr	Val	Thr	Val	Asp	Val	Leu	Asp	Val	Ser	Leu	Thr	Thr	Ser	Thr	Ala	Thr	Val	Thr	Val	Asp	Val	Leu	Asp	Val
465					470					475				480		485					490					495					495
Asn	Glu	Ala	Pro	Ile	Phe	Val	Pro	Pro	Glu	Lys	Arg	Val	Glu	Val	Ser	Asn	Glu	Ala	Pro	Ile	Phe	Val	Pro	Pro	Glu	Lys	Arg	Val	Glu	Val	Ser
Glu	Asp	Phe	Gly	Val	Gly	Gln	Glu	Ile	Thr	Ser	Tyr	Thr	Ala	Gln	Glu	Glu	Asp	Phe	Gly	Val	Gly	Gln	Glu	Ile	Thr	Ser	Tyr	Thr	Ala	Gln	Glu
			500					505					510											515							
Pro	Asp	Thr	Phe	Met	Glu	Gln	Lys	Ile	Thr	Tyr	Arg	Ile	Trp	Arg	Asp	Pro	Asp	Thr	Phe	Met	Glu	Gln	Lys	Ile	Thr	Tyr	Arg	Ile	Trp	Arg	Asp
Thr	Ala	Asn	Trp	Leu	Glu	Ile	Asn	Pro	Asp	Thr	Gly	Ala	Ile	Ser	Thr	Thr	Ala	Asn	Trp	Leu	Glu	Ile	Asn	Pro	Asp	Thr	Gly	Ala	Ile	Ser	Thr
	530					535					540																				
Arg	Ala	Glu	Leu	Asp	Arg	Glu	Asp	Phe	Glu	His	Val	Lys	Asn	Ser	Thr	Arg	Ala	Glu	Leu	Asp	Arg	Glu	Asp	Phe	Glu	His	Val	Lys	Asn	Ser	Thr
545					550					555				560																	
Tyr	Thr	Ala	Leu	Ile	Ile	Ala	Thr	Asp	Asn	Gly	Ser	Pro	Val	Ala	Thr	Tyr	Thr	Ala	Leu	Ile	Ile	Ala	Thr	Asp	Asn	Gly	Ser	Pro	Val	Ala	Thr
					565			570						575																	
Gly	Thr	Gly	Thr	Leu	Leu	Leu	Ile	Leu	Ser	Asp	Val	Asn	Asp	Asn	Ala	Gly	Thr	Gly	Thr	Leu	Leu	Leu	Ile	Leu	Ser	Asp	Val	Asn	Asp	Asn	Ala
			580					585					590																		
Pro	Ile	Pro	Glu	Pro	Arg	Thr	Ile	Phe	Phe	Cys	Glu	Arg	Asn	Pro	Lys	Pro	Ile	Pro	Glu	Pro	Arg	Thr	Ile	Phe	Phe	Cys	Glu	Arg	Asn	Pro	Lys
			595				600						605																		
Pro	Gln	Val	Ile	Asn	Ile	Ile	Asp	Ala	Asp	Leu	Pro	Pro	Asn	Thr	Ser	Pro	Gln	Val	Ile	Asn	Ile	Ile	Asp	Ala	Asp	Leu	Pro	Pro	Asn	Thr	Ser
	610					615					620																				
Pro	Phe	Thr	Ala	Glu	Leu	Thr	His	Gly	Ala	Ser	Ala																				

<210> 38  
 <211> 4521  
 <212> DNA  
 <213> Homo sapiens

<400> 38

```

acttcattca cttgcaaata agtgtgtgcc cacaagagcc agctctccc agcccgtaac 60
cttcgcatcc caagagctgc agtttcagcc gcgacagcaa gaacggcaga gccggcgacc 120
gcggcgccgg cgccggcgga ggcaggagca gcctgggcgg gtcgcagggt ctccgcgggc 180
gcaggaaggc gagcagagat atcctctgag agccaagcaa agaacattaa ggaaggaagg 240
aggaatgagg ctggatacgg tgcagtgaat aaggcacttc caagagtggg gcaactacta 300
cgcacagact cgacggtgcc atcagcatga gaacttaccg ctacttcttg ctgctctttt 360
gggtgggcca gccctaccca actctctcaa ctccactatc aaagaggact agtggtttcc 420
cagcaaagaa aagggccctg gagctctctg gaaacagcaa aaatgagctg aaccgttcaa 480
aaaggagctg gatgtggaat cagttctttc tcctggagga atacacagga tccgattatc 540
agtatgtggg caagttacat tcagaccagg atagaggaga tggatcactt aaatatatcc 600
tttcaggaga tggagcagga gatctcttca ttattaatga aaacacaggc gacatacagg 660
ccaccaagag cgtggacagg gaagaaaaac ccgtttacat ccttcgagct caagctataa 720
acagaaggac agggagaccc gtggagccc agtctgaatt catcatcaag atccatgaca 780
tcaatgacaa tgaaccaata ttcaccaagg aggtttacac agccactgtc cctgaaatgt 840
ctgatgtcgg tacatttgtt gtccaagtca ctgcgacgga tgcagatgat ccaacatatg 900
ggaacagtgc taaagtgtc tacagtattc tacagggaca gccctatttt tcagttgaat 960
cagaaacagg tattatcaag acagctttgc tcaacatgga tcgagaaaac agggagcagt 1020
accaagtggg gattcaagcc aaggatatgg gcggccagat gggaggatta tctgggacca 1080
ccaccgtgaa catcacactg actgatgtca acgacaaccc tccccgattc ccccagagta 1140
cataccagtt taaaactcct gaatcttctc caccggggac accaattggc ayaatcaaag 1200
ccagcgacgc tgatgtggga gaaaatgctg aaattgagta cagcatcaca gacggtgagg 1260
ggctggatat gttttagtgc atcaccgacc aggaaaccca ggaagggatt ataactgtca 1320
aaaagctctt ggactttgaa aagaagaaag tgtataccct taaagtggaa gcctccaatc 1380
cttatgttga gccacgattt ctctacttgg ggcctttcaa agattcagcc acggttagaa 1440
ttgtggtgga ggatgtagat gagccacctg tcttcagcaa actggcctac atcttcaaaa 1500
taagagaaga tgctcagata aacaccacaa taggctccgt cacagcccaa gatccagatg 1560
ctgccaggaa tcctgtcaag tactctgtag atcgacacac agatatggac agaattattca 1620
acattgattc tggaaatggg tcgattttta catcgaaact tcttgaccga gaaacactgc 1680
tatggcaca cttacagtg atagcaacag agatcaataa tccaaagcaa agtagtcgag 1740
tacctctata tattaaagtt ctatagtgta atgacaacgc ccagaattt gctgagtctc 1800
atgaaacttt tgtctgtgaa aaagcaaagg cagatcagtt gattcagacc ctgcatgctg 1860
ttgacaagga tgacccttat agtggacacc aattttcgtt ttccctggcc cctgaagcag 1920
ccagtggctc aaactttacc attcaagaca acaaagacaa cacggcggga atcttaactc 1980
ggaaaaatgg ctataataga cacgagatga gcacctatct cttgcctgtg gtcatttcag 2040
acaacgacta cccagttcaa agcagcactg ggacagtgc tgtccgggtc tgtcatgtg 2100
accaccacgg gaacatgcaa tcctgccatg cggaggcgct catccacccc acgggactga 2160
gcacgggggc tctggttgcc atccttctgt gcatcgtgat cctactagtg acagtgggtc 2220
tgtttgacg tctgaggcgg cagcgaaaaa aagagccctt gatcatttcc aaagaggaca 2280
tcagagataa cattgtcagt tacaacgacg aaggtggtgg agaggaggac acccaggctt 2340
ttgatatcgg caccctgagg aatcctgaag ccatagagga caacaaatta cgaagggaca 2400
ttgtgcccga agcccttttc ctaccccgac ggactccaac agctcgcgac aacaccgatg 2460
tcagagattt cattaaccaa aggttaaagg aaaatgacac ggacccact gccccgccat 2520
acgactcctt ggccacttac gcctatgaag gcactggctc cgtggcggtat tccctgagct 2580
cgctggagtc agtgaccacg gatgcagatc aagactatga ttaccttagt gactggggac 2640
ctcgattcaa aaagcttgca gatatgtatg gaggagtgga cagtgacaaa gactcctaata 2700
ctgttgccct tttcattttc caatacgaca ctgaaatatg tgaagtggct atttctttat 2760
atttatccac tactccgtga aggttctctc gttctaccg ttccaaaagc caatggctgc 2820
agtccgtgtg gatccaatgt tagagacttt tttctagtac acttttatga gcttccaagg 2880
ggcaaatttt tatttttttag tgcatccagt taaccaagtc agcccaacag gcaggtgccg 2940
gaggggagga cagggaaacag tatttccact tgttctcagg gcagcgtgcc cgcttccgct 3000
gtcctgggtgt tttactacac tccatgtcag gtcagccaac tgccctaact gtacatttca 3060

```

```

caggctaattg ggataaagga ctgtgcttta aagataaaaa tatcatcata gtaaaagaaa 3120
tgagggcata tgggctcaca aagagataaaa ctacataggg gtgttttattt gtgtcacaaa 3180
gaatttaaaa taacacttgc ccatgctatt tgttcttcaa gaactttctc tgccatcaac 3240
tactattcaa aacctcaaat ccacccatat gttaaaattc tcattactct taaggaatag 3300
aagcaaatta aacggtaaca tccaaaagca accacaaacc tagtacgact tcattccttc 3360
cactaactca tagtttggtta taccctagac tagacatgcy aaagtttgcc tttgtaccat 3420
ataaaggggg agggaaatag ctaataatgt taaccaagga aatataatttt accatacatt 3480
taaagttttg gccaccacat gtatcacggg tcaattgaaa ttctttcagc tatcagtagg 3540
ctaattgcaa aattgtttta aaattcttga aagaattttc ctgagacaaa ttttaacttc 3600
ttgtctatag ttgtcagtat tattctacta tactgtacat gaaagtagca gtgtgaagta 3660
caataattca tattcttcat atccttctta cagactaag ttgaattagt aaagtttagt 3720
taaataaaaac ttaaattctca ctctaggagt tcagtggaga ggtagagacc agccacactt 3780
gaacctaata ccctgccctt gacatctgga aacctctaca tatattatata acgtgataca 3840
tttgataaaa caacattgag attatgatga aaacctacat attccatgtt tggaagaccc 3900
ttggaagagg aaaattggat tcccttaaac aaaagtgtt aagattgtaa ttaaaatgat 3960
agttgatttt caaaagcatt aatttttttt cattgttttt aactttgctt tcatgaccat 4020
cctgccatcc ttgactttga actaatgata aagtaatgat ctcaaactat gacagaaaag 4080
taatgtaaaa tccatccaat ctattatttt tctaattatg caattagcct catagttatt 4140
atccagagga cccaactgaa ctgaactaat ccttctggca gattcaaacc gtttatttca 4200
cacgctgttc taatggcact tatcattaga atcttacctt gtgcagtcac cagaaattcc 4260
agcgtactat aatgaaaaca tccttgtttt gaaaaccta aagacaggct ctgtatatat 4320
atatacttaa gaatatgctg acttcaacta ttagtcttag ggattttatt tcaattaata 4380
ttaattttct acaaataatt ttagtgtcat ttccatttgg ggatattgtc atatcagcac 4440
atattttctg tttggaaaca cactgttggt tagttaagtt ttaaataaggt gtattacca 4500
agaagtaaaag atggaaacgt t                                     4521

```

&lt;210&gt; 39

&lt;211&gt; 790

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

```

Met Arg Thr Tyr Arg Tyr Phe Leu Leu Leu Phe Trp Val Gly Gln Pro
1          5          10          15
Tyr Pro Thr Leu Ser Thr Pro Leu Ser Lys Arg Thr Ser Gly Phe Pro
20          25          30
Ala Lys Lys Arg Ala Leu Glu Leu Ser Gly Asn Ser Lys Asn Glu Leu
35          40          45
Asn Arg Ser Lys Arg Ser Trp Met Trp Asn Gln Phe Phe Leu Leu Glu
50          55          60
Glu Tyr Thr Gly Ser Asp Tyr Gln Tyr Val Gly Lys Leu His Ser Asp
65          70          75          80
Gln Asp Arg Gly Asp Gly Ser Leu Lys Tyr Ile Leu Ser Gly Asp Gly
85          90          95
Ala Gly Asp Leu Phe Ile Ile Asn Glu Asn Thr Gly Asp Ile Gln Ala
100          105          110
Thr Lys Arg Leu Asp Arg Glu Glu Lys Pro Val Tyr Ile Leu Arg Ala
115          120          125
Gln Ala Ile Asn Arg Arg Thr Gly Arg Pro Val Glu Pro Glu Ser Glu
130          135          140
Phe Ile Ile Lys Ile His Asp Ile Asn Asp Asn Glu Pro Ile Phe Thr
145          150          155          160
Lys Glu Val Tyr Thr Ala Thr Val Pro Glu Met Ser Asp Val Gly Thr
165          170          175
Phe Val Val Gln Val Thr Ala Thr Asp Ala Asp Asp Pro Thr Tyr Gly
180          185          190
Asn Ser Ala Lys Val Val Tyr Ser Ile Leu Gln Gly Gln Pro Tyr Phe
195          200          205

```



Ser Val Glu Ser Glu Thr Gly Ile Ile Lys Thr Ala Leu Leu Asn Met  
 210 215 220  
 Asp Arg Glu Asn Arg Glu Gln Tyr Gln Val Val Ile Gln Ala Lys Asp  
 225 230 235 240  
 Met Gly Gly Gln Met Gly Gly Leu Ser Gly Thr Thr Thr Val Asn Ile  
 245 250 255  
 Thr Leu Thr Asp Val Asn Asp Asn Pro Pro Arg Phe Pro Gln Ser Thr  
 260 265 270  
 Tyr Gln Phe Lys Thr Pro Glu Ser Ser Pro Pro Gly Thr Pro Ile Gly  
 275 280 285  
 Arg Ile Lys Ala Ser Asp Ala Asp Val Gly Glu Asn Ala Glu Ile Glu  
 290 295 300  
 Tyr Ser Ile Thr Asp Gly Glu Gly Leu Asp Met Phe Asp Val Ile Thr  
 305 310 315 320  
 Asp Gln Glu Thr Gln Glu Gly Ile Ile Thr Val Lys Lys Leu Leu Asp  
 325 330 335  
 Phe Glu Lys Lys Lys Val Tyr Thr Leu Lys Val Glu Ala Ser Asn Pro  
 340 345 350  
 Tyr Val Glu Pro Arg Phe Leu Tyr Leu Gly Pro Phe Lys Asp Ser Ala  
 355 360 365  
 Thr Val Arg Ile Val Val Glu Asp Val Asp Glu Pro Pro Val Phe Ser  
 370 375 380  
 Lys Leu Ala Tyr Ile Leu Gln Ile Arg Glu Asp Ala Gln Ile Asn Thr  
 385 390 395 400  
 Thr Ile Gly Ser Val Thr Ala Gln Asp Pro Asp Ala Ala Arg Asn Pro  
 405 410 415  
 Val Lys Tyr Ser Val Asp Arg His Thr Asp Met Asp Arg Ile Phe Asn  
 420 425 430  
 Ile Asp Ser Gly Asn Gly Ser Ile Phe Thr Ser Lys Leu Leu Asp Arg  
 435 440 445  
 Glu Thr Leu Leu Trp His Asn Ile Thr Val Ile Ala Thr Glu Ile Asn  
 450 455 460  
 Asn Pro Lys Gln Ser Ser Arg Val Pro Leu Tyr Ile Lys Val Leu Asp  
 465 470 475 480  
 Val Asn Asp Asn Ala Pro Glu Phe Ala Glu Phe Tyr Glu Thr Phe Val  
 485 490 495  
 Cys Glu Lys Ala Lys Ala Asp Gln Leu Ile Gln Thr Leu His Ala Val  
 500 505 510  
 Asp Lys Asp Asp Pro Tyr Ser Gly His Gln Phe Ser Phe Ser Leu Ala  
 515 520 525  
 Pro Glu Ala Ala Ser Gly Ser Asn Phe Thr Ile Gln Asp Asn Lys Asp  
 530 535 540  
 Asn Thr Ala Gly Ile Leu Thr Arg Lys Asn Gly Tyr Asn Arg His Glu  
 545 550 555 560  
 Met Ser Thr Tyr Leu Leu Pro Val Val Ile Ser Asp Asn Asp Tyr Pro  
 565 570 575  
 Val Gln Ser Ser Thr Gly Thr Val Thr Val Arg Val Cys Ala Cys Asp  
 580 585 590  
 His His Gly Asn Met Gln Ser Cys His Ala Glu Ala Leu Ile His Pro  
 595 600 605  
 Thr Gly Leu Ser Thr Gly Ala Leu Val Ala Ile Leu Leu Cys Ile Val  
 610 615 620  
 Ile Leu Leu Val Thr Val Val Leu Phe Ala Ala Leu Arg Arg Gln Arg  
 625 630 635 640  
 Lys Lys Glu Pro Leu Ile Ile Ser Lys Glu Asp Ile Arg Asp Asn Ile  
 645 650 655  
 Val Ser Tyr Asn Asp Glu Gly Gly Gly Glu Glu Asp Thr Gln Ala Phe  
 660 665 670

Asp Ile Gly Thr Leu Arg Asn Pro Glu Ala Ile Glu Asp Asn Lys Leu  
 675 680 685  
 Arg Arg Asp Ile Val Pro Glu Ala Leu Phe Leu Pro Arg Arg Thr Pro  
 690 695 700  
 Thr Ala Arg Asp Asn Thr Asp Val Arg Asp Phe Ile Asn Gln Arg Leu  
 705 710 715 720  
 Lys Glu Asn Asp Thr Asp Pro Thr Ala Pro Pro Tyr Asp Ser Leu Ala  
 725 730 735  
 Thr Tyr Ala Tyr Glu Gly Thr Gly Ser Val Ala Asp Ser Leu Ser Ser  
 740 745 750  
 Leu Glu Ser Val Thr Thr Asp Ala Asp Gln Asp Tyr Asp Tyr Leu Ser  
 755 760 765  
 Asp Trp Gly Pro Arg Phe Lys Lys Leu Ala Asp Met Tyr Gly Gly Val  
 770 775 780  
 Asp Ser Asp Lys Asp Ser  
 785 790

<210> 40  
 <211> 987  
 <212> DNA  
 <213> Homo sapiens

<400> 40  
 cggagagggg gagaacagac aacgggcggc ggggagcagc atggagccgg cggcggggag 60  
 cagcatggag ccttcggctg actggctggc cagggccgcg gcccggggtc gggtagagga 120  
 ggtgcgggcg ctgctggagg cgggggcgct gcccaacgca ccgaatagtt acggtcggag 180  
 gccgatccag gtcatgatga tgggcagcgc ccgagtggcg gagctgctgc tgctccacgg 240  
 cgcgagccc aactgcgcg accccgccac tctcaccga cccgtgcacg acgctgccc 300  
 ggagggcttc ctggacacgc tgggtgtgct gcaccgggccc ggggcgcggc tggacgtgcg 360  
 cgatgcctgg ggccgtctgc ccgtggacct ggctgaggag ctgggccatc gcgatgtcgc 420  
 acggtacctg cgcgcggtcg cggggggcac cagaggcagt aaccatgccc gcatagatgc 480  
 cgcggaaggt ccctcagaca tccccgattg aaagaaccag agaggctctg agaaacctcg 540  
 ggaaacttag atcatcagtc accgaaggtc ctacagggcc acaactgccc ccgccacaac 600  
 ccaccccgct ttcgtagttt tcatttagaa aatagagctt ttaaaaatgt cctgcctttt 660  
 aacgtagata taagccttcc ccactaccg taaatgtcca tttatatcat tttttatata 720  
 ttcttataaa aatgtaaaaa agaaaaacac cgcttctgcc ttttactgt gttggagt 780  
 tctggagtga gcactcacgc cctaagcgca cattcatgtg ggcatttctt gcgagcctcg 840  
 cagcctccgg aagctgtcga cttcatgaca agcattttgt gaactagga agctcagggg 900  
 gggtactggc ttctcttgag tcacactgct agcaaatggc agaaccaaag ctcaaataaa 960  
 aataaaataa ttttcattca ttcactc 987

<210> 41  
 <211> 156  
 <212> PRT  
 <213> Homo sapiens

<400> 41  
 Met Glu Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu  
 1 5 10 15  
 Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu  
 20 25 30  
 Glu Ala Gly Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro  
 35 40 45  
 Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu  
 50 55 60  
 Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg  
 65 70 75 80

```
<210>: 42
<211> 5142
<212> DNA
<213> Homo sapiens
```

gaattcggcc	gagaggacga	gggggagggc	cagagctgcg	cgtgctgctt	tgcccgagcc	60
cgagcccag	cccagcccg	agcccagacc	cgagcccag	cccgaacgca	agcctgggag	120
cgcgaggccc	ggctagggac	tctctctatt	tatggagcag	gcaccaaca	tggctgagcc	180
ccggggcccc	gtagaccatg	gagtcacgat	tcgcttcac	acagagccag	tgagtgggtc	240
agagatggg	actctacgtc	gaggtggacg	acgcccagct	aaggatgcaa	gagccagtac	300
ctacgggggt	gctgtgcgtg	tgcagggaat	cgctgggcag	ccctttgtgg	tgctcaacag	360
tggggagaaa	ggcgggtgact	cccttgggg	ccaaatcaag	ggggccaatg	accaaggggc	420
ctcaggagct	ctgagctcag	atttggaact	ccctgagaac	ccctactctc	aggtcaaggg	480
atttcctgcc	ccctcgcaga	gcagcacatc	tgatgaggag	cctggggcct	actggaatgg	540
aaagctactc	cgttcccact	cccaggcctc	actggcaggc	cctggcccag	tggatcctag	600
taacagaagc	aacagcatgc	tggagctagc	cccgaaagtg	gcttccccag	gtagcaccat	660
tgacactgct	cccctgtctt	cagtggactc	actcatcaac	aagtttgaca	gtcaacttgg	720
aggccaggcc	cggggtcgga	ctgggcgcgc	aacacggatg	ctaccccctg	aacagcgcaa	780
acggagcaag	agcctggaca	gcgcctccc	acgggcaccc	tttgaggaa	gggagcgcca	840
gtccaccaac	cactggacct	ctagcacaaa	atatgacaac	ctgtgggca	cttcgaagca	900
gccagcccag	agccagaacc	tgagtctct	cagtggcttt	agccgttctc	ctcagactca	960
ggactgggtc	cttcagagtt	ttgaggagcc	gcggaggagt	gcacaggacc	ccaccatgct	1020
gcagttcaaa	tcaactccag	acctctctcg	agaccagcag	gaggcagccc	caccaggcag	1080
tgtggaccat	atgaaggcca	ccatctatgg	catctgagg	gagggaagct	cagaaagtga	1140
aacctctgtg	aggaggaagg	ttagtttgg	gctggagaag	atgcagcctc	tagtgatggt	1200
ttcttctgg	tctactaagg	ccgtggcagg	gcagggtgag	cttaccggaa	aagtggagga	1260
gtctacgcga	aagctggatg	aagaggtgaa	gaagcggcag	aagctagagc	catcccaagt	1320
tgggctggag	cggcagctgg	aggagaaaac	agaagatgc	agccgactgc	aggagctgct	1380
ggagaggagg	aagggggagg	cccagcagag	caacaaggag	ctccagaaca	tgaagcgctt	1440
cttggaaccag	ggtgaagatt	tacgacatgg	gctggagacc	caggtgatgg	agctgcagaa	1500
caagctgaaa	catgtccagg	gtcctgagcc	tgctaaggag	gtgttactga	aggacctgtt	1560
agagacccgg	gaactctctg	aagaggtctt	ggaggggaaa	cagcgagtag	aggagcagct	1620
gaggctgcgg	gagcgggagt	tgacagccct	gaagggggcc	ctgaaagagg	aggtagcctc	1680
ccgtgaccag	gagtggaac	atgtccggca	gcagtaccag	cgagacacag	agcagctccg	1740
caggagcatg	caagatgcaa	cccagacca	tgcatgtcgt	gaggccgaga	ggcagaagat	1800
gtcagccctt	gtgcgagggc	tgcagaggga	gctggaggag	acttcagagg	agacagggca	1860
ttggcagagt	atgttccaga	agaacaagga	ggatcttaga	gccaccaagc	aggaactcct	1920
gcagctgcga	atggagaagg	aggagatgga	agaggagctt	ggagagaaga	tagaggtctt	1980
gcagagggaa	ttagagcagg	cccagactag	tgctggagat	actcgccagg	ttgaggtgct	2040
caagaaggag	ctgctccgga	cacaggagga	gcttaaggaa	ctgcaggcag	aacggcagag	2100
ccaggagggtg	gctgggcgac	accgggaccg	ggagttggag	aagcagctgg	cggtcctgag	2160
ggtcgaggct	gatcgaggtc	gggagctgga	agaacagaac	ctccagctac	aaaagaccct	2220
ccagcagact	cgacaggact	gtgaagaggc	ttccaaggct	aagatggttg	ccgagggcaga	2280
ggcaacagtg	ctggggcagc	ggcgggcgcg	agtggaagcg	acgcttcggg	agaccggagga	2340
ggaaaatgac	gaattccgcc	ggcgcatcct	gggtttggag	cagcagctga	agagactcga	2400

```

aggtctggtg gatggtgggg aagcgggtga ggcacgacta cgggacaagc tgcagcggct 2460
ggaggcagag aaacagcagc tggaggagcg cctgaatgcg tcccaggaag aggaggggag 2520
tctggcagca gccaagcggg cactggagcg acgcctagag gaggtcagc gggggctggc 2580
ccgcctgggg caggagcagc agacactgaa cggggccctg gaggaggaag ggaagcagcg 2640
ggaggtgctc cggcgaggca aggctgagct ggaggagcag aagcgtttgc tggacaggac 2700
tgtggaccga ctgaacaagg agttggagaa gatcggggag gactctaagc aagccctgca 2760
gcagctccag gccagctgg aggattataa ggaaaaggcc cggcgggagg tggcagatgc 2820
ccagcgccag gccaaggatt gggccagtga ggctgagaag acctctggag gactgagccg 2880
acttcaggat gagatccaga ggctgcggca ggccctgcag gcatcccagg ctgagcggga 2940
cacagcccgg ctggacaaag agctactggc ccagcgactg caggggctgg agcaagaggc 3000
agagaacaag aagcgttccc aggacgacag ggcccggcag ctgaagggtc tgcaggaaaa 3060
agtctcacgg ctggaaacag agttagatga ggagaagaac accgtggagc tgctaacaga 3120
tcgggtgaat cgtggccggg accaggtgga tcagctgagg acagagctca tgcaggaaaag 3180
gtctgtcctg caggacctgg agtgtgacaa aatctccttg gagagacaga acaaggacct 3240
gaagaccggg ttggccagct cagaaggctt ccagaagcct agtgccagcc tctctcagct 3300
tgagtcccag aatcagttgt tgcaggagcg gctacaggct gaagagaggg agaagacagt 3360
tctgcagtct accaatcgaa aactggagcg gaaagttaaa gaactatcca tccagattga 3420
agacgagcgg cagcatgtca atgaccagaa agaccagcta agcctgaggg tgaaggcttt 3480
gaagcgtcag gtggatgaag cagaagagga aattgagcga ctggacggcc tgaggaaaga 3540
ggcccagcgt gaggtggagg agcagcatga ggtcaatgaa cagctccagg cccggatcaa 3600
gtctctggag aaggactcct ggcgcaaaagc ttcccgtca gctgctgagt cagctctcaa 3660
aaacgaaggg ctgagctcag atgaggaatt cgacagtgtc tacgatccct cgtccattgc 3720
atcactgctt acggagagca acctacagac cagctcctgt tagctcgtgg tcctcaagga 3780
ctcagaaaacc aggtcagagg cctatcccag caagtgtctg tctgctctgc ccaccctggg 3840
ttctgcattc ctatgggtga cccaattatt cagacctaa acagggaggg gtcagagtga 3900
tggtgataaa aaaaaaaaaa tcatcagcaa taagctgata gatggacttt ccactgtagg 3960
agtggacgtt tcaagccaac tgagcctttt cctcaagtgc cgacacctcc ctcatctctc 4020
ttatagtggg aggatgggtc gcattaggct gatggggact gagaaggata ggaagggata 4080
gaaattgccca tgtgtataaa gctttattct ttagccctta accctaaggc tcagggaaat 4140
accctatgtt atttgtctcc ctggattcct gcaactcatt ttccctccac tctggagcag 4200
ggtgagggga atgttatggg taacagacat gcaggcatgg ctctacccat ttctttgcac 4260
aagtatgggg cccatgtggg agtcccata cccctccagt tcctatatatt ttgtcttctt 4320
cctttccoct ctttgccatt cctaccttgc atttttcctg tcagtgcctt agccaaggca 4380
aggagataag gatgctcttc ttgcttttta tatctgcaca ttcataacct tccaaagacc 4440
agcttttccc cagccagggg cctcagcctt ccctgtgcc ccagtgattg attgagagag 4500
ctgttggggg ttctctgcca atgaccctg ggagagggac tttggtaggg tcatgataaa 4560
gtggcggggg tcttggtcct gctcagggtt ttcctcttcc ctctctccc tcctctgtga 4620
ctgtggatat ggttataagg tggttgcacc tgggagccct gacaactggc tgcacaaatt 4680
ccaaaagtaa aggtgtcagt ccctgtggcc ttcttgggg cttctctgac cacatgtgcc 4740
caacttcaat aagagaacca agggaccttc attttctgag gtgcttggct ctgattcagg 4800
gctttgcaag gggttagaag ctgactgtaa aaatgggaag aggcaacgga agacatttat 4860
ttctcctttg gattttgggg agaaccaagc cctggtaggg aagaggtaag ggggatgatt 4920
cacctccata tttcctaagc aggttgataa gggagccggg ggcaggagga aggctgtttt 4980
cacaaatgac ttgtaatgtc gtgattaaaa aaattcctat attcttctgc aaatcaaacg 5040
ttctttccca atccaatcca gccttggttt tattttaa ataaatattaa aattacacat 5100
ttatattgaa aaaaaaaaaa aaaaaa aaaaaa aa 5142

```

&lt;210&gt; 43

&lt;211&gt; 1203

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 43

```

Met Glu Gln Ala Pro Asn Met Ala Glu Pro Arg Gly Pro Val Asp His
 1             5             10             15
Gly Val Gln Ile Arg Phe Ile Thr Glu Pro Val Ser Gly Ala Glu Met
          20             25             30
Gly Thr Leu Arg Arg Gly Gly Arg Arg Pro Ala Lys Asp Ala Arg Ala

```

[illegible]

500							505							510						
Gln	Glu	Val	Glu	His	Val	Arg	Gln	Gln	Tyr	Gln	Arg	Asp	Thr	Glu	Gln					
		515					520					525								
Leu	Arg	Arg	Ser	Met	Gln	Asp	Ala	Thr	Gln	Asp	His	Ala	Val	Leu	Glu					
		530				535					540									
Ala	Glu	Arg	Gln	Lys	Met	Ser	Ala	Leu	Val	Arg	Gly	Leu	Gln	Arg	Glu					
		545			550					555					560					
Leu	Glu	Glu	Thr	Ser	Glu	Glu	Thr	Gly	His	Trp	Gln	Ser	Met	Phe	Gln					
				565					570					575						
Lys	Asn	Lys	Glu	Asp	Leu	Arg	Ala	Thr	Lys	Gln	Glu	Leu	Leu	Gln	Leu					
			580					585						590						
Arg	Met	Glu	Lys	Glu	Glu	Met	Glu	Glu	Glu	Leu	Gly	Glu	Lys	Ile	Glu					
		595					600					605								
Val	Leu	Gln	Arg	Glu	Leu	Glu	Gln	Ala	Arg	Ala	Ser	Ala	Gly	Asp	Thr					
		610				615					620									
Arg	Gln	Val	Glu	Val	Leu	Lys	Lys	Glu	Leu	Leu	Arg	Thr	Gln	Glu	Glu					
		625			630					635					640					
Leu	Lys	Glu	Leu	Gln	Ala	Glu	Arg	Gln	Ser	Gln	Glu	Val	Ala	Gly	Arg					
				645					650					655						
His	Arg	Asp	Arg	Glu	Leu	Glu	Lys	Gln	Leu	Ala	Val	Leu	Arg	Val	Glu					
			660					665					670							
Ala	Asp	Arg	Gly	Arg	Glu	Leu	Glu	Glu	Gln	Asn	Leu	Gln	Leu	Gln	Lys					
		675				680						685								
Thr	Leu	Gln	Gln	Leu	Arg	Gln	Asp	Cys	Glu	Glu	Ala	Ser	Lys	Ala	Lys					
		690				695					700									
Met	Val	Ala	Glu	Ala	Glu	Ala	Thr	Val	Leu	Gly	Gln	Arg	Arg	Ala	Ala					
		705			710					715				720						
Val	Glu	Thr	Thr	Leu	Arg	Glu	Thr	Gln	Glu	Glu	Asn	Asp	Glu	Phe	Arg					
				725					730					735						
Arg	Arg	Ile	Leu	Gly	Leu	Glu	Gln	Gln	Leu	Lys	Glu	Thr	Arg	Gly	Leu					
			740				745						750							
Val	Asp	Gly	Gly	Glu	Ala	Val	Glu	Ala	Arg	Leu	Arg	Asp	Lys	Leu	Gln					
		755				760						765								
Arg	Leu	Glu	Ala	Glu	Lys	Gln	Gln	Leu	Glu	Glu	Ala	Leu	Asn	Ala	Ser					
		770				775					780									
Gln	Glu	Glu	Glu	Gly	Ser	Leu	Ala	Ala	Ala	Lys	Arg	Ala	Leu	Glu	Ala					
				790						795				800						
Arg	Leu	Glu	Glu	Ala	Gln	Arg	Gly	Leu	Ala	Arg	Leu	Gly	Gln	Glu	Gln					
				805				810						815						
Gln	Thr	Leu	Asn	Arg	Ala	Leu	Glu	Glu	Glu	Gly	Lys	Gln	Arg	Glu	Val					
			820				825						830							
Leu	Arg	Arg	Gly	Lys	Ala	Glu	Leu	Glu	Glu	Gln	Lys	Arg	Leu	Leu	Asp					
		835				840						845								

		965				970				975					
Glu	Leu	Asp	Glu	Glu	Lys	Asn	Thr	Val	Glu	Leu	Leu	Thr	Asp	Arg	Val
		980						985					990		
Asn	Arg	Gly	Arg	Asp	Gln	Val	Asp	Gln	Leu	Arg	Thr	Glu	Leu	Met	Gln
		995					1000					1005			
Glu	Arg	Ser	Ala	Arg	Gln	Asp	Leu	Glu	Cys	Asp	Lys	Ile	Ser	Leu	Glu
		1010				1015					1020				
Arg	Gln	Asn	Lys	Asp	Leu	Lys	Thr	Arg	Leu	Ala	Ser	Ser	Glu	Gly	Phe
		1025			1030					1035				1040	
Gln	Lys	Pro	Ser	Ala	Ser	Leu	Ser	Gln	Leu	Glu	Ser	Gln	Asn	Gln	Leu
			1045					1050					1055		
Leu	Gln	Glu	Arg	Leu	Gln	Ala	Glu	Glu	Arg	Glu	Lys	Thr	Val	Leu	Gln
		1060					1065					1070			
Ser	Thr	Asn	Arg	Lys	Leu	Glu	Arg	Lys	Val	Lys	Glu	Leu	Ser	Ile	Gln
		1075				1080					1085				
Ile	Glu	Asp	Glu	Arg	Gln	His	Val	Asn	Asp	Gln	Lys	Asp	Gln	Leu	Ser
		1090			1095					1100					
Leu	Arg	Val	Lys	Ala	Leu	Lys	Arg	Gln	Val	Asp	Glu	Ala	Glu	Glu	Glu
		1105			1110				1115					1120	
Ile	Glu	Arg	Leu	Asp	Gly	Leu	Arg	Lys	Lys	Ala	Gln	Arg	Glu	Val	Glu
		1125				1130						1135			
Glu	Gln	His	Glu	Val	Asn	Glu	Gln	Leu	Gln	Ala	Arg	Ile	Lys	Ser	Leu
		1140				1145					1150				
Glu	Lys	Asp	Ser	Trp	Arg	Lys	Ala	Ser	Arg	Ser	Ala	Ala	Glu	Ser	Ala
		1155				1160					1165				
Leu	Lys	Asn	Glu	Gly	Leu	Ser	Ser	Asp	Glu	Glu	Phe	Asp	Ser	Val	Tyr
		1170			1175				1180						
Asp	Pro	Ser	Ser	Ile	Ala	Ser	Leu	Leu	Thr	Glu	Ser	Asn	Leu	Gln	Thr
		1185			1190				1195				1200		
Ser	Ser	Cys													

&lt;210&gt; 44

&lt;211&gt; 1925

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 44

```

agtggagtgg gacaggtata taaaggaagt acagggcctg gggaagaggc cctgtctagg 60
tagctggcac caggagccgt gggcaaggga agaggccaca ccctgccctg ctctgctgca 120
gccagaatgg gtgtgaaggc gtctcaaaca ggctttgtgg tcctggtgct gctccagtgc 180
tgctctgcat acaaactggg ctgctactac accagctggt cccagtaccg ggaaggcgat 240
gggagctgct tcccagatgc ccttgaccgc ttctctgtga cccacatcat ctacagcttt 300
gccaatataa gcaacgatca catcgacacc tgggagtggg atgatgtgac gctctacggc 360
atgctcaaca cactcaagaa caggaacccc aacctgaaga ctctcttgct tgtcggagga 420
tggaactttg ggtctcaaag attttccaag atagcctcca acaccagag tcgccggact 480
ttcatcaagt cagtaccgcc attcctgcgc acccatggct ttgatgggct ggaccttgcc 540
tggctctacc ctggacggag agacaaacag cattttacca ccctaataca ggaaatgaag 600
gccgaattta taaaggaagc ccagccaggg aaaaagcagc tcctgctcag cgcagcactg 660
tctgcgggga aggtcaccat tgacagcagc tatgacattg ccaagatata ccaacacctg 720
gatttcatta gcatcatgac ctacgatttt catggagcct ggcggtgggac cacaggccat 780
cacagtcccc tgttccgagg tcaggaggat gcaagtcctg acagattcag caacactgac 840
tatgctgtgg ggtacatggt gaggctgggg gctcctgcca gtaagctggt gatgggcatc 900
cccaccttcg ggaggagctt cactctggct tcttctgaga ctggtgttgg agccccaatc 960
tcaggaccgg gaattccagg ccggttcacc aaggaggcag ggacccttgc ctactatgag 1020
atctgtgact tctccgcgg agccacagtc catagaacct tcggccagca ggtcccctat 1080
gccaccaagg gcaaccagtg ggtaggatac gacgaccagg aaagcgtcaa aagcaagggtg 1140

```

```

cagtacctga aggataggca gctggcaggc gccatggtat gggccctgga cctggatgac 1200
ttccagggct ccttctgcgg ccaggatctg cgcttccctc tcaccaatgc catcaaggat 1260
gcaactcgctg caacgtagcc ctctgttctg cacacagcac gggggccaag gatgccccgt 1320
ccccctctgg ctccagctgg ccgggagcct gatcacctgc cctgtgagt cccaggctga 1380
gcctcagttt cctcccttg gggcctatgc agaggtccac aacacacaga tttgagctca 1440
gccctggtgg gcagagaggt agggatgggg ctgtggggat agtgaggcat cgcaatgtaa 1500
gactcgggat tagtacacac ttgttgatga ttaatggaaa tgtttacaga tccccaaaggc 1560
tggcaaggga atttcttcaa ctccctgccc cctagccctc cttatcaaag gacaccattt 1620
tggcaagctc tatcaccaag gagccaaaca tcctacaaga cacagtgacc atactaatta 1680
taccctctgc aaagccagct tgaaaccttc acttaggaac gtaatcgtgt cccctatcct 1740
acttccccct cctaattcca cagctgctca ataaagtaca agagttaaag agtgtgttgg 1800
cgctttgctt tgggtctatct ttgagcgccc actagaccac ctggactcac ctcccccatc 1860
tcttctgggt tccttcctct gagccttggg acccctgagc ttgcagagat gaaggccgcc 1920
atgtt                                     1925

```

&lt;210&gt; 45

&lt;211&gt; 383

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 45

```

Met Gly Val Lys Ala Ser Gln Thr Gly Phe Val Val Leu Val Leu Leu
 1          5          10          15
Gln Cys Cys Ser Ala Tyr Lys Leu Val Cys Tyr Tyr Thr Ser Trp Ser
 20          25          30
Gln Tyr Arg Glu Gly Asp Gly Ser Cys Phe Pro Asp Ala Leu Asp Arg
 35          40          45
Phe Leu Cys Thr His Ile Ile Tyr Ser Phe Ala Asn Ile Ser Asn Asp
 50          55          60
His Ile Asp Thr Trp Glu Trp Asn Asp Val Thr Leu Tyr Gly Met Leu
 65          70          75          80
Asn Thr Leu Lys Asn Arg Asn Pro Asn Leu Lys Thr Leu Leu Ser Val
 85          90          95
Gly Gly Trp Asn Phe Gly Ser Gln Arg Phe Ser Lys Ile Ala Ser Asn
100          105          110
Thr Gln Ser Arg Arg Thr Phe Ile Lys Ser Val Pro Pro Phe Leu Arg
115          120          125
Thr His Gly Phe Asp Gly Leu Asp Leu Ala Trp Leu Tyr Pro Gly Arg
130          135          140
Arg Asp Lys Gln His Phe Thr Thr Leu Ile Lys Glu Met Lys Ala Glu
145          150          155          160
Phe Ile Lys Glu Ala Gln Pro Gly Lys Lys Gln Leu Leu Leu Ser Ala
165          170          175
Ala Leu Ser Ala Gly Lys Val Thr Ile Asp Ser Ser Tyr Asp Ile Ala
180          185          190
Lys Ile Ser Gln His Leu Asp Phe Ile Ser Ile Met Thr Tyr Asp Phe
195          200          205
His Gly Ala Trp Arg Gly Thr Thr Gly His His Ser Pro Leu Phe Arg
210          215          220
Gly Gln Glu Asp Ala Ser Pro Asp Arg Phe Ser Asn Thr Asp Tyr Ala
225          230          235          240
Val Gly Tyr Met Leu Arg Leu Gly Ala Pro Ala Ser Lys Leu Val Met
245          250          255
Gly Ile Pro Thr Phe Gly Arg Ser Phe Thr Leu Ala Ser Ser Glu Thr
260          265          270
Gly Val Gly Ala Pro Ile Ser Gly Pro Gly Ile Pro Gly Arg Phe Thr
275          280          285
Lys Glu Ala Gly Thr Leu Ala Tyr Tyr Glu Ile Cys Asp Phe Leu Arg

```



290		295		300
Gly Ala Thr Val His Arg	Thr Leu Gly Gln Gln	Val Pro Tyr Ala Thr		
305	310	315	320	
Lys Gly Asn Gln Trp Val	Gly Tyr Asp Asp Gln	Glu Ser Val Lys Ser		
	325	330	335	
Lys Val Gln Tyr Leu Lys	Asp Arg Gln Leu Ala	Gly Ala Met Val Trp		
	340	345	350	
Ala Leu Asp Leu Asp Asp	Phe Gln Gly Ser Phe	Cys Gly Gln Asp Leu		
	355	360	365	
Arg Phe Pro Leu Thr Asn	Ala Ile Lys Asp Ala	Leu Ala Ala Thr		
370	375	380		

&lt;210&gt; 46

&lt;211&gt; 1528

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 46

```

ccggctccca ttccggctcc agcctccaat ccgaccccca ttccggctgc agcctcggac 60
ctagctcccg ccctcggtct atccggttgc atcctccctc cctgttcggg atcttatctt 120
gcgccagcgc ctactccagg atcccgtagc cagacctcaa gccatggctg gtcccttctc 180
ccgtctgctg tccgcccggc cgggactcag gtccttggtt ttggccggag cgggggtctc 240
agccgctggg tttctgctcc gaccggaacc tgtacgagct gccagtgaac gacggaggct 300
gtatcccccg agcgtgtagt acccagacct ccgaaagcac aacaactgca tggccagtca 360
cctgacccca gcagtctatg cacggctctg cgacaagacc acacccactg gttggacgct 420
agatcagtgt atccagactg gcgtggacaa ccctggccac cccttcatca agactgtggg 480
catggtggct ggagatgagg agacctatga ggtatttgct gacctgtttg accctgtgat 540
ccaagagcga cacaatggat atgaccccg gacaatgaag cacaccaagg atctagatgc 600
cagtaaaatc cgttctggct actttgatga gaggtatgta ttgtcctcta gagtcagaac 660
tgcccgaaag atccgaggac tcagtctgcc tcagcttgc actcgagcag agcgacgaga 720
ggtggaacgt gttgtggttg atgcactgag tggcctgaag ggtgacctgg ctggacgtta 780
ctataggctc agtgagatga cagaggctga acagcagcag cttattgatg accactttct 840
gtttgataag cctgtgtccc cgttgctgac tgcagcagga atggctcgag actggccaga 900
tgctcgtgga atttggcaca acaatgagaa gagcttccct atctgggtga atgaggagga 960
tcatacacgg gtgatctcca tggagaaggg tggtaacatg aagagagtgt ttgaaagatt 1020
ctgccgaggg ctcaaagagg tggagagact tatccaagaa cgtggctggg agttcatgtg 1080
gaatgagcgt ttgggataca tcttgacctg tccatctaac ctgggcactg gacttcgggc 1140
aggagtgcac atcaaaactgc ccctgctaag caaagatagc cgcttcccaa agatcctgga 1200
gaacctaaga ctccaaaaac gtggtactgg aggagtggac actgctgcta caggcgggtg 1260
ctttgatatt tctaatttgg accgactagg caaatcagag gtggagctgg tgcaactggt 1320
catcgatgga gtaaactatt tgattgattg tgaacggcgt ctggagagag gccaggatat 1380
ccgcatcccc acacctgtca tccacaccaa gcattaactc cccatcgcca gctgatgact 1440
caagattccc aggagttttg ctcatcttaa tgatggccca ttctacttgc tctggacctg 1500
cccccgcatc ccctgcctcc atcctagt 1528

```

&lt;210&gt; 47

&lt;211&gt; 417

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 47

Met Ala Gly Pro Phe Ser Arg	Leu Leu Ser Ala Arg Pro Gly Leu Arg
1	5 10 15
Leu Leu Ala Leu Ala Gly Ala Gly	Ser Leu Ala Ala Gly Phe Leu Leu
20	25 30
Arg Pro Glu Pro Val Arg Ala Ala	Ser Glu Arg Arg Arg Leu Tyr Pro
35	40 45

Pro Ser Ala Glu Tyr Pro Asp Leu Arg Lys His Asn Asn Cys Met Ala  
 50 55 60  
 Ser His Leu Thr Pro Ala Val Tyr Ala Arg Leu Cys Asp Lys Thr Thr  
 65 70 75 80  
 Pro Thr Gly Trp Thr Leu Asp Gln Cys Ile Gln Thr Gly Val Asp Asn  
 85 90 95  
 Pro Gly His Pro Phe Ile Lys Thr Val Gly Met Val Ala Gly Asp Glu  
 100 105 110  
 Glu Thr Tyr Glu Val Phe Ala Asp Leu Phe Asp Pro Val Ile Gln Glu  
 115 120 125  
 Arg His Asn Gly Tyr Asp Pro Arg Thr Met Lys His Thr Thr Asp Leu  
 130 135 140  
 Asp Ala Ser Lys Ile Arg Ser Gly Tyr Phe Asp Glu Arg Tyr Val Leu  
 145 150 155 160  
 Ser Ser Arg Val Arg Thr Gly Arg Ser Ile Arg Gly Leu Ser Leu Pro  
 165 170 175  
 Pro Ala Cys Thr Arg Ala Glu Arg Arg Glu Val Glu Arg Val Val Val  
 180 185 190  
 Asp Ala Leu Ser Gly Leu Lys Gly Asp Leu Ala Gly Arg Tyr Tyr Arg  
 195 200 205  
 Leu Ser Glu Met Thr Glu Ala Glu Gln Gln Gln Leu Ile Asp Asp His  
 210 215 220  
 Phe Leu Phe Asp Lys Pro Val Ser Pro Leu Leu Thr Ala Ala Gly Met  
 225 230 235 240  
 Ala Arg Asp Trp Pro Asp Ala Arg Gly Ile Trp His Asn Asn Glu Lys  
 245 250 255  
 Ser Phe Leu Ile Trp Val Asn Glu Glu Asp His Thr Arg Val Ile Ser  
 260 265 270  
 Met Glu Lys Gly Gly Asn Met Lys Arg Val Phe Glu Arg Phe Cys Arg  
 275 280 285  
 Gly Leu Lys Glu Val Glu Arg Leu Ile Gln Glu Arg Gly Trp Glu Phe  
 290 295 300  
 Met Trp Asn Glu Arg Leu Gly Tyr Ile Leu Thr Cys Pro Ser Asn Leu  
 305 310 315 320  
 Gly Thr Gly Leu Arg Ala Gly Val His Ile Lys Leu Pro Leu Leu Ser  
 325 330 335  
 Lys Asp Ser Arg Phe Pro Lys Ile Leu Glu Asn Leu Arg Leu Gln Lys  
 340 345 350  
 Arg Gly Thr Gly Gly Val Asp Thr Ala Ala Thr Gly Gly Val Phe Asp  
 355 360 365  
 Ile Ser Asn Leu Asp Arg Leu Gly Lys Ser Glu Val Glu Leu Val Gln  
 370 375 380  
 Leu Val Ile Asp Gly Val Asn Tyr Leu Ile Asp Cys Glu Arg Arg Leu  
 385 390 395 400  
 Glu Arg Gly Gln Asp Ile Arg Ile Pro Thr Pro Val Ile His Thr Lys  
 405 410 415  
 His

&lt;210&gt; 48

&lt;211&gt; 2365

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 48

ggagccggag agcgagcgcg gctgcagccg gcggcatggc tagcacggct tcggagatca 60  
 tcgccttcat ggtctccatc tcaggctggg tactggtgtc ctccacgctg cccaccgact 120

```

actggaaggt gtctaccatc gacggcacgg tcatcacaac cgccacctat tgggcccaacc 180
tgtggaaggc gtgcgttacc gactccacgg gcgtctccaa ctgcaaggac ttcccccca 240
tgctggcgct ggacggttat atacaggcat gtagaggact tatgatcgct gctgtcagcc 300
tgggcttctt tggttccata tttgcgctct ttggaatgaa gtgtacaaa gtcggaggct 360
ccgataaagc caaagctaaa attgcttggt tggctgggat tgtattcata ctgtcagggc 420
tgtgtcaat gactggatgt tccctatatg caaacaaaat cacaacggaa ttctttgatc 480
ctctctttgt tgagcaaaaag tatgaattag gagccgctct gtttattgga tgggcaggag 540
cctcactgtg cataattggt ggtgtcatat tttgcttttc aatatctgac aacaacaaaa 600
caccagata cacatacaac ggggccacat ctgtcatgtc ttctcggaca aagtatcatg 660
gtggagaaga ttttaaaaca acaaacctt caaacagtt tgataaaaat gcttatgtct 720
aaaagagctc gctggcaagc tgcctcttga gtttggtata aaagcgaact gttcacaaaa 780
tgatcccatc aaggccctcc cataattaac actcaaaact atttttaaaa tatgcatttg 840
aagcatctgt tgattgtatg gatgtaagt ttcttacata gttagtata tactaatcat 900
tttctgttgt ggctttctat aaaaaataaa cagtttattt acaggatttg taaaatgttt 960
tctacattta tatagaacat gaaaagcatt tagtacaaa ggttcaagaa gtattcgtac 1020
tctagccttt ttaatcattc atagatagaa gtctttgtac ccaactcctta tgtttctttt 1080
cattcataaa cagggtgtata aggaacaatg tcttataaac agcatggggg caatctgaga 1140
atattcctca aaaggtgtcc aggttaaata gacatgttac tggctgcaca caggcaaatt 1200
ctagtttggt ttttttaagt attctacaac atttatttaa aaaggtaaatt ctttttggtg 1260
aagcagcaag ttatctggtg gaacttaact tctacaggat cagagaggat cttgtcatt 1320
catggccata tccacatgcc catggccact cagtagattg ttgaaaaagc aaagccacac 1380
cattctcttt gatgtatgca gagagttacg tagcagggga tgttctctga tttattccac 1440
tggcaccatt agtgaatatt tagttgtttt cataaacgat gctgtgatga agactcatgt 1500
acatatttag caaattttg tttcttacat gtgcctgtca tgactgtaat tcattatgac 1560
tgctccagga agggctaatt gggccaatat attattgcct gtcatgtggc acatccatgt 1620
taaggggctg aggcgtccct ggcacggaat gcagagccct gagctagggc atcagcagaa 1680
gctgagatag agatattggt catggttgac tgaggagcca attaaaacct gtttatgcct 1740
agtgttccat tattggaaca ctaagcatgt gggagttatt tatatcctac tgctcaagg 1800
catcgccaag gtgtgattgg aaaaattcaa aaaattgcaa cctcaggcat aaatgggtta 1860
aggacatccc aagcccaagt ggtacgtgcc tcaactcagaa ctgacgggcc gagttctatc 1920
taggtgtgtc ttccagaacc tgtttacggc taactggata actgagagac ttgtcatttc 1980
taaagacatt taagttgctc cagggatttc tgaaaaaaga cacaggcttc ttcctagagc 2040
cagccctata taacatgccc acaagggcaa cagttatcac agttcataca cacctttcat 2100
gtcctgtctc actcactcct cacagccatc ctaggagata catattgttt tcatcctgca 2160
tttacagaaa aagaaatgaa aacagagagc ttaaataaatt tgccacagta atgtcgaaac 2220
taggcctttg aaccaaggca gtctagggta aaatatagtt tcaaagtatg aataagaatt 2280
gggtatttggt ttatctttga gtaagaaaact gtccgatatg aatcacacg tgggtgaatg 2340
tagtattttc ctgaagtgtg aaaga 2365

```

&lt;210&gt; 49

&lt;211&gt; 228

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 49

```

Met Ala Ser Thr Ala Ser Glu Ile Ile Ala Phe Met Val Ser Ile Ser
 1           5           10          15
Gly Trp Val Leu Val Ser Ser Thr Leu Pro Thr Asp Tyr Trp Lys Val
 20          25          30
Ser Thr Ile Asp Gly Thr Val Ile Thr Thr Ala Thr Tyr Trp Ala Asn
 35          40          45
Leu Trp Lys Ala Cys Val Thr Asp Ser Thr Gly Val Ser Asn Cys Lys
 50          55          60
Asp Phe Pro Ser Met Leu Ala Leu Asp Gly Tyr Ile Gln Ala Cys Arg
 65          70          75          80
Gly Leu Met Ile Ala Ala Val Ser Leu Gly Phe Phe Gly Ser Ile Phe
 85          90          95
Ala Leu Phe Gly Met Lys Cys Thr Lys Val Gly Gly Ser Asp Lys Ala

```

	100		105		110										
Lys	Ala	Lys	Ile	Ala	Cys	Leu	Ala	Gly	Ile	Val	Phe	Ile	Leu	Ser	Gly
	115						120					125			
Leu	Cys	Ser	Met	Thr	Gly	Cys	Ser	Leu	Tyr	Ala	Asn	Lys	Ile	Thr	Thr
	130						135					140			
Glu	Phe	Phe	Asp	Pro	Leu	Phe	Val	Glu	Gln	Lys	Tyr	Glu	Leu	Gly	Ala
	145					150				155					160
Ala	Leu	Phe	Ile	Gly	Trp	Ala	Gly	Ala	Ser	Leu	Cys	Ile	Ile	Gly	Gly
			165					170							175
Val	Ile	Phe	Cys	Phe	Ser	Ile	Ser	Asp	Asn	Asn	Lys	Thr	Pro	Arg	Tyr
			180					185						190	
Thr	Tyr	Asn	Gly	Ala	Thr	Ser	Val	Met	Ser	Ser	Arg	Thr	Lys	Tyr	His
	195						200					205			
Gly	Gly	Glu	Asp	Phe	Lys	Thr	Thr	Asn	Pro	Ser	Lys	Gln	Phe	Asp	Lys
	210					215					220				
Asn	Ala	Tyr	Val												
	225														

<210> 50  
 <211> 1024  
 <212> DNA  
 <213> Homo sapiens

<400> 50  
 cccacccga aacacactca gcccttgac tgacctgcct tctgattgga ggctggttgc 60  
 ttcggataat gacctccagg accccactgt tggttacagc ctgtttgtat tattcttact 120  
 gcaactcaag acacctgcag cagggcgtga gaaaaagtaa aagaccagta tttcacatt 180  
 gccaggtagc agaaacacag aagactgaca ccgcccactt aagtggggcc agggctggtg 240  
 tctgcccatt ttgccatcct gatgggctgc ttgccacaat gagggatctt cttcaatata 300  
 tcgcttgctt ctttgccctt ttctctgctg gggttttgat tgtggccacc tggactgact 360  
 gttggatggt gaatgctgat gactctctgg aggtgagcac aaaatgccga ggcctctggt 420  
 gggaatgcgt cacaatgct ttgatggga ttgcacctg tgatgagtac gattccatac 480  
 ttgcggagca tcccttgaag ctggtggtaa ctcgagcgtt gatgattact gcagatattc 540  
 tagctgggtt tggatttctc accctgctcc ttggtcttga ctgcgtgaaa ttcctccctg 600  
 atgagccgta cattaaagtc cgcactctgt ttgttgctgg agccacgtta ctaatagcag 660  
 gtaccccagg aatcattggc tctgtgtggt atgctgttga tgtgtatgtg gaacgttcta 720  
 ctttggtttt gcacaatata tttcttggtt tccaatataa atttggttgg tcctgttggc 780  
 tcggaatggc tgggtctctg gggttgcctt tggctggagc tgttctcacc tgcgtgttat 840  
 atctttttta agatgttgg cctgagagaa actatcctta ttccttgagg aaagcctatt 900  
 cagccgcggg tgtttccatg gccaaagtc actcagcccc tcgcacagag acggccaaaa 960  
 tgtatgctgt agacacaagg gtgtaaaatg cacgtttcag ggtgtgtttg catatgattt 1020  
 aatc 1024

<210> 51  
 <211> 305  
 <212> PRT  
 <213> Homo sapiens

<400> 51  
 Met Thr Ser Arg Thr Pro Leu Leu Val Thr Ala Cys Leu Tyr Tyr Ser  
 1 5 10 15  
 Tyr Cys Asn Ser Arg His Leu Gln Gln Gly Val Arg Lys Ser Lys Arg  
 20 25 30  
 Pro Val Phe Ser His Cys Gln Val Pro Glu Thr Gln Lys Thr Asp Thr  
 35 40 45  
 Arg His Leu Ser Gly Ala Arg Ala Gly Val Cys Pro Cys Cys His Pro  
 50 55 60

Asp Gly Leu Leu Ala Thr Met Arg Asp Leu Leu Gln Tyr Ile Ala Cys  
 65 70 75 80  
 Phe Phe Ala Phe Phe Ser Ala Gly Phe Leu Ile Val Ala Thr Trp Thr  
 85 90 95  
 Asp Cys Trp Met Val Asn Ala Asp Asp Ser Leu Glu Val Ser Thr Lys  
 100 105 110  
 Cys Arg Gly Leu Trp Trp Glu Cys Val Thr Asn Ala Phe Asp Gly Ile  
 115 120 125  
 Arg Thr Cys Asp Glu Tyr Asp Ser Ile Leu Ala Glu His Pro Leu Lys  
 130 135 140  
 Leu Val Val Thr Arg Ala Leu Met Ile Thr Ala Asp Ile Leu Ala Gly  
 145 150 155 160  
 Phe Gly Phe Leu Thr Leu Leu Leu Gly Leu Asp Cys Val Lys Phe Leu  
 165 170 175  
 Pro Asp Glu Pro Tyr Ile Lys Val Arg Ile Cys Phe Val Ala Gly Ala  
 180 185 190  
 Thr Leu Leu Ile Ala Gly Thr Pro Gly Ile Ile Gly Ser Val Trp Tyr  
 195 200 205  
 Ala Val Asp Val Tyr Val Glu Arg Ser Thr Leu Val Leu His Asn Ile  
 210 215 220  
 Phe Leu Gly Ile Gln Tyr Lys Phe Gly Trp Ser Cys Trp Leu Gly Met  
 225 230 235 240  
 Ala Gly Ser Leu Gly Cys Phe Leu Ala Gly Ala Val Leu Thr Cys Cys  
 245 250 255  
 Leu Tyr Leu Phe Lys Asp Val Gly Pro Glu Arg Asn Tyr Pro Tyr Ser  
 260 265 270  
 Leu Arg Lys Ala Tyr Ser Ala Ala Gly Val Ser Met Ala Lys Ser Tyr  
 275 280 285  
 Ser Ala Pro Arg Thr Glu Thr Ala Lys Met Tyr Ala Val Asp Thr Arg  
 290 295 300  
 Val  
 305

&lt;210&gt; 52

&lt;211&gt; 1665

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 52

gaaggaactg gttctgctca cacttgctgg cttgcgcac aggactggct ttatctcctg 60  
 actcacgggtg caaaggtgca ctctgcgaac gtttaagtccg tccccagcgc ttggaatcct 120  
 acggccccca cagccggatc ccctcagcct tccaggtcct caactcccgt ggacgctgaa 180  
 caatggcctc catggggcta caggtaatgg gcatcgcgct ggccgtcctg ggctggctgg 240  
 ccgtcatgct gtgctgcgcg ctgcccatgt ggccgtgac ggcccttcac ggcagcaaca 300  
 ttgtcacctc gcagaccatc tgggagggcc tatggatgaa ctgctggtg cagagcaccg 360  
 gccagatgca gtgcaagggtg tacgactcgc tgctggcact gccgcaggac ctgcaggcgg 420  
 cccgcgccct cgtcatcatc agcatcatcg tggctgctct gggcgtgctg ctgtccgtgg 480  
 tggggggcaa gtgtaccaac tgcctggagg atgaaagcgc caaggccaag accatgatcg 540  
 tggcggcggt ggtgttcctg ttggccggcc ttatggtgat agtgccggtg tcctggacgg 600  
 cccacaacat catccaagac ttctacaatc cgctggtggc ctccgggcag aagcgggaga 660  
 tgggtgcctc gctctacgtc ggctggggcc cctccggcct gctgctcctt ggcggggggc 720  
 tgctttgctg caactgtcca cccgcacag acaagcctta ctccgccaa gttattctgctg 780  
 ccgcgtctgc tgctgccagc aactacgtgt aagggtgccac ggctccactc tgttctctc 840  
 tgctttgttc ttccctggac tgagctcagc gcaggctgtg accccaggag ggcctgcc 900  
 cgggccactg cctgctgggg actggggact gggcagagac tgagccaggc aggaaggcag 960  
 cagccttcag cctctctggc ccactcggac aacttcccaa ggccgcctcc tgctagcaag 1020  
 aacagagtcc accctcctct ggatattggg gagggacgga agtgacaggg tgtggtgggtg 1080

```

gagtggggag ctggcttctg ctggccagga tagcttaacc ctgactttgg gatctgcctg 1140
catcggcgtt ggccactgtc cccatttaca ttttccccac tctgtctgcc tgcattctct 1200
ctgttccggg taggccttga tatcacctct gggactgtgc cttgctcacc gaaacccgcg 1260
cccaggagta tggctgaggc cttgccacc cactgcctg ggaagtgcag agtggatgga 1320
cgggtttaga ggggaggggc gaaggtgctg taaacaggtt tgggcagtgg tgggggaggg 1380
ggccagagag gcggctcagg ttgccagct ctgtggcctc aggactctct gcctcaccgc 1440
cttcagccca gggcccctgg agactgatcc cctctgagtc ctctgcccct tccaaggaca 1500
ctaattgagc tgggaggggt gcagggagga ggggacagct tcacccttgg aagtcctggg 1560
gtttttcctc ttctttcttt gtggtttctg ttttgtaatt taagaagagc tattcatcac 1620
tgtaattatt attattttct acaataaatg ggacctgtgc acagg 1665

```

&lt;210&gt; 53

&lt;211&gt; 209

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 53

```

Met Ala Ser Met Gly Leu Gln Val Met Gly Ile Ala Leu Ala Val Leu
 1           5           10          15
Gly Trp Leu Ala Val Met Leu Cys Cys Ala Leu Pro Met Trp Arg Val
          20           25           30
Thr Ala Phe Ile Gly Ser Asn Ile Val Thr Ser Gln Thr Ile Trp Glu
          35           40           45
Gly Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys
 50           55           60
Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala
 65           70           75           80
Arg Ala Leu Val Ile Ile Ser Ile Ile Val Ala Ala Leu Gly Val Leu
          85           90           95
Leu Ser Val Val Gly Gly Lys Cys Thr Asn Cys Leu Glu Asp Glu Ser
          100          105          110
Ala Lys Ala Lys Thr Met Ile Val Ala Gly Val Val Phe Leu Leu Ala
          115          120          125
Gly Leu Met Val Ile Val Pro Val Ser Trp Thr Ala His Asn Ile Ile
          130          135          140
Gln Asp Phe Tyr Asn Pro Leu Val Ala Ser Gly Gln Lys Arg Glu Met
          145          150          155          160
Gly Ala Ser Leu Tyr Val Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu
          165          170          175
Gly Gly Gly Leu Leu Cys Cys Asn Cys Pro Pro Arg Thr Asp Lys Pro
          180          185          190
Tyr Ser Ala Lys Tyr Ser Ala Ala Arg Ser Ala Ala Ala Ser Asn Tyr
          195          200          205
Val

```

&lt;210&gt; 54

&lt;211&gt; 3457

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(3457)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 54

atgaagattt	tgatacttgg	tatttttctg	tttttatgta	gtaccccagc	ctgggcgaaa	60
gaaaagcatt	attacattgg	aattattgaa	acgacttggg	attatgcctc	tgaccatggg	120
gaaaagaaac	ttattttctgt	tgacacggaa	cattccaata	tctatcttca	aaatggccca	180
gatagaattg	ggagactata	taagaaggcc	ctttatcttc	agtacacaga	tgaaaccttt	240
aggacaacta	tagaaaaacc	ggtctggcct	gggttttttag	gccctattat	caaagctgaa	300
actggagata	aagttttatgt	acacttaaaa	aaccttgcct	ctaggcccta	cacctttcat	360
tcacatggaa	taacttacta	taaggaacat	gagggggcca	tctaccctga	taacaccaca	420
gattttcaaa	gagcagatga	caaagtatat	ccaggagagc	agtatacata	catgttgctt	480
gccactgaag	aacaaagtcc	tggggaagga	gatggcaatt	gtgtgactag	gatttaccat	540
tcccacattg	atgctccaaa	agatattgcc	tcaggactca	tcggaccttt	aataatctgt	600
aaaaaagatt	ctctagataa	agaaaaagaa	aaacatattg	accgagaatt	tgtggtgatg	660
ttttctgtgg	tggatgaaaa	tttcagctgg	tacctagaag	acaacattaa	aacctactgc	720
tcagaaccag	agaaagttga	caaagacaac	gaagacttcc	aggagagtaa	cagaatgtat	780
tctgtgaatg	gatacacttt	tgggaagtctc	ccaggactct	ccatgtgtgc	tgaagacaga	840
gtaaaatggg	accttttttg	tatgggtaat	gaagttgatg	tgcacgcagc	tttctttcac	900
gggcaagcac	tgactaacia	gaactaccgt	attgacacaa	tcaacctctt	tcctgctacc	960
ctgtttgatg	cttatatggg	ggcccagaac	cctggagaat	ggatgctcag	ctgtcagaat	1020
ctaaaccatc	tgaagccgg	tttgcaagcc	tttttccagg	tccaggagtg	taacaagtct	1080
tcatacaaag	ataaatccg	tgggaagcat	gttagacact	actacattgc	cgctgaggaa	1140
atcatctgga	actatgctoc	ctctggtata	gacatcttca	ctaaagaaaa	cttaacagca	1200
cctggaagtg	actcagcggg	gttttttgaa	caaggtacca	caagaattgg	aggctcttat	1260
aaaaagctgg	tttatcgtga	gtacacagat	gcctccttca	caaatcgaaa	ggagagaggc	1320
cctgaagaag	agcatcttgg	catcctgggt	cctgtcattt	gggcagaggt	gggagacacc	1380
atcagagtaa	ccttccataa	caaaggagca	tatcccctca	gtattgagcc	gattgggggtg	1440
agattcaata	agaacaacga	gggcacatac	tattccccaa	attacaaccc	ccagagcaga	1500
agtgtgcctc	cttcagcctc	ccatgtggca	cccacagaaa	cattcaccta	tgaatggact	1560
gtccccaaag	aagtaggacc	cactaatgca	gacctgtgt	gtctagctaa	gatgtattat	1620
tctgtctggt	atcccactaa	agatatattc	actgggctta	ttgggccaat	gaaaatgtc	1680
aagaaaggaa	gtttacatgc	aaatgggaga	cagaaagatg	tagacaagga	attctatttg	1740
tttctacag	tatttgatga	gaatgagagt	ttactcctgg	aagataatat	tagaatgttt	1800
acaactgcac	ctgatcaggt	ggataaggaa	gatgaagact	ttcaggaatc	taataaaatg	1860
cactccatga	atggattcat	gtatgggaat	cagccgggtc	tcactatgtg	caaaggagat	1920
tcggtcgtgt	ggtacttatt	cagcgccgga	aatgaggccg	atgtacatgg	aatatacttt	1980
tcaggaaaca	catatctgtg	gagaggagaa	cggagagaca	cagcaaacct	cttccctcaa	2040
acaagtctta	cgctccacat	gtggcctgac	acagagggga	cttttaatgt	tgaatgcctt	2100
acaactgatc	attacacagg	cggcatgaag	caaaaatata	ctgtgaacca	atgcaggcgg	2160
cagctctgagg	attccacctt	ctacctggga	gagaggacat	actatatcgc	agcagtgagg	2220
gtggaatggg	attattcccc	acaaagggag	tgggaaaagg	agctgcatca	tttacaagag	2280
cagaatgttt	caaatgcatt	tttagataag	ggagagtttt	acataggctc	aaagtacaag	2340
aaagttgtgt	atcggcagta	tactgatagc	acattccgtg	ttccagtggg	gagaaaagct	2400
gaagaagaac	atctgggaat	tctaggtcca	caacttcatg	cagatgttgg	agacaaaagtc	2460
aaaattatct	ttaaaaacat	ggccacaagg	ccctactcaa	tacatgcccc	tggggtaaaa	2520
acagagagtt	ctacagttac	tccaacatta	ccaggtgaaa	ctctcactta	cgtatggaaa	2580
atcccagaaa	gatctggagc	tggaaacagag	gattctgctt	gtattccatg	ggcttattat	2640
tcaactgtgg	atcaagttaa	ggacctctac	agtggattaa	ttggccccct	gattgtttgt	2700
cgaagacctt	acttgaaaagt	attcaatccc	agaagggaagc	tggaaattgc	ccttctgttt	2760
ctagtttttg	atgagaatga	atcttggtac	ttagatgaca	acatcaaaac	atactctgat	2820
caccccagaga	aagtaaacia	agatgatgag	gaattcatag	aaagcaataa	aatgcatgct	2880
attaatggaa	gaatgttttg	aaacctacaa	ggcctcacia	tgcacgtggg	agatgaagtc	2940
aactggatc	tgatgggaat	gggcaatgaa	atagacttac	acactgtaca	ttttcacggc	3000
catagcttcc	aatacaagca	caggggagtt	tatagttctg	atgtctttga	cattttccct	3060
ggaacatacc	aaaccttaga	aatgtttcca	agaacacctg	gaatttggtt	actccactgc	3120
catgtgaccg	accacattca	tgctggaatg	gaaaccactt	acaccgttct	acaaaatgaa	3180
ggtgaatatc	cagacaccaa	atctggctga	atgaaataaa	ttggtgataa	gtggaaaaaa	3240
gagaaaaaac	aatgattcat	aacaatgtat	gtgaaagtgt	aaaatagaat	gttactttgg	3300
aatgactata	aacattaaaa	gnagactggn	agcatacaac	tttgtacatt	tgtgggggaa	3360
aactattaat	tttgcccaaa	tggaaagatc	aacagactat	ataatgatac	atgactgaca	3420
ctgtacact	aggtaataaa	actgattcat	acagttct			3457

<210> 55  
 <211> 1069  
 <212> PRT  
 <213> Homo sapiens

<400> 55

Met	Lys	Ile	Leu	Ile	Leu	Gly	Ile	Phe	Leu	Phe	Leu	Cys	Ser	Thr	Pro
1			5					10						15	
Ala	Trp	Ala	Lys	Glu	Lys	His	Tyr	Tyr	Ile	Gly	Ile	Ile	Glu	Thr	Thr
		20					25						30		
Trp	Asp	Tyr	Ala	Ser	Asp	His	Gly	Glu	Lys	Lys	Leu	Ile	Ser	Val	Asp
	35					40					45				
Thr	Glu	His	Ser	Asn	Ile	Tyr	Leu	Gln	Asn	Gly	Pro	Asp	Arg	Ile	Gly
	50				55					60					
Arg	Leu	Tyr	Lys	Lys	Ala	Leu	Tyr	Leu	Gln	Tyr	Thr	Asp	Glu	Thr	Phe
65					70				75						80
Arg	Thr	Thr	Ile	Glu	Lys	Pro	Val	Trp	Leu	Gly	Phe	Leu	Gly	Pro	Ile
			85					90						95	
Ile	Lys	Ala	Glu	Thr	Gly	Asp	Lys	Val	Tyr	Val	His	Leu	Lys	Asn	Leu
		100						105					110		
Ala	Ser	Arg	Pro	Tyr	Thr	Phe	His	Ser	His	Gly	Ile	Thr	Tyr	Tyr	Lys
	115					120						125			
Glu	His	Glu	Gly	Ala	Ile	Tyr	Pro	Asp	Asn	Thr	Thr	Asp	Phe	Gln	Arg
	130					135				140					
Ala	Asp	Asp	Lys	Val	Tyr	Pro	Gly	Glu	Gln	Tyr	Thr	Tyr	Met	Leu	Leu
145					150				155					160	
Ala	Thr	Glu	Glu	Gln	Ser	Pro	Gly	Glu	Gly	Asp	Gly	Asn	Cys	Val	Thr
			165					170						175	
Arg	Ile	Tyr	His	Ser	His	Ile	Asp	Ala	Pro	Lys	Asp	Ile	Ala	Ser	Gly
		180					185						190		
Leu	Ile	Gly	Pro	Leu	Ile	Ile	Cys	Lys	Lys	Asp	Ser	Leu	Asp	Lys	Glu
	195					200						205			
Lys	Glu	Lys	His	Ile	Asp	Arg	Glu	Phe	Val	Val	Met	Phe	Ser	Val	Val
	210				215					220					
Asp	Glu	Asn	Phe	Ser	Trp	Tyr	Leu	Glu	Asp	Asn	Ile	Lys	Thr	Tyr	Cys
225					230					235					240
Ser	Glu	Pro	Glu	Lys	Val	Asp	Lys	Asp	Asn	Glu	Asp	Phe	Gln	Glu	Ser
			245					250						255	
Asn	Arg	Met	Tyr	Ser	Val	Asn	Gly	Tyr	Thr	Phe	Gly	Ser	Leu	Pro	Gly
		260					265						270		
Leu	Ser	Met	Cys	Ala	Glu	Asp	Arg	Val	Lys	Trp	Tyr	Leu	Phe	Gly	Met
	275					280						285			
Gly	Asn	Glu	Val	Asp	Val	His	Ala	Ala	Phe	Phe	His	Gly	Gln	Ala	Leu
	290				295					300					
Thr	Asn	Lys	Asn	Tyr	Arg	Ile	Asp	Thr	Ile	Asn	Leu	Phe	Pro	Ala	Thr
305					310					315					320
Leu	Phe	Asp	Ala	Tyr	Met	Val	Ala	Gln	Asn	Pro	Gly	Glu	Trp	Met	Leu
			325					330						335	
Ser	Cys	Gln	Asn	Leu	Asn	His	Leu	Lys	Ala	Gly	Leu	Gln	Ala	Phe	Phe
		340					345						350		
Gln	Val	Gln	Glu	Cys	Asn	Lys	Ser	Ser	Ser	Lys	Asp	Asn	Ile	Arg	Gly
	355					360						365			
Lys	His	Val	Arg	His	Tyr	Tyr	Ile	Ala	Ala	Glu	Glu	Ile	Ile	Trp	Asn
	370				375					380					
Tyr	Ala	Pro	Ser	Gly	Ile	Asp	Ile	Phe	Thr	Lys	Glu	Asn	Leu	Thr	Ala
385					390					395					400
Pro	Gly	Ser	Asp	Ser	Ala	Val	Phe	Phe	Glu	Gln	Gly	Thr	Thr	Arg	Ile



				405					410					415			
Gly	Gly	Ser	Tyr	Lys	Lys	Leu	Val	Tyr	Arg	Glu	Tyr	Thr	Asp	Ala	Ser		
			420					425					430				
Phe	Thr	Asn	Arg	Lys	Glu	Arg	Gly	Pro	Glu	Glu	Glu	His	Leu	Gly	Ile		
		435					440					445					
Leu	Gly	Pro	Val	Ile	Trp	Ala	Glu	Val	Gly	Asp	Thr	Ile	Arg	Val	Thr		
	450					455					460						
Phe	His	Asn	Lys	Gly	Ala	Tyr	Pro	Leu	Ser	Ile	Glu	Pro	Ile	Gly	Val		
465				470						475					480		
Arg	Phe	Asn	Lys	Asn	Asn	Glu	Gly	Thr	Tyr	Tyr	Ser	Pro	Asn	Tyr	Asn		
			485					490					495				
Pro	Gln	Ser	Arg	Ser	Val	Pro	Pro	Ser	Ala	Ser	His	Val	Ala	Pro	Thr		
		500					505					510					
Glu	Thr	Phe	Thr	Tyr	Glu	Trp	Thr	Val	Pro	Lys	Glu	Val	Gly	Pro	Thr		
	515						520					525					
Asn	Ala	Asp	Pro	Val	Cys	Leu	Ala	Lys	Met	Tyr	Tyr	Ser	Ala	Val	Asp		
	530					535					540						
Pro	Thr	Lys	Asp	Ile	Phe	Thr	Gly	Leu	Ile	Gly	Pro	Met	Lys	Ile	Cys		
545				550						555					560		
Lys	Lys	Gly	Ser	Leu	His	Ala	Asn	Gly	Arg	Gln	Lys	Asp	Val	Asp	Lys		
			565					570					575				
Glu	Phe	Tyr	Leu	Phe	Pro	Thr	Val	Phe	Asp	Glu	Asn	Glu	Ser	Leu	Leu		
		580					585					590					
Leu	Glu	Asp	Asn	Ile	Arg	Met	Phe	Thr	Thr	Ala	Pro	Asp	Gln	Val	Asp		
	595					600					605						
Lys	Glu	Asp	Glu	Asp	Phe	Gln	Glu	Ser	Asn	Lys	Met	His	Ser	Met	Asn		
	610					615					620						
Gly	Phe	Met	Tyr	Gly	Asn	Gln	Pro	Gly	Leu	Thr	Met	Cys	Lys	Gly	Asp		
625				630						635					640		
Ser	Val	Val	Trp	Tyr	Leu	Phe	Ser	Ala	Gly	Asn	Glu	Ala	Asp	Val	His		
			645					650					655				
Gly	Ile	Tyr	Phe	Ser	Gly	Asn	Thr	Tyr	Leu	Trp	Arg	Gly	Glu	Arg	Arg		
	660						665					670					
Asp	Thr	Ala	Asn	Leu	Phe	Pro	Gln	Thr	Ser	Leu	Thr	Leu	His	Met	Trp		
	675						680					685					
Pro	Asp	Thr	Glu	Gly	Thr	Phe	Asn	Val	Glu	Cys	Leu	Thr	Thr	Asp	His		
	690					695					700						
Tyr	Thr	Gly	Gly	Met	Lys	Gln	Lys	Tyr	Thr	Val	Asn	Gln	Cys	Arg	Arg		
705				710						715					720		
Gln	Ser	Glu	Asp	Ser	Thr	Phe	Tyr	Leu	Gly	Glu	Arg	Thr	Tyr	Tyr	Ile		
			725					730					735				
Ala	Ala	Val	Glu	Val	Glu	Trp	Asp	Tyr	Ser	Pro	Gln	Arg	Glu	Trp	Glu		
		740					745					750					
Lys	Glu	Leu	His	His	Leu	Gln	Glu	Gln	Asn	Val	Ser	Asn	Ala	Phe	Leu		
	755						760					765					
Asp	Lys	Gly	Glu	Phe	Tyr	Ile	Gly	Ser	Lys	Tyr	Lys	Lys	Val	Val	Tyr		
	770					775					780						
Arg	Gln	Tyr	Thr	Asp	Ser	Thr	Phe	Arg	Val	Pro	Val	Glu	Arg	Lys	Ala		
785				790						795					800		
Glu	Glu	Glu	His	Leu	Gly	Ile	Leu	Gly	Pro	Gln	Leu	His	Ala	Asp	Val		
			805					810					815				
Gly	Asp	Lys	Val	Lys	Ile	Ile	Phe	Lys	Asn	Met	Ala	Thr	Arg	Pro	Tyr		
		820						825					830				
Ser	Ile	His	Ala	His	Gly	Val	Gln	Thr	Glu	Ser	Ser	Thr	Val	Thr	Pro		
	835						840					845					
Thr	Leu	Pro	Gly	Glu	Thr	Leu	Thr	Tyr	Val	Trp	Lys	Ile	Pro	Glu	Arg		
	850					855					860						
Ser	Gly	Ala	Gly	Thr	Glu	Asp	Ser	Ala	Cys	Ile	Pro	Trp	Ala	Tyr	Tyr		

865		870		875		880
Ser Thr Val Asp Gln Val Lys Asp Leu Tyr Ser Gly Leu Ile Gly Pro						
	885		890		895	
Leu Ile Val Cys Arg Arg Pro Tyr Leu Lys Val Phe Asn Pro Arg Arg						
	900		905		910	
Lys Leu Glu Phe Ala Leu Leu Phe Leu Val Phe Asp Glu Asn Glu Ser						
	915		920		925	
Trp Tyr Leu Asp Asp Asn Ile Lys Thr Tyr Ser Asp His Pro Glu Lys						
	930		935		940	
Val Asn Lys Asp Asp Glu Glu Phe Ile Glu Ser Asn Lys Met His Ala						
	945		950		955	
Ile Asn Gly Arg Met Phe Gly Asn Leu Gln Gly Leu Thr Met His Val						
	965		970		975	
Gly Asp Glu Val Asn Trp Tyr Leu Met Gly Met Gly Asn Glu Ile Asp						
	980		985		990	
Leu His Thr Val His Phe His Gly His Ser Phe Gln Tyr Lys His Arg						
	995		1000		1005	
Gly Val Tyr Ser Ser Asp Val Phe Asp Ile Phe Pro Gly Thr Tyr Gln						
	1010		1015		1020	
Thr Leu Glu Met Phe Pro Arg Thr Pro Gly Ile Trp Leu Leu His Cys						
	1025		1030		1035	
His Val Thr Asp His Ile His Ala Gly Met Glu Thr Thr Tyr Thr Val						
	1045		1050		1055	
Leu Gln Asn Glu Gly Glu Tyr Pro Asp Thr Lys Ser Gly						
	1060		1065			

&lt;210&gt; 56

&lt;211&gt; 2807

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 56

cgtggtgatg	ttttctgtgg	tggatgaaaa	tttcagctgg	tacctagaag	acaacattaa	60
aacctactgc	tcagaaccag	agaaagttga	caaagacaac	gaagacttcc	aggagagtaa	120
cagaatgtat	tctgtgaatg	gatacacttt	tggaagtctc	ccaggactct	ccatgtgtgc	180
tgaagacaga	gtaaaatggg	acctttttgg	tatgggtaat	gaagttgatg	tgcacgcagc	240
tttctttcac	gggcaagcac	tgactaacaa	gaactaccgt	attgacacaa	tcaacctctt	300
tcctgctacc	ctgtttgatg	cttatatggg	ggcccagaac	cctggagaat	ggatgctcag	360
ctgtcagaat	ctaaaccatc	tgaaagccgg	tttgcaagcc	tttttccagg	tccaggagtg	420
taacaagtct	tcatacaagg	ataatatccg	tggaagcat	gttagacact	actacattgc	480
cgctgaggaa	atcatctgga	actatgctcc	ctctggtata	gacatcttca	ctaaagaaaa	540
cttaacagca	cctggaagtg	actcagcggg	gttttttgaa	caaggtacca	caagaattgg	600
aggctcttat	aaaaagctgg	tttatcgtga	gtacacagat	gcctccttca	caaatcgaaa	660
ggagagaggg	cctgaagaag	agcatcttgg	catcctgggt	cctgtcattt	gggcagaggt	720
gggagacacc	atcagagtaa	ccttccataa	caaaggagca	tatccccctca	gtattgagcc	780
gattgggggtg	agattcaata	agaacaacga	gggcacatac	tattcccca	attacaaccc	840
ccagagcaga	agtgtgcctc	cttcagcctc	ccatgtggca	cccacagaaa	cattcaccta	900
tgaatggact	gtcccccagg	aagtaggacc	cactaatgca	gatcctgtgt	gtctagctaa	960
gatgtattat	tctgtctgtg	atcccactaa	agatatattc	actgggctta	ttggggccaat	1020
gaaaatatgc	aagaaaggaa	gtttacatgc	aaatgggaga	cagaaagatg	tagacaagga	1080
attctatttg	tttccctacag	tattttgatga	gaatgagagt	ttactcctgg	aagataatat	1140
tagaatgttt	acaactgcac	ctgatcaggt	ggataaggaa	gatgaagact	ttcaggaatc	1200
taataaaatg	cactccatga	atggattcat	gtatgggaat	cagccgggtc	tcactatgtg	1260
caaaggagat	tcgggtcgtg	ggtacttatt	cagcgccgga	aatgaggccg	atgtacatgg	1320
aatatacttt	tcaggaaaaca	catatctgtg	gagaggagaa	cggagagaca	cagcaaacct	1380
cttccctcaa	acaagtctta	cgctccacat	gtggcctgac	acagagggga	cttttaaatgt	1440
tgaatgcctt	acaactgatc	attacacagg	cggcatgaag	caaaaatata	ctgtgaacca	1500

```

atgcaggcgg cagtctgagg attccacctt ctacctggga gagaggacat actatatcgc 1560
agcagtggag gtggaatggg attattcccc acaaagggag tgggaaaagg agctgcatca 1620
tttacaagag cagaatgttt caaatgcatt tttagataag ggagagtgtt acataggctc 1680
aaagtacaag aaagtttgtg atcggcagta tactgatagc acattccgtg ttccagtggg 1740
gagaaaagct gaagaagaac atctgggaat tctaggtcca caacttcatg cagatgttgg 1800
agacaaaagtc aaaattatct ttaaaaacat ggccacaagg ccctactcaa tacatgcca 1860
tggggtacaa acagagagtt ctacagttac tccaacatta ccaggtgaaa ctctcactta 1920
cgtatggaaa atcccagaaa gatctggagc tggaacagag gattctgctt gtattccatg 1980
ggcttattat tcaactgtgg atcaagttaa ggacctctac agtggattaa ttggccccct 2040
gattgtttgt cgaagacctt acttgaaagt attcaatccc agaaggaaac tgggaatttg 2100
ccttctgttt ctagtgtttg atgagaatga atcttggtag ttagatgaca acatcaaaac 2160
atactctgat ccccccgaga aagtaaacaa agatgatgag gaattcatag aaagcaataa 2220
aatgcatgct attaatggaa gaatgtttgg aaacctacaa ggcctcacia tgcacgtggg 2280
agatgaagtc aactggtatc tgatgggaat gggcaatgaa atagacttac acactgtaca 2340
ttttcacggc catagcttcc aatacaagca caggggagtt tatagttctg atgtctttga 2400
cattttccct ggaacatacc aaaccctaga aatgtttcca agaacacctg gaatttggtt 2460
actccactgc catgtgaccg accacattca tgctggaatg gaaaccactt acaccgttct 2520
acaaaatgaa ggtgaatatc cagacaccaa atctggctga atgaaataaa ttggtgataa 2580
gtggaaaaaa gagaaaaaac aatgattcat aacaatgtat gtgaaagtgt aaaatagaat 2640
gttactttgg aatgactata aacattaaaa gaagactgga agcatacaac tttgtacatt 2700
tgtgggggaa aactattaat tttgcccaaa tggaaagatc aacagactat ataatgatac 2760
atgactgaca cttgtacact aggtaataaa actgattcat acagtct 2807

```

&lt;210&gt; 57

&lt;211&gt; 852

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 57

```

Val Val Met Phe Ser Val Val Asp Glu Asn Phe Ser Trp Tyr Leu Glu
1          5          10          15
Asp Asn Ile Lys Thr Tyr Cys Ser Glu Pro Glu Lys Val Asp Lys Asp
20          25          30
Asn Glu Asp Phe Gln Glu Ser Asn Arg Met Tyr Ser Val Asn Gly Tyr
35          40          45
Thr Phe Gly Ser Leu Pro Gly Leu Ser Met Cys Ala Glu Asp Arg Val
50          55          60
Lys Trp Tyr Leu Phe Gly Met Gly Asn Glu Val Asp Val His Ala Ala
65          70          75          80
Phe Phe His Gly Gln Ala Leu Thr Asn Lys Asn Tyr Arg Ile Asp Thr
85          90          95
Ile Asn Leu Phe Pro Ala Thr Leu Phe Asp Ala Tyr Met Val Ala Gln
100          105          110
Asn Pro Gly Glu Trp Met Leu Ser Cys Gln Asn Leu Asn His Leu Lys
115          120          125
Ala Gly Leu Gln Ala Phe Phe Gln Val Gln Glu Cys Asn Lys Ser Ser
130          135          140
Ser Lys Asp Asn Ile Arg Gly Lys His Val Arg His Tyr Tyr Ile Ala
145          150          155          160
Ala Glu Glu Ile Ile Trp Asn Tyr Ala Pro Ser Gly Ile Asp Ile Phe
165          170          175
Thr Lys Glu Asn Leu Thr Ala Pro Gly Ser Asp Ser Ala Val Phe Phe
180          185          190
Glu Gln Gly Thr Thr Arg Ile Gly Gly Ser Tyr Lys Lys Leu Val Tyr
195          200          205
Arg Glu Tyr Thr Asp Ala Ser Phe Thr Asn Arg Lys Glu Arg Gly Pro
210          215          220
Glu Glu Glu His Leu Gly Ile Leu Gly Pro Val Ile Trp Ala Glu Val

```

225		230		235		240
Gly Asp Thr Ile Arg Val Thr Phe His Asn Lys Gly Ala Tyr Pro Leu						
	245		250		255	
Ser Ile Glu Pro Ile Gly Val Arg Phe Asn Lys Asn Asn Glu Gly Thr						
	260		265		270	
Tyr Tyr Ser Pro Asn Tyr Asn Pro Gln Ser Arg Ser Val Pro Pro Ser						
	275		280		285	
Ala Ser His Val Ala Pro Thr Glu Thr Phe Thr Tyr Glu Trp Thr Val						
	290		295		300	
Pro Lys Glu Val Gly Pro Thr Asn Ala Asp Pro Val Cys Leu Ala Lys						
	305		310		315	
Met Tyr Tyr Ser Ala Val Asp Pro Thr Lys Asp Ile Phe Thr Gly Leu						
	325		330		335	
Ile Gly Pro Met Lys Ile Cys Lys Lys Gly Ser Leu His Ala Asn Gly						
	340		345		350	
Arg Gln Lys Asp Val Asp Lys Glu Phe Tyr Leu Phe Pro Thr Val Phe						
	355		360		365	
Asp Glu Asn Glu Ser Leu Leu Leu Glu Asp Asn Ile Arg Met Phe Thr						
	370		375		380	
Thr Ala Pro Asp Gln Val Asp Lys Glu Asp Glu Asp Phe Gln Glu Ser						
	385		390		395	
Asn Lys Met His Ser Met Asn Gly Phe Met Tyr Gly Asn Gln Pro Gly						
	405		410		415	
Leu Thr Met Cys Lys Gly Asp Ser Val Val Trp Tyr Leu Phe Ser Ala						
	420		425		430	
Gly Asn Glu Ala Asp Val His Gly Ile Tyr Phe Ser Gly Asn Thr Tyr						
	435		440		445	
Leu Trp Arg Gly Glu Arg Arg Asp Thr Ala Asn Leu Phe Pro Gln Thr						
	450		455		460	
Ser Leu Thr Leu His Met Trp Pro Asp Thr Glu Gly Thr Phe Asn Val						
	465		470		475	
Glu Cys Leu Thr Thr Asp His Tyr Thr Gly Gly Met Lys Gln Lys Tyr						
	485		490		495	
Thr Val Asn Gln Cys Arg Arg Gln Ser Glu Asp Ser Thr Phe Tyr Leu						
	500		505		510	
Gly Glu Arg Thr Tyr Tyr Ile Ala Ala Val Glu Val Glu Trp Asp Tyr						
	515		520		525	
Ser Pro Gln Arg Glu Trp Glu Lys Glu Leu His His Leu Gln Glu Gln						
	530		535		540	
Asn Val Ser Asn Ala Phe Leu Asp Lys Gly Glu Phe Tyr Ile Gly Ser						
	545		550		555	
Lys Tyr Lys Lys Val Val Tyr Arg Gln Tyr Thr Asp Ser Thr Phe Arg						
	565		570		575	
Val Pro Val Glu Arg Lys Ala Glu Glu His Leu Gly Ile Leu Gly						
	580		585		590	
Pro Gln Leu His Ala Asp Val Gly Asp Lys Val Lys Ile Ile Phe Lys						
	595		600		605	
Asn Met Ala Thr Arg Pro Tyr Ser Ile His Ala His Gly Val Gln Thr						
	610		615		620	
Glu Ser Ser Thr Val Thr Pro Thr Leu Pro Gly Glu Thr Leu Thr Tyr						
	625		630		635	
Val Trp Lys Ile Pro Glu Arg Ser Gly Ala Gly Thr Glu Asp Ser Ala						
	645		650		655	
Cys Ile Pro Trp Ala Tyr Tyr Ser Thr Val Asp Gln Val Lys Asp Leu						
	660		665		670	
Tyr Ser Gly Leu Ile Gly Pro Leu Ile Val Cys Arg Arg Pro Tyr Leu						
	675		680		685	
Lys Val Phe Asn Pro Arg Arg Lys Leu Glu Phe Ala Leu Leu Phe Leu						

690		695		700
Val Phe Asp Glu Asn Glu Ser Trp Tyr Leu Asp		Asp Asn Ile Lys Thr		
705		710		715
Tyr Ser Asp His Pro Glu Lys Val Asn Lys Asp		Asp Glu Glu Phe Ile		720
		725		730
				735
Glu Ser Asn Lys Met His Ala Ile Asn Gly Arg		Met Phe Gly Asn Leu		
		740		745
				750
Gln Gly Leu Thr Met His Val Gly Asp Glu Val		Asn Trp Tyr Leu Met		
		755		760
				765
Gly Met Gly Asn Glu Ile Asp Leu His Thr Val		His Phe His Gly His		
		770		775
				780
Ser Phe Gln Tyr Lys His Arg Gly Val Tyr Ser		Ser Asp Val Phe Asp		
785		790		795
				800
Ile Phe Pro Gly Thr Tyr Gln Thr Leu Glu Met		Phe Pro Arg Thr Pro		
		805		810
				815
Gly Ile Trp Leu Leu His Cys His Val Thr Asp		His Ile His Ala Gly		
		820		825
				830
Met Glu Thr Thr Tyr Thr Val Leu Gln Asn Glu		Gly Glu Tyr Pro Asp		
		835		840
				845
Thr Lys Ser Gly				
850				

&lt;210&gt; 58

&lt;211&gt; 3321

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 58

atgaagattt	tgataacttg	tatttttctg	tttttatgta	gtacccacgc	ctgggcgaaa	60
gaaaagcatt	attacattgg	aattattgaa	acgacttggg	attatgcctc	tgaccatggg	120
gaaaagaaac	ttattttctgt	tgacacggaa	cattccaata	tctatcttca	aaatggccca	180
gatagaattg	ggagactata	taagaaggcc	ctttatcttc	agtacacaga	tgaaaccttt	240
aggacaacta	tagaaaaacc	ggtctggctt	gggttttttag	gccctattat	caaagctgaa	300
actggagata	aagtttatgt	acacttaaaa	aaccttgcct	ctaggcccta	cacctttcat	360
tcacattgaa	taacttacta	taaggaacat	gagggggcca	tctaccctga	taacaccaca	420
gattttcaaa	gagcagatga	caaagtatat	ccaggagagc	agtatacata	catgttgctt	480
gccactgaa	aacaaagtcc	tggggaagga	gatggcaatt	gtgtgactag	gatttaccat	540
tcccacattg	atgctccaaa	agatattgcc	tcaggactca	tcggaccttt	aataatctgt	600
aaaaaagatt	ctctagataa	agaaaaagaa	aaacatatgt	accgagaatt	tgtggtgatg	660
ttttctgtgg	tgatgaaaa	tttcagctgg	tacctagaag	acaacattaa	aacctactgc	720
tcagaaccag	agaaagttga	caaagacaac	gaagacttcc	aggagagtaa	cagaatgtat	780
tctgtgaatg	gatacacttt	tggaagtctc	ccaggactct	ccatgtgtgc	tgaagacaga	840
gtaaaatggt	accttttttg	tatgggtaat	gaagttgatg	tgacgcgcgc	tttctttcac	900
gggcaagcac	tgactaacia	gaactaccgt	attgacacaa	tcaacctctt	tcctgtacc	960
ctgtttgatg	cttatatggt	ggcccagaac	cctggagaat	ggatgctcag	ctgtcagaat	1020
ctaaaccatc	tgaaagccgg	tttgcaagcc	tttttccagg	tccaggagtg	taacaagtct	1080
tcatacaagg	ataatatccg	tggaagcat	gttagacact	actacattgc	cgctgaggaa	1140
atcatctgga	actatgctcc	ctctgtgata	gacatcttca	ctaaagaaaa	cttaacagca	1200
cctggaagtg	actcagcggg	gttttttgaa	caaggtacca	caagaattgg	aggctcttat	1260
aaaaagctgg	tttatcgtga	gtacacagat	gcctccttca	caaatcgaaa	ggagagaggc	1320
cctgaagaag	agcatcttgg	catcctgggt	cctgtcattt	gggcagagg	gggagacacc	1380
atcagagtaa	ccttccataa	caaaggagca	tatccctcca	gtattgagcc	gattggggtg	1440
agattcaata	agaacaacga	gggcacatac	tattcccaaa	attacaaccc	ccagagcaga	1500
agtgtgcctc	cttcagcctc	ccatgtggca	cccacagaaa	cattcaccta	tgaatggact	1560
gtccccaag	aagttagacc	cactaatgca	gatcctgtgt	gtctagctaa	gatgtattat	1620
tctgtctgtg	atcccaacta	agatatattc	actgggctta	ttggggccaa	gaaaatatgc	1680
aagaaaggaa	gtttacatgc	aaatgggaga	cagaaagatg	tagacaagga	attctatttg	1740

```

tttcctacag tatttgatga gaatgagagt ttactcctgg aagataatat tagaatgttt 1800
acaactgcac ctgatcaggt ggataaggaa gatgaagact ttcaggaatc taataaaatg 1860
cactccatga atggattcat gtatgggaat cagccgggtc tcactatgtg caaaggagat 1920
tcgggtcgtgt ggtacttatt cagcgccgga aatgaggccg atgtacatgg aatatacttt 1980
tcaggaaaca catatctgtg gagaggagaa cggagagaca cagcaaacct cttccctcaa 2040
acaagtctta cgctccacat gtggcctgac acagagggga cttttaatgt tgaatgcctt 2100
acaactgac attacacagg cggcatgaag caaaaatata ctgtgaacca atgcaggcgg 2160
cagtctgagg attccacctt ctacctggga gagaggacat actatatcgc agcagtggag 2220
gtggaatggg attattcccc acaaaggagg tgggaaaagg agctgcatca tttacaagag 2280
cagaatgttt caaatgcatt tttagataag ggagagtgtt acataggctc aaagtacaag 2340
aaagtgtgt atcggcagta tactgatagc acattccgtg ttccagtgga gagaaaagct 2400
gaagaagaac atctgggaat tctaggtcca caacttcatg cagatgttgg agacaaaagtc 2460
aaaattatct ttaaaaacat ggccacaagg ccctactcaa tacatgcccc tggggtacaa 2520
acagagagtt ctacagttac tccaacatta ccagggtgaaa ctctcactta cgtatggaaa 2580
atcccagaaa gatctggagc tggaacagag gattctgctt gtaattccatg ggcttattat 2640
tcaactgtgg atcaagttaa ggacctctac agtggattaa ttggccccct gattgtttgt 2700
cgaagacctt acttgaaagt attcaatccc agaaggaagc tggaattttgc ccttctgttt 2760
ctagtttttg atgagaatga atcttggtag ttagatgaca acatcaaaac atactctgat 2820
caccgcgaga aagtaaacaa agatgatgag gaattcatag aaagcaataa aatgcatgct 2880
attaatggaa gaatgtttgg aaacctacaa ggcctcacia tgcacgtggg agatgaagtc 2940
aactggtatc tgatgggaat gggcaatgaa atagacttac acactgtaca ttttcacggc 3000
catagcttcc aatacaagca caggggagtt tatagttctg atgtctttga cattttccct 3060
ggaacatacc aaacctaga aatgtttcca agaaccactg gaatttggtt actccactgc 3120
catgtgaccg accacattca tgctggaatg gaaaccactt acaccgttct acaaaatgaa 3180
gacaccaaat ctggctgaat gaaataaatt ggtgataagt ggaaaaaaga gaaaaaccaa 3240
tgattcataa caatgtatgt gaaagtgtaa aatagaatgt tactttggaa tgactataaa 3300
cattaaaga gactggagca t 3321

```

&lt;210&gt; 59

&lt;211&gt; 1065

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 59

```

Met Lys Ile Leu Ile Leu Gly Ile Phe Leu Phe Leu Cys Ser Thr Pro
 1           5           10           15
Ala Trp Ala Lys Glu Lys His Tyr Tyr Ile Gly Ile Ile Glu Thr Thr
      20           25           30
Trp Asp Tyr Ala Ser Asp His Gly Glu Lys Lys Leu Ile Ser Val Asp
      35           40           45
Thr Glu His Ser Asn Ile Tyr Leu Gln Asn Gly Pro Asp Arg Ile Gly
      50           55           60
Arg Leu Tyr Lys Lys Ala Leu Tyr Leu Gln Tyr Thr Asp Glu Thr Phe
      65           70           75           80
Arg Thr Thr Ile Glu Lys Pro Val Trp Leu Gly Phe Leu Gly Pro Ile
      85           90           95
Ile Lys Ala Glu Thr Gly Asp Lys Val Tyr Val His Leu Lys Asn Leu
      100          105          110
Ala Ser Arg Pro Tyr Thr Phe His Ser His Gly Ile Thr Tyr Tyr Lys
      115          120          125
Glu His Glu Gly Ala Ile Tyr Pro Asp Asn Thr Thr Asp Phe Gln Arg
      130          135          140
Ala Asp Asp Lys Val Tyr Pro Gly Glu Gln Tyr Thr Tyr Met Leu Leu
      145          150          155          160
Ala Thr Glu Glu Gln Ser Pro Gly Glu Gly Asp Gly Asn Cys Val Thr
      165          170          175
Arg Ile Tyr His Ser His Ile Asp Ala Pro Lys Asp Ile Ala Ser Gly
      180          185          190

```

Leu Ile Gly Pro Leu Ile Ile Cys Lys Lys Asp Ser Leu Asp Lys Glu  
 195 200 205  
 Lys Glu Lys His Ile Asp Arg Glu Phe Val Val Met Phe Ser Val Val  
 210 215 220  
 Asp Glu Asn Phe Ser Trp Tyr Leu Glu Asp Asn Ile Lys Thr Tyr Cys  
 225 230 235 240  
 Ser Glu Pro Glu Lys Val Asp Lys Asp Asn Glu Asp Phe Gln Glu Ser  
 245 250 255  
 Asn Arg Met Tyr Ser Val Asn Gly Tyr Thr Phe Gly Ser Leu Pro Gly  
 260 265 270  
 Leu Ser Met Cys Ala Glu Asp Arg Val Lys Trp Tyr Leu Phe Gly Met  
 275 280 285  
 Gly Asn Glu Val Asp Val His Ala Ala Phe Phe His Gly Gln Ala Leu  
 290 295 300  
 Thr Asn Lys Asn Tyr Arg Ile Asp Thr Ile Asn Leu Phe Pro Ala Thr  
 305 310 315 320  
 Leu Phe Asp Ala Tyr Met Val Ala Gln Asn Pro Gly Glu Trp Met Leu  
 325 330 335  
 Ser Cys Gln Asn Leu Asn His Leu Lys Ala Gly Leu Gln Ala Phe Phe  
 340 345 350  
 Gln Val Gln Glu Cys Asn Lys Ser Ser Ser Lys Asp Asn Ile Arg Gly  
 355 360 365  
 Lys His Val Arg His Tyr Tyr Ile Ala Ala Glu Glu Ile Ile Trp Asn  
 370 375 380  
 Tyr Ala Pro Ser Gly Ile Asp Ile Phe Thr Lys Glu Asn Leu Thr Ala  
 385 390 395 400  
 Pro Gly Ser Asp Ser Ala Val Phe Phe Glu Gln Gly Thr Thr Arg Ile  
 405 410 415  
 Gly Gly Ser Tyr Lys Lys Leu Val Tyr Arg Glu Tyr Thr Asp Ala Ser  
 420 425 430  
 Phe Thr Asn Arg Lys Glu Arg Gly Pro Glu Glu Glu His Leu Gly Ile  
 435 440 445  
 Leu Gly Pro Val Ile Trp Ala Glu Val Gly Asp Thr Ile Arg Val Thr  
 450 455 460  
 Phe His Asn Lys Gly Ala Tyr Pro Leu Ser Ile Glu Pro Ile Gly Val  
 465 470 475 480  
 Arg Phe Asn Lys Asn Asn Glu Gly Thr Tyr Tyr Ser Pro Asn Tyr Asn  
 485 490 495  
 Pro Gln Ser Arg Ser Val Pro Pro Ser Ala Ser His Val Ala Pro Thr  
 500 505 510  
 Glu Thr Phe Thr Tyr Glu Trp Thr Val Pro Lys Glu Val Gly Pro Thr  
 515 520 525  
 Asn Ala Asp Pro Val Cys Leu Ala Lys Met Tyr Tyr Ser Ala Val Asp  
 530 535 540  
 Pro Thr Lys Asp Ile Phe Thr Gly Leu Ile Gly Pro Met Lys Ile Cys  
 545 550 555 560  
 Lys Lys Gly Ser Leu His Ala Asn Gly Arg Gln Lys Asp Val Asp Lys  
 565 570 575  
 Glu Phe Tyr Leu Phe Pro Thr Val Phe Asp Glu Asn Glu Ser Leu Leu  
 580 585 590  
 Leu Glu Asp Asn Ile Arg Met Phe Thr Thr Ala Pro Asp Gln Val Asp  
 595 600 605  
 Lys Glu Asp Glu Asp Phe Gln Glu Ser Asn Lys Met His Ser Met Asn  
 610 615 620  
 Gly Phe Met Tyr Gly Asn Gln Pro Gly Leu Thr Met Cys Lys Gly Asp  
 625 630 635 640  
 Ser Val Val Trp Tyr Leu Phe Ser Ala Gly Asn Glu Ala Asp Val His  
 645 650 655

Gly Ile Tyr Phe Ser Gly Asn Thr Tyr Leu Trp Arg Gly Glu Arg Arg  
 660 665 670  
 Asp Thr Ala Asn Leu Phe Pro Gln Thr Ser Leu Thr Leu His Met Trp  
 675 680 685  
 Pro Asp Thr Glu Gly Thr Phe Asn Val Glu Cys Leu Thr Thr Asp His  
 690 695 700  
 Tyr Thr Gly Gly Met Lys Gln Lys Tyr Thr Val Asn Gln Cys Arg Arg  
 705 710 715 720  
 Gln Ser Glu Asp Ser Thr Phe Tyr Leu Gly Glu Arg Thr Tyr Tyr Ile  
 725 730 735  
 Ala Ala Val Glu Val Glu Trp Asp Tyr Ser Pro Gln Arg Glu Trp Glu  
 740 745 750  
 Lys Glu Leu His His Leu Gln Glu Gln Asn Val Ser Asn Ala Phe Leu  
 755 760 765  
 Asp Lys Gly Glu Phe Tyr Ile Gly Ser Lys Tyr Lys Lys Val Val Tyr  
 770 775 780  
 Arg Gln Tyr Thr Asp Ser Thr Phe Arg Val Pro Val Glu Arg Lys Ala  
 785 790 795 800  
 Glu Glu Glu His Leu Gly Ile Leu Gly Pro Gln Leu His Ala Asp Val  
 805 810 815  
 Gly Asp Lys Val Lys Ile Ile Phe Lys Asn Met Ala Thr Arg Pro Tyr  
 820 825 830  
 Ser Ile His Ala His Gly Val Gln Thr Glu Ser Ser Thr Val Thr Pro  
 835 840 845  
 Thr Leu Pro Gly Glu Thr Leu Thr Tyr Val Trp Lys Ile Pro Glu Arg  
 850 855 860  
 Ser Gly Ala Gly Thr Glu Asp Ser Ala Cys Ile Pro Trp Ala Tyr Tyr  
 865 870 875 880  
 Ser Thr Val Asp Gln Val Lys Asp Leu Tyr Ser Gly Leu Ile Gly Pro  
 885 890 895  
 Leu Ile Val Cys Arg Arg Pro Tyr Leu Lys Val Phe Asn Pro Arg Arg  
 900 905 910  
 Lys Leu Glu Phe Ala Leu Leu Phe Leu Val Phe Asp Glu Asn Glu Ser  
 915 920 925  
 Trp Tyr Leu Asp Asp Asn Ile Lys Thr Tyr Ser Asp His Pro Glu Lys  
 930 935 940  
 Val Asn Lys Asp Asp Glu Glu Phe Ile Glu Ser Asn Lys Met His Ala  
 945 950 955 960  
 Ile Asn Gly Arg Met Phe Gly Asn Leu Gln Gly Leu Thr Met His Val  
 965 970 975  
 Gly Asp Glu Val Asn Trp Tyr Leu Met Gly Met Gly Asn Glu Ile Asp  
 980 985 990  
 Leu His Thr Val His Phe His Gly His Ser Phe Gln Tyr Lys His Arg  
 995 1000 1005  
 Gly Val Tyr Ser Ser Asp Val Phe Asp Ile Phe Pro Gly Thr Tyr Gln  
 1010 1015 1020  
 Thr Leu Glu Met Phe Pro Arg Thr Pro Gly Ile Trp Leu Leu His Cys  
 1025 1030 1035 1040  
 His Val Thr Asp His Ile His Ala Gly Met Glu Thr Thr Tyr Thr Val  
 1045 1050 1055  
 Leu Gln Asn Glu Asp Thr Lys Ser Gly  
 1060 1065

&lt;210&gt; 60

&lt;211&gt; 3881

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens



&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(3881)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 60

```

agaaagcttt atttataaaa ttgcctgctc ctgattttac ttcattttctt ctcaggctcc 60
aagaagggga aaaaaatgaa gatttttgata cttgggtattt ttctgttttt atgtagtacc 120
ccagcctggg cgaaagaaaa gcattattac attggaatta ttgaaacgac ttgggattat 180
gcctctgacc atggggaaaa gaaacttatt tctgttgaca cggaacattc caatatctat 240
cttcaaaatg gccagatag aattggggaga ctatataaga aggcccttta tcttcagtac 300
acagatgaaa cttttaggac aactatagaa aaaccggtct ggcttgggtt tttaggccct 360
attatcaaag ctgaaactgg agataaagtt tatgtacact taaaaaacct tgcctctagg 420
ccctacacct ttcattcaca tggataaact tactataagg aacatgaggg ggccatctac 480
cctgataaca ccacagattt tcaaagagca gatgacaaag tatatccagg agagcagtat 540
acatacatgt tgcttgccac tgaagaacaa agtcctgggg aaggagatgg caattgtgtg 600
actaggattt accattccca cattgatgct ccaaaagata ttgcctcagg actcatcgga 660
cctttaataa tctgtaaaaa agattctcta gataaagaaa aagaaaaaca tattgaccga 720
gaatttgtgg tgatgttttc tgtggtggat gaaaatttca gctggtacct agaagacaac 780
attaaaacct actgctcaga accagagaaa gttgacaaag acaacgaaga cttccaggag 840
agtaacagaa tgtattctgt gaatggatac acttttggaa gtctcccagg actctccatg 900
tgtgtgaag acagagtaaa atggtacctt tttggtatgg gtaatgaagt tgatgtgcac 960
gcagctttct ttcacgggca agcactgact aacaagaact accgtattga cacaatcaac 1020
ctctttcctg ctaccctgtt tgatgcttat atggtggccc agaaccctgg agaatggatg 1080
ctcagctgtc agaatctaaa ccatctgaaa gccggtttgc aagccttttt ccagggtccag 1140
gagtgtaaac agtcttcac aaaggataat atccgtggga agcatgttag acactactac 1200
attgccgtcg aggaatcat ctggaactat gctccctctg gtatagacat cttcactaaa 1260
gaaaacttaa cagcacctgg aagtgactca gcggtgtttt ttgaacaagg taccacaaga 1320
attggaggct cttataaaaa gctggtttat cgtgagtaca cagatgcctc cttcacaaat 1380
cgaaaggaga gaggccctga agaagagcat cttggcatcc tgggtcctgt catttgggca 1440
gagtgaggag acaccatcag agtaaccttc catacaaaag gagcatatcc cctcagtatt 1500
gagccgattg gggtgagatt caataagaac aacgagggca catactattc cccaaattac 1560
aacccccaga gcagaagtgt gcctccttca gcctcccatg tggcaccac agaaacattc 1620
acctatgaat ggactgtccc caaagaagta ggaccacta atgcagatcc tgtgtgtcta 1680
gctaagatgt attattctgc tgtggatccc actaaagata tattcactgg gcttattggg 1740
ccaatgaaaa tatgcaagaa aggaagttaa catgcaaatg ggagacagaa agatgtagac 1800
aaggaattct atttgtttcc tacagtattt gatgagaatg agagtttact cctggaagat 1860
aatattagaa tgtttacaac tgcacctgat cagggtggata aggaagatga agactttcag 1920
gaatctaata aaatgcactc catgaatgga ttcattgtat ggaatcagcc ggggtctcact 1980
atgtgcaaaag gagattcggc cgtgtggtac ttattcagcg ccggaatga ggccgatgta 2040
catggaatat acttttcagg aaacacatat ctgtggagag gagaacggag agacacagca 2100
aacctcttcc ctcaaacaag tcttacgctc cacatgtggc ctgacacaga ggggactttt 2160
aatgttgaat gccttacaac tgatcattac acaggcgga tgaagcaaaa atatactgtg 2220
aaccaatgca ggcggcagtc tgaggattcc accttctacc tgggagagag gacatactat 2280
atcgccagcag tggaggtgga atgggattat tccccacaaa gggagtggga aaaggagctg 2340
catcatttac aagagcagaa tgtttcaaat gcatttttag ataagggaga gttttacata 2400
ggctcaaagt acaagaaagt tgtgtatcgg cagtatactg atagcacatt ccgtgttcca 2460
gtggagagaa aagctgaaga agaacatctg ggaattctag gtccacaact tcatgcagat 2520
gttgagagaa aagtcaaaat tatctttaaa aacatggcca caaggcccta ctcaatacat 2580
gcccatgggg taaaaacaga gagttctaca gttactccaa cattaccagg tgaaactctc 2640
acttaagtat ggaaaatccc agaaagatct ggagctggaa cagaggattc tgcttgtatt 2700
ccatgggctt attattcaac tgtggatcaa gttaaggacc tctacagtgg attaattggc 2760
ccctctattg tttgtcgaag accttacttg aaagtattca atcccagaag gaagctggaa 2820
tttgcccttc tgtttctagt ttttgatgag atgaatctt ggtacttaga tgacaacatc 2880
aaaacatact ctgatcacc cgagaaagta aacaaagatg atgaggaatt catagaaagc 2940
aataaaatgc atgctattaa tggagaatg tttggaaacc tacaaggcct cacaatgcac 3000
gtgggagatg aagtcaactg gtatctgatg ggaatgggca atgaaataga cttacacact 3060

```

```

gtacattttc acggccatag cttccaatac aagcacaggg gagtttatag ttctgatgtc 3120
tttgacattt tccctggaac ataccaaacc ctagaaatgt ttccaagaac acctggaatt 3180
tggttactcc actgcatgt gaccgaccac attcatgctg gaatggaac cacttacacc 3240
gtttacaaa atgaagcatc ttctgagact cacaggagaa tatggaatgt gatctaccca 3300
atcacagtca gtgtgattat tttattccaa atatctacca aggaatgacc aggagaataa 3360
gatcctccga tgttcgcaat ggtgtggtgt caggaggctg cctcttagac aatctccaga 3420
tggttactgt atgtgagttt gaaaaagagt tcctgaagta ccacatctgg gagacatgcc 3480
actagctgag cttcccaaaa gtctaccaag agctgaggaa ttgtatcttc atccttgac 3540
aaagcacctt aaaaacagta aaaggagcct ctatattcca gataaatata gcactgataa 3600
agcgacagct gggcntgaat atcacagcat cacatgggcc acgcaatcaa taatttacca 3660
ttagcattag cgccatggca aaagcaaatt tagacatttt taaaaggaaa cagattctag 3720
gatgtacaaa taaagtttct acagatatag tcttttaatt agtactttta tcttataaac 3780
tgattatgta tgtctgtttt ttcaataaac aaacaaatga aaaaaaaaaa aaaaaaatgg 3840
cggccgcaag cttattancc tttagtgagg gttaatttta a 3881

```

&lt;210&gt; 61

&lt;211&gt; 1090

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 61

```

Met Lys Ile Leu Ile Leu Gly Ile Phe Leu Phe Leu Cys Ser Thr Pro
 1           5           10           15
Ala Trp Ala Lys Glu Lys His Tyr Tyr Ile Gly Ile Ile Glu Thr Thr
 20           25           30
Trp Asp Tyr Ala Ser Asp His Gly Glu Lys Lys Leu Ile Ser Val Asp
 35           40           45
Thr Glu His Ser Asn Ile Tyr Leu Gln Asn Gly Pro Asp Arg Ile Gly
 50           55           60
Arg Leu Tyr Lys Lys Ala Leu Tyr Leu Gln Tyr Thr Asp Glu Thr Phe
 65           70           75           80
Arg Thr Thr Ile Glu Lys Pro Val Trp Leu Gly Phe Leu Gly Pro Ile
 85           90           95
Ile Lys Ala Glu Thr Gly Asp Lys Val Tyr Val His Leu Lys Asn Leu
100           105           110
Ala Ser Arg Pro Tyr Thr Phe His Ser His Gly Ile Thr Tyr Tyr Lys
115           120           125
Glu His Glu Gly Ala Ile Tyr Pro Asp Asn Thr Thr Asp Phe Gln Arg
130           135           140
Ala Asp Asp Lys Val Tyr Pro Gly Glu Gln Tyr Thr Tyr Met Leu Leu
145           150           155           160
Ala Thr Glu Glu Gln Ser Pro Gly Glu Gly Asp Gly Asn Cys Val Thr
165           170           175
Arg Ile Tyr His Ser His Ile Asp Ala Pro Lys Asp Ile Ala Ser Gly
180           185           190
Leu Ile Gly Pro Leu Ile Ile Cys Lys Lys Asp Ser Leu Asp Lys Glu
195           200           205
Lys Glu Lys His Ile Asp Arg Glu Phe Val Val Met Phe Ser Val Val
210           215           220
Asp Glu Asn Phe Ser Trp Tyr Leu Glu Asp Asn Ile Lys Thr Tyr Cys
225           230           235           240
Ser Glu Pro Glu Lys Val Asp Lys Asp Asn Glu Asp Phe Gln Glu Ser
245           250           255
Asn Arg Met Tyr Ser Val Asn Gly Tyr Thr Phe Gly Ser Leu Pro Gly
260           265           270
Leu Ser Met Cys Ala Glu Asp Arg Val Lys Trp Tyr Leu Phe Gly Met
275           280           285
Gly Asn Glu Val Asp Val His Ala Ala Phe Phe His Gly Gln Ala Leu

```

290		295		300
Thr Asn Lys Asn Tyr Arg	Ile Asp Thr Ile Asn	Leu Phe Pro Ala Thr		
305	310	315		320
Leu Phe Asp Ala Tyr Met	Val Ala Gln Asn Pro	Gly Glu Trp Met Leu		
	325	330		335
Ser Cys Gln Asn Leu Asn	His Leu Lys Ala Gly	Leu Gln Ala Phe Phe		
	340	345		350
Gln Val Gln Glu Cys Asn	Lys Ser Ser Ser Lys	Asp Asn Ile Arg Gly		
	355	360		365
Lys His Val Arg His Tyr	Tyr Ile Ala Ala Glu	Glu Ile Ile Trp Asn		
	370	375		380
Tyr Ala Pro Ser Gly Ile	Asp Ile Phe Thr Lys	Glu Asn Leu Thr Ala		
385	390	395		400
Pro Gly Ser Asp Ser Ala	Val Phe Phe Glu Gln	Gly Thr Thr Arg Ile		
	405	410		415
Gly Gly Ser Tyr Lys Lys	Leu Val Tyr Arg Glu	Tyr Thr Asp Ala Ser		
	420	425		430
Phe Thr Asn Arg Lys Glu	Arg Gly Pro Glu Glu	Glu His Leu Gly Ile		
	435	440		445
Leu Gly Pro Val Ile Trp	Ala Glu Val Gly Asp	Thr Ile Arg Val Thr		
	450	455		460
Phe His Asn Lys Gly Ala	Tyr Pro Leu Ser Ile	Glu Pro Ile Gly Val		
465	470	475		480
Arg Phe Asn Lys Asn Asn	Glu Gly Thr Tyr Tyr	Ser Pro Asn Tyr Asn		
	485	490		495
Pro Gln Ser Arg Ser Val	Pro Pro Ser Ala Ser	His Val Ala Pro Thr		
	500	505		510
Glu Thr Phe Thr Tyr Glu	Trp Thr Val Pro Lys	Glu Val Gly Pro Thr		
	515	520		525
Asn Ala Asp Pro Val Cys	Leu Ala Lys Met Tyr	Tyr Ser Ala Val Asp		
	530	535		540
Pro Thr Lys Asp Ile Phe	Thr Gly Leu Ile Gly	Pro Met Lys Ile Cys		
545	550	555		560
Lys Lys Gly Ser Leu His	Ala Asn Gly Arg Gln	Lys Asp Val Asp Lys		
	565	570		575
Glu Phe Tyr Leu Phe Pro	Thr Val Phe Asp Glu	Asn Glu Ser Leu Leu		
	580	585		590
Leu Glu Asp Asn Ile Arg	Met Phe Thr Thr Ala	Pro Asp Gln Val Asp		
	595	600		605
Lys Glu Asp Glu Asp Phe	Gln Glu Ser Asn Lys	Met His Ser Met Asn		
	610	615		620
Gly Phe Met Tyr Gly Asn	Gln Pro Gly Leu Thr	Met Cys Lys Gly Asp		
625	630	635		640
Ser Val Val Trp Tyr Leu	Phe Ser Ala Gly Asn	Glu Ala Asp Val His		
	645	650		655
Gly Ile Tyr Phe Ser Gly	Asn Thr Tyr Leu Trp	Arg Gly Glu Arg Arg		
	660	665		670
Asp Thr Ala Asn Leu Phe	Pro Gln Thr Ser Leu	Thr Leu His Met Trp		
	675	680		685
Pro Asp Thr Glu Gly Thr	Phe Asn Val Glu Cys	Leu Thr Thr Asp His		
	690	695		700
Tyr Thr Gly Gly Met Lys	Gln Lys Tyr Thr Val	Asn Gln Cys Arg Arg		
705	710	715		720
Gln Ser Glu Asp Ser Thr	Phe Tyr Leu Gly Glu	Arg Thr Tyr Tyr Ile		
	725	730		735
Ala Ala Val Glu Val Glu	Trp Asp Tyr Ser Pro	Gln Arg Glu Trp Glu		
	740	745		750
Lys Glu Leu His His Leu	Gln Glu Gln Asn Val	Ser Asn Ala Phe Leu		

755	760	765
Asp Lys Gly Glu Phe Tyr Ile Gly Ser Lys Tyr Lys Lys Val Val Tyr		
770	775	780
Arg Gln Tyr Thr Asp Ser Thr Phe Arg Val Pro Val Glu Arg Lys Ala		
785	790	795
Glu Glu Glu His Leu Gly Ile Leu Gly Pro Gln Leu His Ala Asp Val		
805	810	815
Gly Asp Lys Val Lys Ile Ile Phe Lys Asn Met Ala Thr Arg Pro Tyr		
820	825	830
Ser Ile His Ala His Gly Val Gln Thr Glu Ser Ser Thr Val Thr Pro		
835	840	845
Thr Leu Pro Gly Glu Thr Leu Thr Tyr Val Trp Lys Ile Pro Glu Arg		
850	855	860
Ser Gly Ala Gly Thr Glu Asp Ser Ala Cys Ile Pro Trp Ala Tyr Tyr		
865	870	875
Ser Thr Val Asp Gln Val Lys Asp Leu Tyr Ser Gly Leu Ile Gly Pro		
885	890	895
Leu Ile Val Cys Arg Arg Pro Tyr Leu Lys Val Phe Asn Pro Arg Arg		
900	905	910
Lys Leu Glu Phe Ala Leu Leu Phe Leu Val Phe Asp Glu Asn Glu Ser		
915	920	925
Trp Tyr Leu Asp Asp Asn Ile Lys Thr Tyr Ser Asp His Pro Glu Lys		
930	935	940
Val Asn Lys Asp Asp Glu Glu Phe Ile Glu Ser Asn Lys Met His Ala		
945	950	955
Ile Asn Gly Arg Met Phe Gly Asn Leu Gln Gly Leu Thr Met His Val		
965	970	975
Gly Asp Glu Val Asn Trp Tyr Leu Met Gly Met Gly Asn Glu Ile Asp		
980	985	990
Leu His Thr Val His Phe His Gly His Ser Phe Gln Tyr Lys His Arg		
995	1000	1005
Gly Val Tyr Ser Ser Asp Val Phe Asp Ile Phe Pro Gly Thr Tyr Gln		
1010	1015	1020
Thr Leu Glu Met Phe Pro Arg Thr Pro Gly Ile Trp Leu Leu His Cys		
1025	1030	1035
His Val Thr Asp His Ile His Ala Gly Met Glu Thr Thr Tyr Thr Val		
1045	1050	1055
Leu Gln Asn Glu Ala Ser Ser Glu Thr His Arg Arg Ile Trp Asn Val		
1060	1065	1070
Ile Tyr Pro Ile Thr Val Ser Val Ile Ile Leu Phe Gln Ile Ser Thr		
1075	1080	1085
Lys Glu		
1090		

&lt;210&gt; 62

&lt;211&gt; 969

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 62

```

agctttgggg ttgtccctgg acttgtcttg gttccagaac ctgacgaccc ggcgacggcg 60
acgtctcttt tgactaaaag acagtgtcca gtgtctccagc ctaggagtct acggggaccg 120
cctcccgcg cgccaccatg cccaacttct ctggcaactg gaaaatcatc cgatcggaaa 180
acttgagga attgctcaaa gtgctggggg tgaatgtgat gctgaggaag attgctgtgg 240
ctgcagcgtc caagccagca gtggagatca aacaggaggg agacactttc tacatcaaaa 300
cctccaccac cgtgcgcacc acagagatta acttcaaggt tggggaggag tttgaggagc 360
agactgtgga tgggaggccc tgtaagagcc tgggtgaaatg ggagagttag aataaaatgg 420

```

```

tctgtgagca gaagctcctg aagggagagg gccccaagac ctcgtggacc agagaactga 480
ccaacgatgg ggaactgata ctgaccatga cggcggatga cggtgtgtgc accagggctc 540
acgtccgaga gtgagtggcc acaggtagaa ccgcggccga agccccaccac tggccatgct 600
caccgccctg cttcactgcc ccctccgtcc caccgccctcc ttctaggata gcgctcccct 660
taccccagtc acttctgggg gtcactggga tgcctcttgc agggctcttgc tttctttgac 720
ctcttctctc ctccccctaca ccaacaaaga ggaatggctg caagagccca gatcacccat 780
tccgggttca ctccccgcct cccaagtca gcagtcctag ccccaaacca gccagagca 840
gggtctctct aaaggggact tgagggcctg agcaggaaag actggccctc tagcttctac 900
cctttgtccc tgtagcctat acagtttaga atatttattt gttaatttta ttaaaatgct 960
ttaaaaaaa

```

&lt;210&gt; 63

&lt;211&gt; 138

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 63

```

Met Pro Asn Phe Ser Gly Asn Trp Lys Ile Ile Arg Ser Glu Asn Phe
1          5          10          15
Glu Glu Leu Leu Lys Val Leu Gly Val Asn Val Met Leu Arg Lys Ile
20          25          30
Ala Val Ala Ala Ala Ser Lys Pro Ala Val Glu Ile Lys Gln Glu Gly
35          40          45
Asp Thr Phe Tyr Ile Lys Thr Ser Thr Thr Val Arg Thr Thr Glu Ile
50          55          60
Asn Phe Lys Val Gly Glu Glu Phe Glu Glu Gln Thr Val Asp Gly Arg
65          70          75          80
Pro Cys Lys Ser Leu Val Lys Trp Glu Ser Glu Asn Lys Met Val Cys
85          90          95
Glu Gln Lys Leu Leu Lys Gly Glu Gly Pro Lys Thr Ser Trp Thr Arg
100          105          110
Glu Leu Thr Asn Asp Gly Glu Leu Ile Leu Thr Met Thr Ala Asp Asp
115          120          125
Val Val Cys Thr Arg Val Tyr Val Arg Glu
130          135

```

&lt;210&gt; 64

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 64

```

ggaagttag gttaactgtc ttaaatttcc aaagctgtaa tcattatttt cattctcaaa 60
gtgatggcct tgtgttttgc tcctctcctc cagggccaga ctgagcccag gttgatttca 120
ggcggacacc aatagactcc acagcagctc caggagccca gacaccggcg gccagaagca 180
aggctaggag ctgctgcagc catgtcggcc ctcagcctcc tcattctggg cctgctcagc 240
gcagtgccac ctgccagctg tcagcaaggc ctggggaacc ttcagccctg gatgcagggc 300
cttatcgagg tggccgtgtt cctggctcctc gttgcaatcg cctttgcagt caaccacttc 360
tggtgccagg aggagccgga gcctgcacac atgatcctga ccgtcggaaa caaggcagat 420
ggagtcttgg tgggaacaga tggaaagtac tcttcgatgg cggccagttt caggtccagt 480
gagcatgaga atgcctatga gaatgtgccc gaggaggaag gcaagggtccg cagcaccocg 540
atgtaacctt ctctgtggct ccaaccccaa gactcccagg cacatgggat ggtgtccag 600
tgctaccacc caagccccct ccttctttgt gtggaatctg caatagtggg ctgactccct 660
ccagccccat gccggcccta cccgcccttg aagtatagcc agccaagggt ggagctcaga 720
ccgtgtctag gttggggctc ggctgtggcc ctgggggtctc ctgctcagct cagaagagcc 780
ttctggagag gacagttagc tgagcacctc ccatcctgct cacacgtcct tccccataac 840
tatggaaatg gccctaattt ctgtgaaata aagacttttt gtatttcttg ggctgaggct 900

```

cagcaacagc ccctcaggct tccaaaa .

927

&lt;210&gt; 65

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 65

```

Met Ser Ala Leu Ser Leu Leu Ile Leu Gly Leu Leu Thr Ala Val Pro
 1           5           10           15
Pro Ala Ser Cys Gln Gln Gly Leu Gly Asn Leu Gln Pro Trp Met Gln
      20           25           30
Gly Leu Ile Ala Val Ala Val Phe Leu Val Leu Val Ala Ile Ala Phe
      35           40           45
Ala Val Asn His Phe Trp Cys Gln Glu Glu Pro Glu Pro Ala His Met
      50           55           60
Ile Leu Thr Val Gly Asn Lys Ala Asp Gly Val Leu Val Gly Thr Asp
      65           70           75           80
Gly Arg Tyr Ser Ser Met Ala Ala Ser Phe Arg Ser Ser Glu His Glu
      85           90           95
Asn Ala Tyr Glu Asn Val Pro Glu Glu Glu Gly Lys Val Arg Ser Thr
      100          105          110
Pro Met

```

&lt;210&gt; 66

&lt;211&gt; 3641

&lt;212&gt; DNA .

&lt;213&gt; Homo sapiens

&lt;400&gt; 66

```

ctgcactgaa gagggagagc gagagagaga ctggagacgc acagatcccc ccaaggtctc 60
ccaagcctac cgtccacacag attattgtac agagcccca aaatcgaaac agaggaaacg 120
aacagcagtt gaacatggac gaaggaattc ctcatcttga agagagacag ttactggaac 180
atagagattt tataggactg gactattcct ctttgtatat gtgtaaacc aaaggagca 240
tgaaacgaga cgacaccaag gatacctaca aattaccgca cagattaata gaaaagaaaa 300
gaagagaccg aattaatgaa tgcattgctc agctgaaaga tttactgcct gaacatctga 360
aatgacaac tctgggacat ctggagaaaag ctgtagtctt ggaattaact ttgaaacact 420
taaaagcttt aaccgcctta accgagcaac agcatcagaa gataattgct ttacagaatg 480
gggagcgatc tctgaaatcg cccattcagt ccgacttggg tgcgttccac tcgggatttc 540
aaacatgcgc caaagaagtc ttgcaatacc tctcccggtt tgagagctgg acaccagggg 600
agccgcggtg tgtccagctg atcaaccact tgcacgcgtg ggccaccag ttcttgccca 660
ccccgcagct gttgactcaa caggtccctc tgagcaaagg caccggcgct ccctcgcccg 720
ccgggtccgc ggccgcccc tgcttgagc gcgcggggca gaagctggag cccctcgctt 780
actgcgtgcc cgtcatccag cggactcagc ccagcgccga gctcgccgc gagaacgaca 840
cggacaccga cagcggtac ggcgcggaag ccgaggcccg gccggaccgc gagaagga 900
aaggcgcggg ggcgagccgc gtcaccatca agcaggagcc tccgggggag gactcgccgg 960
cgcccaagag gatgaagctg gattccgcgc gcggcggcag cggcggcggc ccggggggcg 1020
gcgcggcggc ggcggcagcc gcgcttctgg ggcccgacc tgccgcgcgc gccgcgctgc 1080
tgagaccga cgccgccctg ctgagctcgc tgggtggcgtt cggcgagggc ggaggcgcg 1140
ccttcgccga gccgcggcc gccgcggccc ccttctgcct gcccttctgc ttctctcgc 1200
cttctgcagc tgccgcctac gtgcagccct tcttggaaca gagcgccctg gagaagtatc 1260
tgtaccgcgc ggcggtgcc gcccgttcc cgctgctata ccccgccatc cccgcccccg 1320
cggcagccgc ggagccgcc gccgcgctg ccgcgcgcgc cgccgcgttc ccctgcctgt 1380
cctcggtggt gtcgccccct cccgagaagg cggcgccgc cgccgcgacc ctctgcgcgc 1440
acgaggtggc gcccttggg gcgcgcacc cccagcacc gcacggcgcc acccactgc 1500
ccttcgcggc gcccgcgag ccggggaacc cggagagctc tgctcaggaa gatccctcgc 1560

```

```

agccaggaaa ggaagctccc tgaatccttg cgtcccgaag gacggaggtt caagcagagt 1620
gagaagttaa aataccctta aggagggttca agcagagtga gaagttaaaa tacccttaag 1680
gtctttaagg gaggaagtgt aatagatgca cgacaggcat aaacaagaac aacaaaacag 1740
gtgttatgtg tacattcgga gttcctgttt tgetcatccc gcaccacccc accctccaca 1800
cactaacatc cctttcttcc ccccaccagc tgtaaaagat cctatgcgaa agacactggc 1860
tctttttttt aatcccccaa ataaattttg ccccttttta ggccatgttc cattatctct 1920
taaaattgga acctaattcg agaggaagta agaaggggtct gttctgtggc tgagctaggt 1980
gaaccccggt gtaggggaaa gatgttaaca ctttgacgt ctttgaggtt gacatggaac 2040
agcaggtagt tgttatgtag agctagttct caaagctgcc ctgcctgttt taggaggcgt 2100
tccacaaaca gattgaggct ctttttagaa ttgaatttac tcttcagtat tttctaagt 2160
tcagctttct aaaaggcata ttttttcaa agaagtgagg atgcagtttc tcacgttgca 2220
acctattctg aagtgggttta aatggtatct cttagtaact tgcaactcgtt aaagaaacac 2280
ggagctgggc catcgtcaga actaagtcag ggaaggagat ggatgagaag gccagaatca 2340
ttcctagtac atttgctaac actttattga gaaattgacc atgaattaat ggactcatct 2400
taatttcttc taagtcata tatagataga tatctatctg tacagatttc tatttatcca 2460
tagataggta tctatacata cacatctcaa gtgcatctat tcccactctc attaatccat 2520
catgttccta aatttttgta atcttactgt aaaaaaagt gcactgaact tcaaaacaaa 2580
acaaaaaaca acaacaacaa aaaacaagtc caaactgata tatcctatat tctgttaaaa 2640
ttcaaaagt gaaagaaagca tttaactggc cagttttgat tgcaaatgct gtaaagatat 2700
agaatgaagt cctgtgaggc cttcctatct ccaagtctat gtattttctg gagaccacac 2760
cagataccag ataatacaca agaaagcttt tttaataagg cttaaaccaa gaccttgtct 2820
agatattttt agtttggtgc caaggtagca ctgtgagaaa tctcacttgg atgttatgta 2880
aggggtgaga cacaacagtc tgactatgag tgaggaaaat atctgggtct tttcgtcagt 2940
ttgggtgcatt tgctgctgct gttgctactg ttgacctcaa acgctgtgtt taaacaacgt 3000
taaactctta gcctacaagg tggctcttat gtacatagtt gtaatacat ccaattaatg 3060
atgtctgaca tgctattttt gtagggagaa aatatgtgct aatgatattt tgagttaaaa 3120
tatcttttgg ggaggatttg ctgaaaagtt gcacttttgt tacaatgctt atgcttggtta 3180
caagcttatg ctgtcttaaa ttatttttaa aaaattaaat actgtctgtg agaaaccagc 3240
tggtttagaa aagtttagta tgtgacgata aactagaaat tacctttata ttctagtatt 3300
ttcagcactc cataaattct attacctaaa tattgccaca ctattttgtg atttaaaaaat 3360
tcttactaag gaataaaaac tttaatatat gatatgatat tgtctaataa ttaaaaaaga 3420
cataatggat gctcaattag ttttaagata tctataacta tagggataca aatcactaca 3480
gttctcagat ttacaccttt tttttgtcat tggcttgatg tcacacattt ccaatctctt 3540
gcaagcctcc aggtctctggc tttgtctacc tgctcgttcc caatgtatct taatgaaaaa 3600
tgcaaaagaa aaacctacca attaaaaaaa aaaaaaaaaa a 3641

```

&lt;210&gt; 67

&lt;211&gt; 482

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 67

```

Met Asp Glu Gly Ile Pro His Leu Gln Glu Arg Gln Leu Leu Glu His
1          5          10          15
Arg Asp Phe Ile Gly Leu Asp Tyr Ser Ser Leu Tyr Met Cys Lys Pro
20        25        30
Lys Arg Ser Met Lys Arg Asp Asp Thr Lys Asp Thr Tyr Lys Leu Pro
35        40        45
His Arg Leu Ile Glu Lys Lys Arg Arg Asp Arg Ile Asn Glu Cys Ile
50        55        60
Ala Gln Leu Lys Asp Leu Leu Pro Glu His Leu Lys Leu Thr Thr Leu
65        70        75        80
Gly His Leu Glu Lys Ala Val Val Leu Glu Leu Thr Leu Lys His Leu
85        90        95
Lys Ala Leu Thr Ala Leu Thr Glu Gln Gln His Gln Lys Ile Ile Ala
100       105       110
Leu Gln Asn Gly Glu Arg Ser Leu Lys Ser Pro Ile Gln Ser Asp Leu
115       120       125

```

Asp Ala Phe His Ser Gly Phe Gln Thr Cys Ala Lys Glu Val Leu Gln  
 130 135 140  
 Tyr Leu Ser Arg Phe Glu Ser Trp Thr Pro Arg Glu Pro Arg Cys Val  
 145 150 155 160  
 Gln Leu Ile Asn His Leu His Ala Val Ala Thr Gln Phe Leu Pro Thr  
 165 170 175  
 Pro Gln Leu Leu Thr Gln Gln Val Pro Leu Ser Lys Gly Thr Gly Ala  
 180 185 190  
 Pro Ser Ala Ala Gly Ser Ala Ala Ala Pro Cys Leu Glu Arg Ala Gly  
 195 200 205  
 Gln Lys Leu Glu Pro Leu Ala Tyr Cys Val Pro Val Ile Gln Arg Thr  
 210 215 220  
 Gln Pro Ser Ala Glu Leu Ala Ala Glu Asn Asp Thr Asp Thr Asp Ser  
 225 230 235 240  
 Gly Tyr Gly Gly Glu Ala Glu Ala Arg Pro Asp Arg Glu Lys Gly Lys  
 245 250 255  
 Gly Ala Gly Ala Ser Arg Val Thr Ile Lys Gln Glu Pro Pro Gly Glu  
 260 265 270  
 Asp Ser Pro Ala Pro Lys Arg Met Lys Leu Asp Ser Arg Gly Gly Gly  
 275 280 285  
 Ser Gly Gly Gly Pro Gly Gly Gly Ala Ala Ala Ala Ala Ala Leu  
 290 295 300  
 Leu Gly Pro Asp Pro Ala Ala Ala Ala Ala Leu Leu Arg Pro Asp Ala  
 305 310 315 320  
 Ala Leu Leu Ser Ser Leu Val Ala Phe Gly Gly Gly Gly Ala Pro  
 325 330 335  
 Phe Pro Gln Pro Ala Ala Ala Ala Ala Pro Phe Cys Leu Pro Phe Cys  
 340 345 350  
 Phe Leu Ser Pro Ser Ala Ala Ala Ala Tyr Val Gln Pro Phe Leu Asp  
 355 360 365  
 Lys Ser Gly Leu Glu Lys Tyr Leu Tyr Pro Ala Ala Ala Ala Pro  
 370 375 380  
 Phe Pro Leu Leu Tyr Pro Gly Ile Pro Ala Pro Ala Ala Ala Ala  
 385 390 395 400  
 Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Phe Pro Cys Leu Ser  
 405 410 415  
 Ser Val Leu Ser Pro Pro Pro Glu Lys Ala Gly Ala Ala Ala Thr  
 420 425 430  
 Leu Leu Pro His Glu Val Ala Pro Leu Gly Ala Pro His Pro Gln His  
 435 440 445  
 Pro His Gly Arg Thr His Leu Pro Phe Ala Gly Pro Arg Glu Pro Gly  
 450 455 460  
 Asn Pro Glu Ser Ser Ala Gln Glu Asp Pro Ser Gln Pro Gly Lys Glu  
 465 470 475 480  
 Ala Pro

&lt;210&gt; 68

&lt;211&gt; 3624

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 68

tagtctaact cgcggtgtc accgccactg cagcggagcc ggccggccgg gcgctgcggg 60  
 acgggagggc ggctgccggc aggagcgcc gagccgggtg actgccgcgg cgggcacagt 120  
 ccggggccac agcgccgagc ccgggcggga gtggccccgc gcaggcaggg agcggcgccg 180  
 cgcaactcaa cccggcgggc acctcggggg cgggcgcggg gcgcagcctt ctgctcccg 240



```

cctctgtgac aagcgccccg gagccgggag cccgattgcc gggctcgggg tgggcgcgga 300
cgcaggcact gggctcgtgc ggggccccgg gcgtcgcgat gaacatcgtg gtggagtct 360
tcgtgggtcac tttcaaagtg ctctgggctg tcgtgctggc cgcggcgcg cgtggtggtgc 420
ggcccaagga gaagagcgtg gcgggccagg tgtgcctcat caccggcgcc ggcagcggcc 480
tgggcgcgct ctctcgctg gagttcgccc ggcgtcgggg gctgctggtg ctgtgggaca 540
tcaacacgca aagcaacgag gagacggctg gcatggtgcg ccacatctac cgcgacctgg 600
aggcgggcga cgcgctgctg ctgcaagctg ggaatggtga ggaagaaatt ctgccccact 660
gtaacttgca ggtttttacc tacacctgtg acgtggggaa gagggagAAC gtctacctga 720
cggctgaaag agtccgcaag gaggttggcg aagtctcagt cctggtcaat aatgctggtg 780
tgggtctctgg gcatcacctt ctggaatgtc ctgatgagct cattgagaga accatgatgg 840
tcaattgcca tgcacacttc tggaccacta aggcttttct tcctacgatg ctggagatta 900
atcatggtca tattgtgaca gttgcaagtt ccttgggatt gttcagtact gccggagtgtg 960
aggattactg tgccagtaaa tttggagtgt tgggttttca tgaatccctg agccatgaac 1020
taaaggctgc tgaaaaggat ggaattaaaa caaccttgggt ttgcccttat ctgttagaca 1080
ctggcatgtt cagaggctgc cgaatcagga aagaaattga gccttttctg ccacctctga 1140
agcctgatta ctgtgtgaag caggccatga aggccatcct cactgaccag cccatgatct 1200
gcactccccg cctcatgtac atcgtgacct tcataagag cactctacca tttgaagcag 1260
ttgtgtgcat gtabcggttc ctaggagcgg acaagtgtat gtaccctttt attgctcaaa 1320
gaaagcaagc cacaacaat aatgaagcaa aaaaatggaat ctaagaatct tttgtatgg 1380
aatattactt ctatcagaag atgatcaaga tgtttcagtc cagtgcacat cagcattgct 1440
gacattttat ggattctaaa cttgtgttgt ttctttttta aatcaacttt ttaaaaaaat 1500
aaagtgtaaa ttaaccgact agagtacttg gaaaatgtga tcagtacaag tgaacttagg 1560
ttgttgccaa cagggtcctt ttaggcagaa cccagaaacc agtcaaatct gtagagaagc 1620
agtgtgacat cttcagggtta ccattatttt ttaatgagca ggaagtctag aaatgataac 1680
tagactgtat gtttcatgtg tgtgattttt cagaattccc agagtttact cattcttgtt 1740
attaaactct agccagttga catcttcgca atttcaagga ctgatagtgc tgtattttct 1800
cacgttttct agctttcgt tttgcaaggc ctaggtgact ttttcatggt gtttgtatgt 1860
ttagctcttt tgaaaaggaa ttttgaaatc tccatcaact gaagttaaag atgtctgagt 1920
gttacagtwa aggtgaccaa gtctctttct taaagtcaca atgactaaag tattagttag 1980
attttttttt ttttttttga tggagtctcg ctctgtcacc aggtctggagt gcagtagcac 2040
aatcacggct cactgcaatc tctgcctccc rgtttcaagt gattctgctg tctcagcctc 2100
ccaagtagct gggactacag gcatgcgcca ccacgcccag ctaatttttg tattttttag 2160
agagacgggg tttcaccatg ttggtcagga tgggtctccat ctcttgacat tgtgatccac 2220
ctgctcggc ctcccaaagt gctgggatta caggcatgag ccactgcacc cagccttgaa 2280
tttttaatt tatctctgat atacttcatt aagtgtctgg agacctaat atcctaaaag 2340
atcatacatt ttctacctat gaattttgct gcatacagaa agtgccttt cctcaggaag 2400
ttgtgtgtt tcatttcttt ggatggactc ttatctagaa tacatagcag ctctgcaaag 2460
aaacagtttt taaaaatggg aacttctaca ttgaaaagtc cccatttttg tgccaactat 2520
gattagttag aggaagaaat cttattctat ggcataatga tggagggtg taaagattct 2580
tttgaaagg ttaattcacat tgtagaacag caaatgacat ttttacagta tttttttgta 2640
aagcaaacta ttttgtgcct tgaatttgggt atatgtgtat tagtgaaaca ttgtaaagg 2700
gaacttctac ctctgtatct aaatgtatac catccacttg taaatgacta taaactatta 2760
tgtgattgct ttttttttta gaatgtcttg tttaaatagt ggccaatgtt taaggctgtt 2820
aaaataagcc aacttttact aattggggag ttttataaat gactgattaa atttaaagaa 2880
ttaacttaca tgcaattgtg tgattattag ttatcagcag tgttgaagg aaaattattg 2940
tgtttttttt tatgatcatt atcccacttt aggtaaagaa aaatattgga atggaatagt 3000
gttgggaaac agacattaac aacctagggt gcctgcactc aaatagccga tgttactgtc 3060
cctagattag agacttgatt aagggttgt ttgtaccaa agtggggaaa caatgccatg 3120
acctgtgtt tagtttggct gcaccacaga tcaaatctgc actgtgtcta catataggaa 3180
aggctcctgt gtgtgcta atgttccaatg caggacttga ggaagagctc tttataacaa tggaggcact 3300
ttccatttct ctttatcaaa gataaccaa ccttatggcc cttataacaa tctgaagggt ctcaacaatg 3360
ggctgcctct taattttcaa tcatggacct tcagagatta tccaggtctg cctcccagcg agcctggagt 3420
ccagggtggg acagatatata aatctgttat atttatacaa cccacttatc caccttaaaa 3480
acaccagacc ctctagaga atctaatatt attcttgtgt gttataactt aaacctattt 3540
ctgaggaaa tctgttttac atctaatttt attcttgtgt gttataactt aaacctattt 3600
ctatttttgt ttgttattgc cttataaagg gtgtccatct ccaagttcaa taaactaatt 3600
catttaaaaa aaaaaaaaaa aaaa 3624

```

<210> 69  
 <211> 341  
 <212> PRT  
 <213> Homo sapiens

<400> 69

```

Met Asn Ile Val Val Glu Phe Phe Val Val Thr Phe Lys Val Leu Trp
 1          5          10          15
Ala Phe Val Leu Ala Ala Ala Arg Trp Leu Val Arg Pro Lys Glu Lys
          20          25          30
Ser Val Ala Gly Gln Val Cys Leu Ile Thr Gly Ala Gly Ser Gly Leu
          35          40          45
Gly Arg Leu Phe Ala Leu Glu Phe Ala Arg Arg Arg Ala Leu Leu Val
          50          55          60
Leu Trp Asp Ile Asn Thr Gln Ser Asn Glu Glu Thr Ala Gly Met Val
          65          70          75          80
Arg His Ile Tyr Arg Asp Leu Glu Ala Ala Asp Ala Ala Ala Leu Gln
          85          90          95
Ala Gly Asn Gly Glu Glu Glu Ile Leu Pro His Cys Asn Leu Gln Val
          100          105          110
Phe Thr Tyr Thr Cys Asp Val Gly Lys Arg Glu Asn Val Tyr Leu Thr
          115          120          125
Ala Glu Arg Val Arg Lys Glu Val Gly Glu Val Ser Val Leu Val Asn
          130          135          140
Asn Ala Gly Val Val Ser Gly His His Leu Leu Glu Cys Pro Asp Glu
          145          150          155          160
Leu Ile Glu Arg Thr Met Met Val Asn Cys His Ala His Phe Trp Thr
          165          170          175
Thr Lys Ala Phe Leu Pro Thr Met Leu Glu Ile Asn His Gly His Ile
          180          185          190
Val Thr Val Ala Ser Ser Leu Gly Leu Phe Ser Thr Ala Gly Val Glu
          195          200          205
Asp Tyr Cys Ala Ser Lys Phe Gly Val Val Gly Phe His Glu Ser Leu
          210          215          220
Ser His Glu Leu Lys Ala Ala Glu Lys Asp Gly Ile Lys Thr Thr Leu
          225          230          235          240
Val Cys Pro Tyr Leu Val Asp Thr Gly Met Phe Arg Gly Cys Arg Ile
          245          250          255
Arg Lys Glu Ile Glu Pro Phe Leu Pro Pro Leu Lys Pro Asp Tyr Cys
          260          265          270
Val Lys Gln Ala Met Lys Ala Ile Leu Thr Asp Gln Pro Met Ile Cys
          275          280          285
Thr Pro Arg Leu Met Tyr Ile Val Thr Phe Met Lys Ser Ile Leu Pro
          290          295          300
Phe Glu Ala Val Val Cys Met Tyr Arg Phe Leu Gly Ala Asp Lys Cys
          305          310          315          320
Met Tyr Pro Phe Ile Ala Gln Arg Lys Gln Ala Thr Asn Asn Asn Glu
          325          330          335
Ala Lys Asn Gly Ile
          340

```

<210> 70  
 <211> 1428  
 <212> DNA  
 <213> Homo sapiens

<400> 70

```

ggcacgagggc ggagacagag acttcacgac tcccagttc ctctcgcgcg cggccgcccgc 60
ctctccttctc tctcctcctc ctcttctctc tctcctcctc ctcccacagc catgtctgct 120
tagaccagag cagccccaca gccaaactagg gcagctgccg ccgccacaac agcaaggaca 180
gccgctgccg ccgcccgtga gcgatgacag gagtgtttga cagaagggtc cccagcatcc 240
gatccggcga cttccaagct ccgttccaga cgtccgcagc tatgcacat ccgtctcagg 300
aatcgccaac tttgcccag tcttcagcta ccgattctga ctactacagc cctacggggg 360
gagccccgca cggctactgc tctcctacct cggcttccta tggcaaagct ctcaaccct 420
accagtatca gtatcacggc gtgaacggct ccgcccggag ctaccagcc aaagcttatg 480
ccgactatag ctacgctagc tcctaccacc agtacggcgg cgctacaac cgcgtcccaa 540
gcgccaccaa ccagccagag aaagaagtga ccgagcccga ggtgagaatg gtgaatggca 600
aaccaaagaa agttcgtaaa cccaggacta tttattccag ctttcagctg gccgcattac 660
agagaagggt tcagaagact cagtacctcg ccttgccgga acgcgcgcgag ctggccgcct 720
cgctgggatt gacacaaaca caggtgaaaa tctggtttca gaacaaaaga tccaagatca 780
agaagatcat gaaaaacggg gagatgcctc cggagcacag tcccagctcc agcgacccaa 840
tggcgtgtaa ctgcgcgcag tctccagcgg tgtgggagcc ccagggtcgc tcccgcctgc 900
tcagccacca ccctcatgcc caccctccga cctccaacca gtcccagcg tccagctacc 960
tggagaactc tgcctcctgg tacacaagtg cagccagctc aatcaattcc cacctgccgc 1020
cgccgggctc cttacagcac ccgctggcgc tggcctccgg gacactctat tagatgggct 1080
gtctctctct actctcttt ttgggactac tgtgttttg tgttctagaa aatcataaag 1140
aaaggaattc atatggggaa gttcggaaaa ctgaaaaaga ttcattgtga aagctttttt 1200
ttgcatgtaa gttattgcat ttcaaaagac ccccccttt tttacagagg actttttttg 1260
cgcaactgtg gacactttca atggtgcctt gaaatctat acctcaact ttcaaaagac 1320
ttttttcaat gttattttag ccatgtaaat aagtgtagat agaggaatta aactgtatat 1380
tctggataaa taaaattatt tcgaccatga aaaaaaaaa aaaaaaaa 1428

```

&lt;210&gt; 71

&lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 71

```

Met Thr Gly Val Phe Asp Arg Arg Val Pro Ser Ile Arg Ser Gly Asp
 1           5           10          15
Phe Gln Ala Pro Phe Gln Thr Ser Ala Ala Met His His Pro Ser Gln
 20          25          30
Glu Ser Pro Thr Leu Pro Glu Ser Ser Ala Thr Asp Ser Asp Tyr Tyr
 35          40          45
Ser Pro Thr Gly Gly Ala Pro His Gly Tyr Cys Ser Pro Thr Ser Ala
 50          55          60
Ser Tyr Gly Lys Ala Leu Asn Pro Tyr Gln Tyr Gln Tyr His Gly Val
 65          70          75          80
Asn Gly Ser Ala Gly Ser Tyr Pro Ala Lys Ala Tyr Ala Asp Tyr Ser
 85          90          95
Tyr Ala Ser Ser Tyr His Gln Tyr Gly Gly Ala Tyr Asn Arg Val Pro
100          105          110
Ser Ala Thr Asn Gln Pro Glu Lys Glu Val Thr Glu Pro Glu Val Arg
115          120          125
Met Val Asn Gly Lys Pro Lys Lys Val Arg Lys Pro Arg Thr Ile Tyr
130          135          140
Ser Ser Phe Gln Leu Ala Ala Leu Gln Arg Arg Phe Gln Lys Thr Gln
145          150          155          160
Tyr Leu Ala Leu Pro Glu Arg Ala Glu Leu Ala Ala Ser Leu Gly Leu
165          170          175
Thr Gln Thr Gln Val Lys Ile Trp Phe Gln Asn Lys Arg Ser Lys Ile
180          185          190
Lys Lys Ile Met Lys Asn Gly Glu Met Pro Pro Glu His Ser Pro Ser
195          200          205
Ser Ser Asp Pro Met Ala Cys Asn Ser Pro Gln Ser Pro Ala Val Trp

```

210		215		220
Glu Pro Gln Gly Ser Ser Arg Ser Leu Ser His		His Pro His Ala His		
225		230		235
Pro Pro Thr Ser Asn Gln Ser Pro Ala Ser Ser Tyr Leu Glu Asn Ser				240
		245		250
				255
Ala Ser Trp Tyr Thr Ser Ala Ala Ser Ser Ile Asn Ser His Leu Pro				
		260		265
				270
Pro Pro Gly Ser Leu Gln His Pro Leu Ala Leu Ala Ser Gly Thr Leu				
		275		280
				285

Tyr

<210> 72  
 <211> 2036  
 <212> DNA  
 <213> Homo sapiens

<400> 72

gacagcttga	accattcccc	tggccagagt	ggattcctca	gctatggctc	cagcttcagc	60
acctcaccca	ctggacagag	cccatacacc	taccagatgc	acggcacaaac	agggttctat	120
caaggaggaa	atggactggg	caacgcagcc	ggtttcggga	gtgtgcacca	ggactatcct	180
tcctaccccg	gcttccccca	gagccagtac	ccccagtatt	acggctcatc	ctacaaccct	240
ccctacgtcc	cggccagcag	catctgccct	tcgcccctct	ccacgtccac	ctacgtcctc	300
caggaggcat	ctcacaacgt	cccccaaccag	agttccgagt	cacttgctgg	tgaatacaac	360
acacacaatg	gaccttccac	accagcgaaa	gagggagaca	cagacaggcc	gcaccggggc	420
tccgacggga	agctccgagg	ccggtctaag	aggagcagt	acccgtcccc	ggcagggggc	480
aatgagattg	agcgtgtggt	cgtgtgggac	ttggatgaga	caataattat	ttttcactcc	540
ttactcacgg	ggacatttgc	atccagatac	gggaaggaca	ccacgacgtc	cgtgcgcatt	600
ggccttatga	tggaagagat	gatcttcaac	cttgagata	cacatctgtt	cttcaatgac	660
ctggaggatt	gtgaccagat	ccacgttgat	gacgtctcat	cagatgacaa	tggccaagat	720
ttaagcacat	acaacttctc	cgctgacggc	ttccacagtt	cggccccagg	agccaacctg	780
tgcctgggct	ctggcggtga	cggcggtg	gactggatga	ggaagctggc	cttccgctac	840
cggcggttga	aggagatgta	caatacctac	aagaacaacg	ttggtgggtt	gataggcact	900
ccaaaagg	agacctggct	acagctccga	gctgagctgg	aagctctcac	agacctctgg	960
ctgacctact	ccctgaaggc	actaaacctc	atcaactccc	ggcccaactg	tgtcaatgtg	1020
ctggtcacca	ccactcaact	aattcctgcc	ctggccaaag	tcctgctata	tggtctgggg	1080
tctgtgttct	ctattgagaa	catctacagt	gcaaccaaga	caggaagga	gagctgcttc	1140
gagaggataa	tgagagatt	cggcagaaaa	gctgtctacg	tggtgatcgg	tgatggtgtg	1200
gaagaggagc	aaggagcgaa	aaagcacaa	atgcctttct	ggcggtatct	ctgccacgca	1260
gacctggagg	cactgaggca	cgcctggag	ctggagtatt	tatagcagga	tcagcagcat	1320
ctccacctgc	catctcacc	tcagaccccc	tcgcttccc	cacctcccc	ccgagaactc	1380
cagagaccca	gatgttgac	accaggaagg	ggccccacag	ccgagacgac	gtgtccagt	1440
accatctcag	aagccgtcca	tcagtccaaa	tgggggttct	gagaaggaaa	gtacccaaca	1500
ttggcttcgg	agtatttgac	tttggggaaa	agggctggct	cggagtctag	actcttctgt	1560
aagactcaca	gaacaaaagc	aaggaattgc	caatttgggg	ggtgcctggt	gatgaggagg	1620
ggatgggttt	gtcttgtctt	ctttttaatt	tatggactag	tctcattact	ccagaattat	1680
gctcttgtag	ctgtgtggct	gggtttctta	gtcgttggtt	tgggttggtt	ttttgaactg	1740
gtatgtagg	tggttcacag	ttctaattgta	agcactctct	tctccaagtt	gtgctttgtg	1800
gggacaatca	ttctttgaac	attagagagg	aaggcagttc	aagctgttga	aaagactatt	1860
gcttattttt	gtttttaaag	acctacttga	cgtcatgtgg	acagtgcacg	tgctttacgc	1920
tacatcttgt	tttctaggaa	gagggggatg	ctgggaagga	atgggtgctt	tgtgatggat	1980
aaaaggcatt	aaataaaacc	acgtttacat	tttgaaaaaa	aaaaaaaaaa	aaaaaa	2036

<210> 73  
 <211> 434  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 73

Asp Ser Leu Asn His Ser Pro Gly Gln Ser Gly Phe Leu Ser Tyr Gly  
 1 5 10 15  
 Ser Ser Phe Ser Thr Ser Pro Thr Gly Gln Ser Pro Tyr Thr Tyr Gln  
 20 25 30  
 Met His Gly Thr Thr Gly Phe Tyr Gln Gly Gly Asn Gly Leu Gly Asn  
 35 40 45  
 Ala Ala Gly Phe Gly Ser Val His Gln Asp Tyr Pro Ser Tyr Pro Gly  
 50 55 60  
 Phe Pro Gln Ser Gln Tyr Pro Gln Tyr Tyr Gly Ser Ser Tyr Asn Pro  
 65 70 75 80  
 Pro Tyr Val Pro Ala Ser Ser Ile Cys Pro Ser Pro Leu Ser Thr Ser  
 85 90 95  
 Thr Tyr Val Leu Gln Glu Ala Ser His Asn Val Pro Asn Gln Ser Ser  
 100 105 110  
 Glu Ser Leu Ala Gly Glu Tyr Asn Thr His Asn Gly Pro Ser Thr Pro  
 115 120 125  
 Ala Lys Glu Gly Asp Thr Asp Arg Pro His Arg Ala Ser Asp Gly Lys  
 130 135 140  
 Leu Arg Gly Arg Ser Lys Arg Ser Ser Asp Pro Ser Pro Ala Gly Asp  
 145 150 155 160  
 Asn Glu Ile Glu Arg Val Phe Val Trp Asp Leu Asp Glu Thr Ile Ile  
 165 170 175  
 Ile Phe His Ser Leu Leu Thr Gly Thr Phe Ala Ser Arg Tyr Gly Lys  
 180 185 190  
 Asp Thr Thr Thr Ser Val Arg Ile Gly Leu Met Met Glu Glu Met Ile  
 195 200 205  
 Phe Asn Leu Ala Asp Thr His Leu Phe Phe Asn Asp Leu Glu Asp Cys  
 210 215 220  
 Asp Gln Ile His Val Asp Asp Val Ser Ser Asp Asp Asn Gly Gln Asp  
 225 230 235 240  
 Leu Ser Thr Tyr Asn Phe Ser Ala Asp Gly Phe His Ser Ser Ala Pro  
 245 250 255  
 Gly Ala Asn Leu Cys Leu Gly Ser Gly Val His Gly Gly Val Asp Trp  
 260 265 270  
 Met Arg Lys Leu Ala Phe Arg Tyr Arg Arg Val Lys Glu Met Tyr Asn  
 275 280 285  
 Thr Tyr Lys Asn Asn Val Gly Gly Leu Ile Gly Thr Pro Lys Arg Glu  
 290 295 300  
 Thr Trp Leu Gln Leu Arg Ala Glu Leu Glu Ala Leu Thr Asp Leu Trp  
 305 310 315 320  
 Leu Thr His Ser Leu Lys Ala Leu Asn Leu Ile Asn Ser Arg Pro Asn  
 325 330 335  
 Cys Val Asn Val Leu Val Thr Thr Thr Gln Leu Ile Pro Ala Leu Ala  
 340 345 350  
 Lys Val Leu Leu Tyr Gly Leu Gly Ser Val Phe Pro Ile Glu Asn Ile  
 355 360 365  
 Tyr Ser Ala Thr Lys Thr Gly Lys Glu Ser Cys Phe Glu Arg Ile Met  
 370 375 380  
 Gln Arg Phe Gly Arg Lys Ala Val Tyr Val Val Ile Gly Asp Gly Val  
 385 390 395 400  
 Glu Glu Glu Gln Gly Ala Lys Lys His Asn Met Pro Phe Trp Arg Ile  
 405 410 415  
 Ser Cys His Ala Asp Leu Glu Ala Leu Arg His Ala Leu Glu Leu Glu  
 420 425 430  
 Tyr Leu

<210> 74  
 <211> 1907  
 <212> DNA  
 <213> Homo sapiens

<400> 74

```

cggccagata cctcagcgct acctggcgga actggatttc tctcccgct gccggcctgc 60
ctgccacagc cggactccgc cactccggta gcctcatggc tgcaacctgt gagattagca 120
acatttttag caactacttc agtgcgatgt acagctcgga ggactccacc ctggcctctg 180
ttccccctgc tgccaccttt ggggccgatg acttgggtact gaccctgagc aacccccaga 240
tgtcattgga gggtagacag aaggccagct ggttggggga acagccccag ttctggctga 300
agacgcaggt totggactgg atcagctacc aagtggagaa gaacaagtac gacgcaagcg 360
ccattgactt ctcacgatgt gacatggatg gcgccaccct ctgcaattgt gcccttgagg 420
agctgcgtct ggtctttggg cctctggggg accaactcca tgcccagctg cgagacctca 480
cttccagctc ttctgatgag ctgagttgga tcattgagct gctggagaag gatggcatgg 540
ccttcaggga gggcctagac ccaggggcct ttgaccaggg cagccccttt gccaggagc 600
tgctggacga cggtagcaaa gccagcccct accaccggc cagctgtggc gcaggagccc 660
cctccccctg cagctctgac gtctccaccg cagggtactg tgcttctcgg agctccact 720
cctcagactc cgggtggaagt gacgtggacc tggatccac tgatggcaag ctcttcccca 780
gcatggttt tctgactgac aagaagggg atcccaagca cgggaagcgg aaacgaggcc 840
ggccccgaaa gctgagcaaa gactactggg actgtctcga gggcaagaag agcaagcacg 900
cgcccagagg caccacactg tgggagttca tccgggacat cctcatccac ccggagctca 960
acgagggcct catgaagtgg gagaatcggc atgaaggcgt cttcaagttc ctgcgctccg 1020
aggctgtggc ccaactatgg ggccaaaaga aaaagaacag caacatgacc tacgagaagc 1080
tgagccgggc catgaggtac tactacaaac gggagatcct ggaacgggtg gatggccggc 1140
gactcgtcta caagtttggc aaaaactcaa gcggctggaa ggaggaagag gttctccaga 1200
gtcggaaactg agggttgga ctatacccg gaccaaactc acggaccact cgaggcctgc 1260
aaaccttcct gggaggacag gcaggccaga tggcccctcc actggggaat gctcccagct 1320
gtgctgtgga gagaagctga tgttttggg tattgtcagc catcgtcctt ggactcggag 1380
actatggcct cgcctcccca ccctcctctt ggaattacaa gccctggggg ttgaagctga 1440
ctttatagct gcaagtgtat ctcttttat ctggtgcctc ctcaaaccac gtctcagaca 1500
cttaaatgca gacaacacct tcttcctgca gacacttggc ctgagccaag gaggcttggg 1560
aggccctagg gagcaccgtg atggagagga cagagcaggg gctccagcac ttctttctgg 1620
actggcggtc acctccctgc tcagtgttg ggctccacgg gcaggggtca gagcactccc 1680
taatttatgt gctatataaa tatgtcagat gtacatagag atctattttt tctaaaacat 1740
tccccctccc actcctctcc cacagagtgc tggactgttc caggccctcc agtgggctga 1800
tgctgggacc cttaggatgg ggctcccagc tcctttctcc tgtgaatgga ggcagagacc 1860
tccaataaag tgccttctgg gctttttcta aaaaaaaaa aaaaaaa 1907

```

<210> 75  
 <211> 371  
 <212> PRT  
 <213> Homo sapiens

<400> 75

```

Met Ala Ala Thr Cys Glu Ile Ser Asn Ile Phe Ser Asn Tyr Phe Ser
 1           5           10          15
Ala Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val Pro Pro Ala
 20          25          30
Ala Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser Asn Pro Gln
 35          40          45
Met Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro
 50          55          60
Gln Phe Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val
 65          70          75          80
Glu Lys Asn Lys Tyr Asp Ala Ser Ala Ile Asp Phe Ser Arg Cys Asp

```

85

				85					90					95		
Met	Asp	Gly	Ala	Thr	Leu	Cys	Asn	Cys	Ala	Leu	Glu	Glu	Leu	Arg	Leu	
			100						105					110		
Val	Phe	Gly	Pro	Leu	Gly	Asp	Gln	Leu	His	Ala	Gln	Leu	Arg	Asp	Leu	
		115					120						125			
Thr	Ser	Ser	Ser	Ser	Asp	Glu	Leu	Ser	Trp	Ile	Ile	Glu	Leu	Leu	Glu	
		130				135					140					
Lys	Asp	Gly	Met	Ala	Phe	Gln	Glu	Ala	Leu	Asp	Pro	Gly	Pro	Phe	Asp	
		145			150					155					160	
Gln	Gly	Ser	Pro	Phe	Ala	Gln	Glu	Leu	Leu	Asp	Asp	Gly	Gln	Gln	Ala	
				165					170					175		
Ser	Pro	Tyr	His	Pro	Gly	Ser	Cys	Gly	Ala	Gly	Ala	Pro	Ser	Pro	Gly	
		180					185						190			
Ser	Ser	Asp	Val	Ser	Thr	Ala	Gly	Thr	Gly	Ala	Ser	Arg	Ser	Ser	His	
		195					200					205				
Ser	Ser	Asp	Ser	Gly	Gly	Ser	Asp	Val	Asp	Leu	Asp	Pro	Thr	Asp	Gly	
		210				215					220					
Lys	Leu	Phe	Pro	Ser	Asp	Gly	Phe	Arg	Asp	Cys	Lys	Lys	Gly	Asp	Pro	
		225			230				235						240	
Lys	His	Gly	Lys	Arg	Lys	Arg	Gly	Arg	Pro	Arg	Lys	Leu	Ser	Lys	Glu	
				245					250					255		
Tyr	Trp	Asp	Cys	Leu	Glu	Gly	Lys	Lys	Ser	Lys	His	Ala	Pro	Arg	Gly	
		260					265						270			
Thr	His	Leu	Trp	Glu	Phe	Ile	Arg	Asp	Ile	Leu	Ile	His	Pro	Glu	Leu	
		275					280					285				
Asn	Glu	Gly	Leu	Met	Lys	Trp	Glu	Asn	Arg	His	Glu	Gly	Val	Phe	Lys	
		290				295					300					
Phe	Leu	Arg	Ser	Glu	Ala	Val	Ala	Gln	Leu	Trp	Gly	Gln	Lys	Lys	Lys	
		305			310				315						320	
Asn	Ser	Asn	Met	Thr	Tyr	Glu	Lys	Leu	Ser	Arg	Ala	Met	Arg	Tyr	Tyr	
			325					330					335			
Tyr	Lys	Arg	Glu	Ile	Leu	Glu	Arg	Val	Asp	Gly	Arg	Arg	Leu	Val	Tyr	
		340					345					350				
Lys	Phe	Gly	Lys	Asn	Ser	Ser	Gly	Trp	Lys	Glu	Glu	Glu	Val	Leu	Gln	
		355					360					365				
Ser	Arg	Asn														
		370														

&lt;210&gt; 76

&lt;211&gt; 3951

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(3951)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 76

```

nngacccaacg cgtccgggtg cggctctggac acgtctccgg ggtgggtcgt ccggccttcg 60
atcttagacg aattttacaa tgtgaagttc tgcataagatg ccagtcaacc agatgttgga 120
agctgggtca agtacattag attcgtctggc tgttatgatc agcacaacct tgttgcatgc 180
cagataaatg atcagatatt ctatagagta gttgcagaca ttgcgcggg agaggagctt 240
ctgctgttca tgaagagcga agactatccc catgaaacta tggcgccgga tatccacgaa 300
gaacggcaat atcgctgcga agactgtgac cagctctttg aatctaaggc tgaactagca 360
gatcaccaaa agtttccatg cagtactcct cactcagcat tttcaatggt tgaagaggac 420
tttcagcaaa aactcgaaag cgagaatgat ctccaagaga tacacacgat ccaggagtgt 480

```

aaggaatgtg	accaagtttt	tcttgatttg	caaagcctgg	agaaacacat	gctgtcacat	540
actgaagaga	gggaatacaa	gtgtgatcag	tgtcccaagg	catttaactg	gaagtccaat	600
ttaattcgcc	accagatgtc	acatgacagt	ggaaagcact	atgaatgtga	aaactgtgcc	660
aaggttttca	cggaccctag	caaccttcag	cggcacattc	gctctcagca	tgctcggtgcc	720
cgggcccattg	catgcccgga	gtgtggcaaa	acgtttgcc	cttcgtcggg	cctcaaacaa	780
cacaagcaca	tccacagcag	tgtgaagccc	tttatctcat	tctctcaatc	aatgtacca	840
tttctgata	gagacttgag	atcgttacct	ttgaaaatgg	aaccccaatc	accaggtgaa	900
gtaaagaaac	tgcagaagg	cagctctgag	tcccccttg	atctcaccac	taagcgaaag	960
gatgagaagc	ccttgactcc	agtcacctcc	aagcctccag	tgacacctgc	cacaagccaa	1020
gaccagcccc	tggatctaag	tatgggcagt	aggagtagag	ccagtgggac	aaagctgact	1080
gagcctcgaa	aaaaccacgt	gtttggggga	aaaaaaggaa	gcaacgtcga	atcaagacct	1140
gcttcagatg	gttccttgca	gcatgcaaga	cccactcctt	tctttatgga	ccctatattac	1200
agagtagaga	aaagaaaact	aactgaccca	cttgaagctt	taaaagagaa	atacttgagg	1260
ccttctccag	gattcttggt	tcaccacaa	atgtcagcta	ttgaaaacat	ggcagaaaag	1320
ctagagagct	tcagtgcctt	gaaacctgag	gccagtgcgc	tcttacagtc	agtgccctct	1380
atgttcaact	tcagggcgcc	tcccaatgcc	ctgccagaga	accttctgcg	gaaggggaaag	1440
gagcgctata	cctgcagata	ctgtggcaag	atttttccaa	ggtctgcaaa	cctaacacgg	1500
cacttgagaa	cccacacagg	agagcagcct	tacagatgca	aatactgtga	cagatcattt	1560
agcatatctt	ctaacttgca	aaggcatggt	cgcaacatcc	acaataaaga	gaagccattt	1620
aagtgtcact	tatgtgtag	gtgttttggt	caacaacca	atttagacag	acaccttaag	1680
aaacatgaga	atgggaacat	gtccggtaca	gcaacatcgt	cgcctcattc	tgaactggaa	1740
agtacagggtg	cgattctgga	tgacaaagaa	gatgcttact	tcacagaaat	tcgaaatttc	1800
attgggaaca	gcaaccatgg	cagccaatct	cccaggaatg	tggaggagag	aatgaatggc	1860
agtcatttta	aagatgaaaa	ggctttgggtg	accagtcaaa	attcagactt	gctggatgat	1920
gaagaagttg	aagatgaggt	gttggttagat	gaggaggatg	aagacaatga	tattactgga	1980
aaaacaggaa	aggaaccagt	gacaagtaat	ttacatgaag	gaaaccctga	ggatgactat	2040
gaagaaacca	gtgccctgga	gatgagttgc	aagacatccc	cagtgcagga	taaagaggaa	2100
gaatataaaa	tgggactttc	tgctctagat	catataaggc	acttcacaga	tagcctcaaa	2160
atgaggaaaa	tgggaagataa	tcaatattct	gaagctgagc	tgctctcttt	tagtaacttc	2220
catgtgccag	aggaacttaa	gcagccgtta	cacagaaagt	ccaaatcgca	ggcatatgct	2280
atgatgctgt	cactgtctga	caaggagtcc	ctccattcta	catcccacag	ttcttccaac	2340
gtgtggcaca	gtatggccag	ggctgcggcg	gaatccagtg	ctatccagtc	cataagccac	2400
gtatgacgtt	atcaaggttg	accagagtgg	gaccaagtcc	aacagtagca	tggctctttc	2460
atataggact	atttacaaga	ctgctgagca	gaatgcctta	taaacctgca	gggtcactca	2520
tctaaagtct	agtacctta	aactgaatga	tttaaaaaag	aaaagaaaga	aaaaagaaac	2580
tatttattct	cgataattttg	ttttgcacag	caaaggcagc	tgctgacttc	tggagatca	2640
atcaatgcga	cttaaaagtga	ttcagtga	acaaaaaact	tgggtggctg	aaggcatctt	2700
ccagtttacc	ccaccttagg	gtatgggtgg	gtgagaagg	cagttgagat	ggcagcattg	2760
atatgaatga	acactccata	gaaactgaat	tctcttttgt	acaagatcac	ctgacatgat	2820
tgggaacagt	tgcttttaat	tacagattta	atttttttct	tcgttaaagt	tttatgtaat	2880
ttaacctttt	gaagacagaa	gtagtggat	gaaatgcaca	gtcaattatt	atagaaactg	2940
ataacaggga	gtacttggtc	ccccttttgc	cttcttaagt	acattgttta	aaactaggga	3000
aaaagggtat	gtgtatattg	taaactatgg	atgttaacac	ttcaaagagg	ttaagtcagt	3060
gargtaacct	attcatcacc	agtaccgctg	taccactaat	aaattgtttg	ccaaatcctt	3120
gtaataacat	cttaatttta	gacaatcatg	tcaactgttt	taattgtttat	ttttttgtgt	3180
gtgttgcggt	tatcatgtat	ttatttggtg	gcaaactatt	gtttgttgat	taaaatagca	3240
ctgttccagt	cagccactac	tttatgacgt	ctgaggcaca	cccctttccg	aatttcaagg	3300
accaaggtga	cccagacctg	gtatgagagt	gccaaatggt	gtttggcttt	tcttaacatt	3360
cctttttgtt	tgtttggttt	gttttccttc	ttaatgaact	aaatacgaat	agatgcaact	3420
tagtttttgt	aatactgaaa	tncgattcaa	ttgtataaac	gattataatt	tctttcatgg	3480
aagcatgatt	cttctgatta	aaaactgtac	tccatatttt	atgctgggtg	tctgcaagct	3540
tgtgcgatgt	tatgttcatg	ttaatcctat	ttgtaaaatg	aagtgttccc	aaccttatng	3600
ttaaaagaga	gaangtaaat	aacagactgt	attcagttat	tttgcctttt	attgagggaac	3660
cagattttgt	ttctttttgt	ttgtaatctc	attttngaaa	taatcagcaa	gttgagggtac	3720
tttcttcaaa	tgctttgtac	aatataaact	gttatgcctt	tcagtgcatt	actatgggag	3780
gagcaactaa	aaaataaaga	cttacaacaaa	ggagtatttt	taaagaacaa	aaacttgagg	3840
gggggcccgg	tacccaattc	gccctatagt	gagtagtatt	acaattcact	ggccgtcggt	3900
ttacaacgtc	gtgactggga	aaaccctggg	ttaccaact	taatcgtctt	n	3951



<210> 77  
 <211> 718  
 <212> PRT  
 <213> Homo sapiens

<400> 77

Met	Lys	Ser	Glu	Asp	Tyr	Pro	His	Glu	Thr	Met	Ala	Pro	Asp	Ile	His
1				5					10					15	
Glu	Glu	Arg	Gln	Tyr	Arg	Cys	Glu	Asp	Cys	Asp	Gln	Leu	Phe	Glu	Ser
			20					25					30		
Lys	Ala	Glu	Leu	Ala	Asp	His	Gln	Lys	Phe	Pro	Cys	Ser	Thr	Pro	His
	35						40					45			
Ser	Ala	Phe	Ser	Met	Val	Glu	Glu	Asp	Phe	Gln	Gln	Lys	Leu	Glu	Ser
	50					55					60				
Glu	Asn	Asp	Leu	Gln	Glu	Ile	His	Thr	Ile	Gln	Glu	Cys	Lys	Glu	Cys
65				70					75					80	
Asp	Gln	Val	Phe	Pro	Asp	Leu	Gln	Ser	Leu	Glu	Lys	His	Met	Leu	Ser
			85						90					95	
His	Thr	Glu	Glu	Arg	Glu	Tyr	Lys	Cys	Asp	Gln	Cys	Pro	Lys	Ala	Phe
			100					105					110		
Asn	Trp	Lys	Ser	Asn	Leu	Ile	Arg	His	Gln	Met	Ser	His	Asp	Ser	Gly
	115						120					125			
Lys	His	Tyr	Glu	Cys	Glu	Asn	Cys	Ala	Lys	Val	Phe	Thr	Asp	Pro	Ser
	130					135					140				
Asn	Leu	Gln	Arg	His	Ile	Arg	Ser	Gln	His	Val	Gly	Ala	Arg	Ala	His
145				150						155				160	
Ala	Cys	Pro	Glu	Cys	Gly	Lys	Thr	Phe	Ala	Thr	Ser	Ser	Gly	Leu	Lys
			165						170					175	
Gln	His	Lys	His	Ile	His	Ser	Ser	Val	Lys	Pro	Phe	Ile	Ser	Phe	Ser
			180					185					190		
Gln	Ser	Met	Tyr	Pro	Phe	Pro	Asp	Arg	Asp	Leu	Arg	Ser	Leu	Pro	Leu
	195						200					205			
Lys	Met	Glu	Pro	Gln	Ser	Pro	Gly	Glu	Val	Lys	Lys	Leu	Gln	Lys	Gly
	210					215					220				
Ser	Ser	Glu	Ser	Pro	Phe	Asp	Leu	Thr	Thr	Lys	Arg	Lys	Asp	Glu	Lys
225				230						235				240	
Pro	Leu	Thr	Pro	Val	Pro	Ser	Lys	Pro	Pro	Val	Thr	Pro	Ala	Thr	Ser
			245							250				255	
Gln	Asp	Gln	Pro	Leu	Asp	Leu	Ser	Met	Gly	Ser	Arg	Ser	Arg	Ala	Ser
			260					265					270		
Gly	Thr	Lys	Leu	Thr	Glu	Pro	Arg	Lys	Asn	His	Val	Phe	Gly	Gly	Lys
	275						280					285			
Lys	Gly	Ser	Asn	Val	Glu	Ser	Arg	Pro	Ala	Ser	Asp	Gly	Ser	Leu	Gln
	290					295					300				
His	Ala	Arg	Pro	Thr	Pro	Phe	Phe	Met	Asp	Pro	Ile	Tyr	Arg	Val	Glu
305				310						315				320	
Lys	Arg	Lys	Leu	Thr	Asp	Pro	Leu	Glu	Ala	Leu	Lys	Glu	Lys	Tyr	Leu
			325						330					335	
Arg	Pro	Ser	Pro	Gly	Phe	Leu	Phe	His	Pro	Gln	Met	Ser	Ala	Ile	Glu
			340					345					350		
Asn	Met	Ala	Glu	Lys	Leu	Glu	Ser	Phe	Ser	Ala	Leu	Lys	Pro	Glu	Ala
	355					360						365			
Ser	Glu	Leu	Leu	Gln	Ser	Val	Pro	Ser	Met	Phe	Asn	Phe	Arg	Ala	Pro
	370					375					380				
Pro	Asn	Ala	Leu	Pro	Glu	Asn	Leu	Leu	Arg	Lys	Gly	Lys	Glu	Arg	Tyr
385				390						395				400	
Thr	Cys	Arg	Tyr	Cys	Gly	Lys	Ile	Phe	Pro	Arg	Ser	Ala	Asn	Leu	Thr

```
<210> 78
<211> 4950
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(4950)
<223> n = A,T,C or G
```

<400> 78							
nngaccacag	cgtccgggtg	cggctctggac	acgtctccgg	ggtgggtcgt	ccggccttcg	60	
atcttagacg	aattttacaa	tgtgaagttc	tgcatagatg	ccagtcaacc	agatgttgga	120	
agctggctca	agtacattag	attcgctggc	tgttatgatc	agcacaaact	tggtgcatgc	180	
cagataaatg	atcagatatt	ctatagagta	gttcgagaca	ttgcgccggg	agaggagctt	240	
ctgctgtttc	tgaagagcga	agactatccc	catgaaacta	tggcgccggg	tatccacgaa	300	
gaacggcaat	atcgctgcga	agactctqac	cagctctttg	aatctaaggc	tgaactagca	360	

gataccaaaa	agtttccatg	cagtactcct	cactcagcat	tttcaatggt	tgaagaggac	420
tttcagcaaa	aactcgaaag	cgagaatgat	ctccaagaga	tacacacgat	ccaggagtgt	480
aaggaatgtg	accaagtttt	tcctgatttg	caaagcctgg	agaaacacat	gctgtcacat	540
actgaagaga	gggaatacaa	gtgtgatcag	tgtcccaagg	catttaactg	gaagtccaat	600
ttaattcgcc	accagatgtc	acatgacagt	ggaaagcact	atgaatgtga	aaactgtgcc	660
aaggttttca	cggaccctag	caaccttcag	cggcacattc	gctctcagca	tgtcggtgcc	720
cgggcccattg	catgcccggga	gtgtggcaaa	acgtttgcca	cttcgtcggg	cctcaaacaa	780
cacaagcaca	tccacagcag	tgtgaagccc	tttatctgtg	aggtctgcca	taaactcctat	840
actcagtttt	caaacctttg	ccgtcataag	cgcatgcatg	ctgattgcag	aacccaaatc	900
aagtgc aaag	aactgtggaca	aatgttcagc	actacgtctt	ccttaaataa	acacaggagg	960
ttttgtgagg	gcaagaacca	ttttgcggca	ggtggatttt	ttggccaagg	catttcactt	1020
cctggaaccc	cagctatgga	taaaacgtcc	atggttaata	tgagtcatgc	caaccggggc	1080
cttgctgact	attttggcgc	caataggcat	cctgctggtc	ttacctttcc	aacagctcct	1140
ggattttctt	ttagcttccc	tggtctgttt	ccttcgggt	tgtaccacag	gcctcctttg	1200
atacctgcta	gttctcctgt	taaaggacta	tcaagtactg	aacagacaaa	caaaagtcaa	1260
agtccccctca	tgacacatcc	tcagatactg	ccagctacac	aggatatttt	gaaggcacta	1320
tctaaacacc	catctgtagg	ggacaataag	ccagtggagc	tccagcccga	gaggtcctct	1380
gaagagaggc	cctttgagaa	aatcagtgac	cagtcagaga	gtagtacct	tgatgatgtc	1440
agtaaccaca	gtggcagtg	cctggaaaca	acctcgggt	ctgatctgga	aagtgcatt	1500
gaaagtgata	agagaaaatt	taaaagaaat	ggtaaaatgt	tcaaagacaa	agtaagccct	1560
cttcagaatc	tggtctcaat	aaataataag	aaagaatata	gcaatcattc	cattttctca	1620
ccatcttttag	aggagcagac	tgcggtgtca	ggagctgtga	atgattctat	aaaggctatt	1680
gcttctattg	ctgaaaaata	ctttggttca	acaggactgg	tggggctgca	agacaaaaaa	1740
gttgaggctt	taccttacc	ttccatgttt	cccctcccat	tttttccagc	attctctcaa	1800
tcaatgtacc	catttcctga	tagagacttg	agatcgttac	ctttgaaaat	ggaaccccaa	1860
tcaccaggtg	aagtaaagaa	actgcagaag	ggcagctctg	agtccccctt	tgatctcacc	1920
actaagcgaa	aggatgagaa	gcccttgact	ccagtcacct	ccaagcctcc	agtgcacct	1980
gccacaagcc	agaccagcc	cctggatcta	agtatgggca	gtaggagtag	agccagtggg	2040
acaaagctga	ctgagcctcg	aaaaaaccac	gtgtttgggg	gaaaaaaagg	aagcaacgtc	2100
gaatcaagac	ctgcttcaga	tggttccttg	cagcatgcaa	gacccactcc	tttctttatg	2160
gaccctattt	acagagtaga	gaaaagaaaa	ctaactgacc	cacttgaagc	tttaaaagag	2220
aaatacttga	ggccttctcc	aggattcttg	tttcccccac	aattccaact	gcctgatcag	2280
agaacttgga	tgtcagctat	tgaaaacatg	gcagaaaagc	tagagagctt	cagtgccttg	2340
aaacctgagg	ccagtgcagc	cttacagtca	gtgccctcta	tgttcaactt	cagggcgctt	2400
cccaatgccc	tgccagagaa	ccttctgcgg	aagggaagg	agcgctatac	ctgcagatac	2460
tgtggcaaga	tttttccaag	gtctgcaaac	ctaacacggc	acttgagaac	ccacacagga	2520
gagcagcctt	acagatgcaa	atactgtgac	agatcattta	gcatatcttc	taacttgcaa	2580
aggcatgttc	gcaacatcca	caataaagag	aagccattta	agtgtcactt	atgtgatagg	2640
tgttttggtc	aacaaaccaa	tttagacaga	cacctaaaga	aacatgagaa	tggaacatg	2700
tccggtacag	caacatcgtc	gcctcattct	gaactggaaa	gtacagggtg	gattctggat	2760
gacaaagaag	atgcttactt	cacagaaatt	cgaaatttca	ttgggaacag	caaccatggc	2820
agccaatctc	ccaggaatgt	ggaggagaga	atgaatggca	gtcattttta	agatgaaaag	2880
gctttggtga	ccagtcaaaa	ttcagacttg	ctggatgatg	aagaagttga	agatgagggtg	2940
ttgttagatg	aggaggatga	agacaatgat	attactggaa	aaacaggaaa	ggaaccagtg	3000
acaagtaatt	tacatgaagg	aaacctgag	gatgactatg	aagaaaccag	tgccctggag	3060
atgagttgca	agacatcccc	agtgaggtat	aaagaggaag	aataataaag	tggaactttct	3120
gctctagatc	atataaggca	cttcacagat	agcctcaaaa	tgaggaaaat	ggaagataat	3180
caatattctg	aagctgagct	gtcttctttt	agtacttccc	atgtgccaga	ggaacttaag	3240
cagccgttac	acagaaagtc	caaatcgag	gcatatgcta	tgatgctgtc	actgtctgac	3300
aaggagtccc	tccattctac	atcccacagt	tcttccaacg	tgtggcacag	tatggccagg	3360
gctgcggcgg	aatccagtc	tatccagtc	ataagccacg	tatgacgtta	tcaaggttga	3420
ccagagtggg	accaagtcca	acagtagcat	ggctctttca	tataggacta	tttacaagac	3480
tgctgagcag	aatgccttat	aaacctgcag	ggtcactcat	ctaaagtcta	gtgaccttaa	3540
actgaatgat	ttaaaaaaga	aaagaaagaa	aaaagaaact	atattattctc	gatattttgt	3600
tttgacagc	aaaggcagct	gctgacttct	ggaagatcaa	tcaatgcgac	ttaaagtgat	3660
tcagtga aaa	caaaaaactt	ggtgggctga	aggcatcttc	cagtttacc	caccttaggg	3720
tatgggtggg	tgagaagggc	agttgagatg	gcagcattga	tatgaatgaa	cactccatag	3780
aaactgaatt	ctcttttgta	caagatcacc	tgacatgatt	gggaacagtt	gcttttaatt	3840

```

acagatttaa ttttttctt cgtaaagtt ttatgtaatt taaccctttg aagacagaag 3900
tagttggatg aaatgcacag tcaattatta tagaaactga taacagggag tacttggtcc 3960
cccttttgcc ttcttaagta cattgtttaa aactagggaa aaagggtatg tgtatattgt 4020
aaactatgga tgtaaacact tcaaagaggt taagtcagtg argtaaccta ttcacacca 4080
gtaccgctgt accactaata aattgtttgc caaatccttg taataacatc ttaatttttag 4140
acaatcatgt cactgttttt aatgtttatt tttttgtgtg tggtgcgtgt atcatgtatt 4200
tatttggttg caaactattg tttgttgatt aaaatagcac tgttccagtc agccactact 4260
ttatgacgtc tgaggcacac ccctttccga atttcaagga ccaagggtgac ccgacctgtg 4320
tatgagagtg ccaaagtgtg tttggctttt cttaacattc ctttttggtt gtttggtttg 4380
ttttccttct taatgaacta aatacgaata gatgcaactt agtttttgta atactgaaat 4440
ncgattcaat tgtataaacg attataattt ctttcatgga agcatgattc ttctgattaa 4500
aaactgtact ccataattta tgctggttgt ctgcaagctt gtgcgatggt atgttcatgt 4560
taatcctatt tgtaaaatga agtgttccca accttatngt taaaagagag aangtaata 4620
acagactgta ttcagttatt ttgcccttta ttgaggaacc agatttggtt tcttttggtt 4680
tgtaatctca ttttngaaat aatcagcaag ttgaggtact ttcttcaaat gctttgtaca 4740
atataaaactg ttatgccttt cagtgcatta ctatgggagg agcaactaaa aaataaagac 4800
ttacaaaaag gagtatTTTT aaagaacaaa aacttgaggg ggggcccggt acccaattcg 4860
ccctatagtg agtagtatta caattcactg gccgtcggtt tacaacgtcg tgactgggaa 4920
aaccctgggt tacccaactt aatcgtcttn 4950

```

&lt;210&gt; 79

&lt;211&gt; 1051

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 79

```

Met Lys Ser Glu Asp Tyr Pro His Glu Thr Met Ala Pro Asp Ile His
 1          5          10          15
Glu Glu Arg Gln Tyr Arg Cys Glu Asp Cys Asp Gln Leu Phe Glu Ser
 20          25          30
Lys Ala Glu Leu Ala Asp His Gln Lys Phe Pro Cys Ser Thr Pro His
 35          40          45
Ser Ala Phe Ser Met Val Glu Glu Asp Phe Gln Gln Lys Leu Glu Ser
 50          55          60
Glu Asn Asp Leu Gln Glu Ile His Thr Ile Gln Glu Cys Lys Glu Cys
 65          70          75          80
Asp Gln Val Phe Pro Asp Leu Gln Ser Leu Glu Lys His Met Leu Ser
 85          90          95
His Thr Glu Glu Arg Glu Tyr Lys Cys Asp Gln Cys Pro Lys Ala Phe
100          105          110
Asn Trp Lys Ser Asn Leu Ile Arg His Gln Met Ser His Asp Ser Gly
115          120          125
Lys His Tyr Glu Cys Glu Asn Cys Ala Lys Val Phe Thr Asp Pro Ser
130          135          140
Asn Leu Gln Arg His Ile Arg Ser Gln His Val Gly Ala Arg Ala His
145          150          155          160
Ala Cys Pro Glu Cys Gly Lys Thr Phe Ala Thr Ser Ser Gly Leu Lys
165          170          175
Gln His Lys His Ile His Ser Ser Val Lys Pro Phe Ile Cys Glu Val
180          185          190
Cys His Lys Ser Tyr Thr Gln Phe Ser Asn Leu Cys Arg His Lys Arg
195          200          205
Met His Ala Asp Cys Arg Thr Gln Ile Lys Cys Lys Asp Cys Gly Gln
210          215          220
Met Phe Ser Thr Thr Ser Ser Leu Asn Lys His Arg Arg Phe Cys Glu
225          230          235          240
Gly Lys Asn His Phe Ala Ala Gly Gly Phe Phe Gly Gln Gly Ile Ser
245          250          255

```

Leu Pro Gly Thr Pro Ala Met Asp Lys Thr Ser Met Val Asn Met Ser  
 260 265 270  
 His Ala Asn Pro Gly Leu Ala Asp Tyr Phe Gly Ala Asn Arg His Pro  
 275 280 285  
 Ala Gly Leu Thr Phe Pro Thr Ala Pro Gly Phe Ser Phe Ser Val Pro  
 290 295 300  
 Gly Leu Phe Pro Ser Gly Leu Tyr His Arg Pro Pro Leu Ile Pro Ala  
 305 310 315 320  
 Ser Ser Pro Val Lys Gly Leu Ser Ser Thr Glu Gln Thr Asn Lys Ser  
 325 330 335  
 Gln Ser Pro Leu Met Thr His Pro Gln Ile Leu Pro Ala Thr Gln Asp  
 340 345 350  
 Ile Leu Lys Ala Leu Ser Lys His Pro Ser Val Gly Asp Asn Lys Pro  
 355 360 365  
 Val Glu Leu Gln Pro Glu Arg Ser Ser Glu Glu Arg Pro Phe Glu Lys  
 370 375 380  
 Ile Ser Asp Gln Ser Glu Ser Ser Asp Leu Asp Asp Val Ser Thr Pro  
 385 390 395 400  
 Ser Gly Ser Asp Leu Glu Thr Thr Ser Gly Ser Asp Leu Glu Ser Asp  
 405 410 415  
 Ile Glu Ser Asp Lys Glu Lys Phe Lys Glu Asn Gly Lys Met Phe Lys  
 420 425 430  
 Asp Lys Val Ser Pro Leu Gln Asn Leu Ala Ser Ile Asn Asn Lys Lys  
 435 440 445  
 Glu Tyr Ser Asn His Ser Ile Phe Ser Pro Ser Leu Glu Glu Gln Thr  
 450 455 460  
 Ala Val Ser Gly Ala Val Asn Asp Ser Ile Lys Ala Ile Ala Ser Ile  
 465 470 475 480  
 Ala Glu Lys Tyr Phe Gly Ser Thr Gly Leu Val Gly Leu Gln Asp Lys  
 485 490 495  
 Lys Val Gly Ala Leu Pro Tyr Pro Ser Met Phe Pro Leu Pro Phe Phe  
 500 505 510  
 Pro Ala Phe Ser Gln Ser Met Tyr Pro Phe Pro Asp Arg Asp Leu Arg  
 515 520 525  
 Ser Leu Pro Leu Lys Met Glu Pro Gln Ser Pro Gly Glu Val Lys Lys  
 530 535 540  
 Leu Gln Lys Gly Ser Ser Glu Ser Pro Phe Asp Leu Thr Thr Lys Arg  
 545 550 555 560  
 Lys Asp Glu Lys Pro Leu Thr Pro Val Pro Ser Lys Pro Pro Val Thr  
 565 570 575  
 Pro Ala Thr Ser Gln Asp Gln Pro Leu Asp Leu Ser Met Gly Ser Arg  
 580 585 590  
 Ser Arg Ala Ser Gly Thr Lys Leu Thr Glu Pro Arg Lys Asn His Val  
 595 600 605  
 Phe Gly Gly Lys Lys Gly Ser Asn Val Glu Ser Arg Pro Ala Ser Asp  
 610 615 620  
 Gly Ser Leu Gln His Ala Arg Pro Thr Pro Phe Phe Met Asp Pro Ile  
 625 630 635 640  
 Tyr Arg Val Glu Lys Arg Lys Leu Thr Asp Pro Leu Glu Ala Leu Lys  
 645 650 655  
 Glu Lys Tyr Leu Arg Pro Ser Pro Gly Phe Leu Phe His Pro Gln Phe  
 660 665 670  
 Gln Leu Pro Asp Gln Arg Thr Trp Met Ser Ala Ile Glu Asn Met Ala  
 675 680 685  
 Glu Lys Leu Glu Ser Phe Ser Ala Leu Lys Pro Glu Ala Ser Glu Leu  
 690 695 700  
 Leu Gln Ser Val Pro Ser Met Phe Asn Phe Arg Ala Pro Pro Asn Ala  
 705 710 715 720

Leu Pro Glu Asn Leu Leu Arg Lys Gly Lys Glu Arg Tyr Thr Cys Arg  
 725 730 735  
 Tyr Cys Gly Lys Ile Phe Pro Arg Ser Ala Asn Leu Thr Arg His Leu  
 740 745 750  
 Arg Thr His Thr Gly Glu Gln Pro Tyr Arg Cys Lys Tyr Cys Asp Arg  
 755 760 765  
 Ser Phe Ser Ile Ser Ser Asn Leu Gln Arg His Val Arg Asn Ile His  
 770 775 780  
 Asn Lys Glu Lys Pro Phe Lys Cys His Leu Cys Tyr Arg Cys Phe Gly  
 785 790 795 800  
 Gln Gln Thr Asn Leu Asp Arg His Leu Lys Lys His Glu Asn Gly Asn  
 805 810 815  
 Met Ser Gly Thr Ala Thr Ser Ser Pro His Ser Glu Leu Glu Ser Thr  
 820 825 830  
 Gly Ala Ile Leu Asp Asp Lys Glu Asp Ala Tyr Phe Thr Glu Ile Arg  
 835 840 845  
 Asn Phe Ile Gly Asn Ser Asn His Gly Ser Gln Ser Pro Arg Asn Val  
 850 855 860  
 Glu Glu Arg Met Asn Gly Ser His Phe Lys Glu Glu Lys Ala Leu Val  
 865 870 875 880  
 Pro Ser Gln Asn Ser Asp Leu Leu Asp Asp Glu Glu Val Glu Asp Glu  
 885 890 895  
 Val Leu Leu Asp Glu Glu Asp Glu Asp Tyr Asp Ile Thr Gly Lys Thr  
 900 905 910  
 Gly Lys Glu Pro Val Thr Ser Asn Leu His Glu Gly Asn Pro Glu Asp  
 915 920 925  
 Asp Tyr Glu Glu Thr Ser Ala Leu Glu Met Ser Cys Lys Thr Ser Pro  
 930 935 940  
 Val Arg Tyr Lys Glu Glu Glu Tyr Lys Ser Gly Leu Ser Ala Leu Asp  
 945 950 955 960  
 His Ile Arg His Phe Thr Asp Ser Leu Lys Met Arg Lys Met Glu Asp  
 965 970 975  
 Asn Gln Tyr Ser Glu Ala Glu Leu Ser Ser Phe Ser Thr Ser His Val  
 980 985 990  
 Pro Glu Glu Leu Lys Gln Pro Leu His Arg Lys Ser Lys Ser Gln Ala  
 995 1000 1005  
 Tyr Ala Met Met Leu Ser Leu Ser Asp Lys Glu Ser Leu His Ser Thr  
 1010 1015 1020  
 Ser His Ser Ser Ser Asn Val Trp His Ser Met Ala Arg Ala Ala Ala  
 1025 1030 1035 1040  
 Glu Ser Ser Ala Ile Gln Ser Ile Ser His Val  
 1045 1050

&lt;210&gt; 80

&lt;211&gt; 3978

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(3978)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 80

nngacccacg cgtccgggtg cggctcggac acgtctccgg ggtgggtcgt ccggccttcg 60  
 atcttagacg aattttacaa tgtgaagttc tgcatagatg ccagtcaacc agatgttgga 120  
 agctggctca agtacattag attcgtctgc tggttatgatc agcacaacct tgttgcattg 180

cagataaatg	atcagatatt	ctatagagta	gttgagaca	ttgcgcggg	agaggagctt	240
ctgctgttca	tgaagagcga	agactatccc	catgaaacta	tggcgccgga	tatccacgaa	300
gaacggcaat	atcgctgcga	agactgtgac	cagctctttg	aatctaaggc	tgaactagca	360
gatcaccaaa	agttttccatg	cagtactcct	cactcagcat	tttcaatggt	tgaagaggac	420
tttcagcaaa	aactcgaaag	cgagaatgat	ctccaagaga	tacacacgat	ccaggagtgt	480
aaggaatgtg	accaagtttt	tctgtatttg	caaagcctgg	agaaacacat	gctgtcacat	540
actgaagaga	gggaatacaa	gtgtgatcag	tgtcccaagg	catttaactg	gaagtccaat	600
ttaattcgcc	accagatgtc	acatgacagt	ggaaagcact	atgaatgtga	aaactgtgcc	660
aaggttttca	cggaccctag	caaccttcag	cggcacattc	gctctcagca	tgtcggtgcc	720
cgggccccatg	catgcccgga	gtgtggcaaa	acgttttgcca	cttcgtcggg	cctcaaacaa	780
cacaagcaca	tccacagcag	tgtgaagccc	tttatctcat	tctctcaatc	aatgtacca	840
tttcttgata	gagacttgag	atcgttacct	ttgaaaatgg	aaccccaatc	accaggtgaa	900
gtaaagaaac	tgcagaaggg	cagctctgag	tccccctttg	atctcaccac	taagcgaaag	960
gatgagaagc	ccttgactcc	agtccctcc	aagcctccag	tgacacctgc	cacaagccaa	1020
gaccagcccc	tggatctaag	tatgggcagt	aggagtagag	ccagtgggac	aaagctgact	1080
gagcctcgaa	aaaaccacgt	gtttggggga	aaaaaaggaa	gcaacgtcga	atcaagacct	1140
gcttcagatg	gttccttgca	gcatgcaaga	cccactcctt	tctttatgga	ccctattttac	1200
agagtagaga	aaagaaaact	aactgaccca	cttgaagctt	taaaagagaa	atacttgagg	1260
ccttctccag	gattcttggt	tcacccacaa	ttccaactgc	ctgatcagag	aacttggtat	1320
tcagctattg	aaaacatggc	agaaaagcta	gagagcttca	gtgccctgaa	acctgaggcc	1380
agtgaagctc	tacagtacgt	gcctctatg	ttcaacttca	gggcgcctcc	caatgccctg	1440
ccagagaacc	ttctgcggaa	gggaaaggag	cgctatacct	gcagatactg	tggcaagatt	1500
tttccaaggt	ctgcaaacct	aacacggcac	ttgagaaccc	acacaggaga	gcagccttac	1560
agatgcaaat	actgtgacag	atcatttagc	atatcttcta	acttgcaaag	gcatgttcgc	1620
aacatccaca	ataaagagaa	gccattttaag	tgctcacttat	gtgatagggt	ttttgggtcaa	1680
caaaccaatt	tagacagaca	cctaaagaaa	catgagaatg	ggaacatgtc	cggtagacga	1740
acatcgtcgc	ctcattctga	actggaaaagt	acaggtgcga	ttctggatga	caaagaagat	1800
gcttacttca	cagaaaattcg	aaatttcatt	gggaacagca	accatggcag	ccaatctccc	1860
aggaatgtgg	aggagagaa	gaatggcagt	cattttaaa	atgaaaaggc	tttgggtgacc	1920
agtcaaaatt	cagacttgct	ggatgatgaa	gaagttgaag	atgaggtgtt	gttagatgag	1980
gaggatgaag	acaatgatata	tactggaaaa	acaggaaagg	aaccagtgc	aagtaattta	2040
catgaaggaa	accctgagga	tgactatgaa	gaaaccagtgc	ccctggagat	gagttgcaag	2100
acatccccag	tgaggtataa	agaggaagaa	tataaaagtgc	gactttctgc	tctagatcat	2160
ataaggcact	tcacagatag	cctcaaaatg	aggaaaatgg	aagataatca	atattctgaa	2220
gctgagctgt	cttcttttag	tacttcccat	gtgccagagg	aacttaagca	gccgttacac	2280
agaaagtcca	aactgcaggc	atatgctatg	atgctgtcac	tgtctgacaa	ggagtccctc	2340
cattctacat	cccacagtgc	ttccaacgtg	tgccacagta	tggccagggc	tgcggcgga	2400
tccagtgcata	tccagtccat	aagccacgta	tgacgttatc	aaggttgacc	agagtgggac	2460
caagtccaac	agtagcatgg	ctctttcata	taggactatt	tacaagactg	ctgagcagaa	2520
tgctttataa	acctgcaggg	tcactcatct	aaagtctagt	gaccttaaac	tgaatgattt	2580
aaaaaagaaa	agaaagaaaa	aagaaactat	ttattctcga	tattttgttt	tgacacgaa	2640
aggcagctgc	tgacttctgg	aagatcaatc	aatgcgactt	aaagtgattc	agtgaataca	2700
aaaaacttgg	tgggctgaag	gcatcttcca	gtttacccca	ccttaggggt	tgggtgggtg	2760
agaagggcag	ttgagatggc	agcattgata	tgaatgaaca	ctccatagaa	actgaattct	2820
cttttgtaca	agatcacctg	acatgattgg	gaacagttgc	ttttaattac	agatttaatt	2880
tttttcttcg	ttaaagtttt	atgtaattta	accctttgaa	gacagaagta	gttggatgaa	2940
atgcacagtc	aattattata	gaaactgata	acaggagta	cttgttcccc	cttttgcctt	3000
cttaagtaca	ttgtttaaaa	ctagggaaaa	agggtatgtg	tatatgttaa	actatggatg	3060
ttacacttcc	aaagagggtta	agtcagtgar	gtaacctatt	catcaccagt	accgctgtac	3120
cactaataaa	ttgtttgcca	aatccttgta	ataacatctt	aatttttagac	aatcatgtca	3180
ctgttttttaa	tgttttatttt	tttgtgtgtg	ttgcgtgtat	catgtattta	tttgttggca	3240
aactattggt	tgttgattaa	aatagcactg	ttccagtcag	ccactacttt	atgacgtctg	3300
aggcacaccc	ctttccgaat	ttcaaggacc	aaggtgaccc	gacctgtgta	tgagagtgcc	3360
aaatggtgct	tggcttttct	taacattcct	ttttgtttgt	ttgtttgttt	ttccttctta	3420
atgaactaaa	tacgaataga	tgcaacttag	ttttgttaat	actgaaatnc	gattcaattg	3480
tataaacgat	tataattttot	ttcatggaag	catgattcct	ctgattaaaa	actgtactcc	3540
atatttttatg	ctggttgtct	gcaagcttgt	gcgatgttat	gttcatgtta	atcctattttg	3600
taaaatgaag	tgttcccaac	cttatngtta	aaagagagaa	ngtaaataac	agactgtatt	3660

cagttatttt gccctttatt gaggaaccag atttgttttc tttttgtttg taatctcatt 3720  
 ttngaaataa tcagcaagtt gaggtacttt cttcaaagtc tttgtacaat ataaactgtt 3780  
 atgcctttca gtgcattact atgggaggag caactaaaaa ataaagactt acaaaaagga 3840  
 gtatttttaa agaacaaaaa cttgaggggg ggcccgggtac ccaattcgcc ctatagttag 3900  
 tagtattaca attcactggc cgctcgttta caacgctcgtg actgggaaaa ccctggggtta 3960  
 cccaacttaa tcgtcttn 3978

<210> 81

<211> 727

<212> PRT

<213> Homo sapiens

<400> 81

Met	Lys	Ser	Glu	Asp	Tyr	Pro	His	Glu	Thr	Met	Ala	Pro	Asp	Ile	His
1				5					10					15	
Glu	Glu	Arg	Gln	Tyr	Arg	Cys	Glu	Asp	Cys	Asp	Gln	Leu	Phe	Glu	Ser
			20					25					30		
Lys	Ala	Glu	Leu	Ala	Asp	His	Gln	Lys	Phe	Pro	Cys	Ser	Thr	Pro	His
	35						40					45			
Ser	Ala	Phe	Ser	Met	Val	Glu	Glu	Asp	Phe	Gln	Gln	Lys	Leu	Glu	Ser
	50					55					60				
Glu	Asn	Asp	Leu	Gln	Glu	Ile	His	Thr	Ile	Gln	Glu	Cys	Lys	Glu	Cys
65					70					75				80	
Asp	Gln	Val	Phe	Leu	Asp	Leu	Gln	Ser	Leu	Glu	Lys	His	Met	Leu	Ser
			85						90					95	
His	Thr	Glu	Glu	Arg	Glu	Tyr	Lys	Cys	Asp	Gln	Cys	Pro	Lys	Ala	Phe
		100						105					110		
Asn	Trp	Lys	Ser	Asn	Leu	Ile	Arg	His	Gln	Met	Ser	His	Asp	Ser	Gly
	115						120					125			
Lys	His	Tyr	Glu	Cys	Glu	Asn	Cys	Ala	Lys	Val	Phe	Thr	Asp	Pro	Ser
	130					135					140				
Asn	Leu	Gln	Arg	His	Ile	Arg	Ser	Gln	His	Val	Gly	Ala	Arg	Ala	His
145					150					155				160	
Ala	Cys	Pro	Glu	Cys	Gly	Lys	Thr	Phe	Ala	Thr	Ser	Ser	Gly	Leu	Lys
			165						170					175	
Gln	His	Lys	His	Ile	His	Ser	Ser	Val	Lys	Pro	Phe	Ile	Ser	Phe	Ser
		180						185					190		
Gln	Ser	Met	Tyr	Pro	Phe	Pro	Asp	Arg	Asp	Leu	Arg	Ser	Leu	Pro	Leu
		195					200					205			
Lys	Met	Glu	Pro	Gln	Ser	Pro	Gly	Glu	Val	Lys	Lys	Leu	Gln	Lys	Gly
	210					215					220				
Ser	Ser	Glu	Ser	Pro	Phe	Asp	Leu	Thr	Thr	Lys	Arg	Lys	Asp	Glu	Lys
225					230					235				240	
Pro	Leu	Thr	Pro	Val	Pro	Ser	Lys	Pro	Pro	Val	Thr	Pro	Ala	Thr	Ser
			245							250				255	
Gln	Asp	Gln	Pro	Leu	Asp	Leu	Ser	Met	Gly	Ser	Arg	Ser	Arg	Ala	Ser
		260						265					270		
Gly	Thr	Lys	Leu	Thr	Glu	Pro	Arg	Lys	Asn	His	Val	Phe	Gly	Gly	Lys
		275					280					285			
Lys	Gly	Ser	Asn	Val	Glu	Ser	Arg	Pro	Ala	Ser	Asp	Gly	Ser	Leu	Gln
	290					295					300				
His	Ala	Arg	Pro	Thr	Pro	Phe	Phe	Met	Asp	Pro	Ile	Tyr	Arg	Val	Glu
305					310					315				320	
Lys	Arg	Lys	Leu	Thr	Asp	Pro	Leu	Glu	Ala	Leu	Lys	Glu	Lys	Tyr	Leu
			325						330					335	
Arg	Pro	Ser	Pro	Gly	Phe	Leu	Phe	His	Pro	Gln	Phe	Gln	Leu	Pro	Asp
			340					345					350		
Gln	Arg	Thr	Trp	Met	Ser	Ala	Ile	Glu	Asn	Met	Ala	Glu	Lys	Leu	Glu



355	360	365
Ser Phe Ser Ala Leu Lys Pro Glu Ala Ser Glu Leu Leu Gln Ser Val		
370	375	380
Pro Ser Met Phe Asn Phe Arg Ala Pro Pro Asn Ala Leu Pro Glu Asn		
385	390	395
Leu Leu Arg Lys Gly Lys Glu Arg Tyr Thr Cys Arg Tyr Cys Gly Lys		
405	410	415
Ile Phe Pro Arg Ser Ala Asn Leu Thr Arg His Leu Arg Thr His Thr		
420	425	430
Gly Glu Gln Pro Tyr Arg Cys Lys Tyr Cys Asp Arg Ser Phe Ser Ile		
435	440	445
Ser Ser Asn Leu Gln Arg His Val Arg Asn Ile His Asn Lys Glu Lys		
450	455	460
Pro Phe Lys Cys His Leu Cys Tyr Arg Cys Phe Gly Gln Gln Thr Asn		
465	470	475
Leu Asp Arg His Leu Lys Lys His Glu Asn Gly Asn Met Ser Gly Thr		
485	490	495
Ala Thr Ser Ser Pro His Ser Glu Leu Glu Ser Thr Gly Ala Ile Leu		
500	505	510
Asp Asp Lys Glu Asp Ala Tyr Phe Thr Glu Ile Arg Asn Phe Ile Gly		
515	520	525
Asn Ser Asn His Gly Ser Gln Ser Pro Arg Asn Val Glu Glu Arg Met		
530	535	540
Asn Gly Ser His Phe Lys Glu Glu Lys Ala Leu Val Pro Ser Gln Asn		
545	550	555
Ser Asp Leu Leu Asp Asp Glu Glu Val Glu Asp Glu Val Leu Leu Asp		
565	570	575
Glu Glu Asp Glu Asp Tyr Asp Ile Thr Gly Lys Thr Gly Lys Glu Pro		
580	585	590
Val Thr Ser Asn Leu His Glu Gly Asn Pro Glu Asp Asp Tyr Glu Glu		
595	600	605
Thr Ser Ala Leu Glu Met Ser Cys Lys Thr Ser Pro Val Arg Tyr Lys		
610	615	620
Glu Glu Glu Tyr Lys Ser Gly Leu Ser Ala Leu Asp His Ile Arg His		
625	630	635
Phe Thr Asp Ser Leu Lys Met Arg Lys Met Glu Asp Asn Gln Tyr Ser		
645	650	655
Glu Ala Glu Leu Ser Ser Phe Ser Thr Ser His Val Pro Glu Glu Leu		
660	665	670
Lys Gln Pro Leu His Arg Lys Ser Lys Ser Gln Ala Tyr Ala Met Met		
675	680	685
Leu Ser Leu Ser Asp Lys Glu Ser Leu His Ser Thr Ser His Ser Ser		
690	695	700
Ser Asn Val Trp His Ser Met Ala Arg Ala Ala Glu Ser Ser Ala		
705	710	715
Ile Gln Ser Ile Ser His Val		720
725		

&lt;210&gt; 82

&lt;211&gt; 4923

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(4923)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 82

```

nngacccacg cgtccgggtg cggctctggac acgtctccgg ggtgggtcgt ccggccttcg 60
atcttagacg aattttacaa tgtgaagttc tgcatagatg ccagtcaacc agatgttga 120
agctggctca agtacattag attcgctggc tgttatgatc agcacaacct tgttgcatgc 180
cagataaatg atcagatatt ctatagagta gttgcagaca ttgcgccggg agaggagctt 240
ctgctgttca tgaagagcga agactatccc catgaaacta tggcgccgga tatccacgaa 300
gaacggcaat atcgctgcga agactgtgac cagctctttg aatctaaggc tgaactagca 360
gatcaccaaa agtttccatg cagtactcct cactcagcat tttcaatggt tgaagaggac 420
tttcagcaaa aactcgaaag cgagaatgat ctccaagaga tacacacgat ccaggagtgt 480
aaggaatgtg accaagtttt tcctgatttg caaagcctgg agaaacacat gctgtcacat 540
actgaagaga gggaatacaa gtgtgatcag tgtcccaagg catttaactg gaagtccaat 600
ttaattcgcc accagatgtc acatgacagt ggaaagcact atgaatgtga aaactgtgcc 660
aagggttttca cggaccctag caaccttcag cggcacattc gctctcagca tgtcggtgcc 720
cgggcccattg catgcccgga gtgtggcaaa acgtttgcca ctctcgtcggg cctcaaacaa 780
cacaagcaca tccacagcag tgtgaagccc tttatctgtg aggtctgcca taaatcctat 840
actcagtttt caaacctttg ccgtcataag ccatgcatg ctgattgcag aacccaaatc 900
aagtgcгааг аатgttgaca аатgttcagc actacgtctt ccttaaataa аcaаaggagg 960
ttttgtgagg gcaagaacca ttttgccgca ggttgatttt ttggccaagg catttcactt 1020
cctggaaccc cagctatgga taaaacgtcc atggttaata tgagtcatgc caaccggggc 1080
cttgctgact attttggcgc caataggcat cctgctggtc ttacctttcc aacagctcct 1140
ggattttctt ttagcttccc tggctctgtt ccttccggct tgtaccacag gcctcctttg 1200
atacctgcta gttctcctgt taaaggacta tcaagtactg aacagacaaa caaaagtcaa 1260
agtccccctc tgacacatcc tcagatactg ccagctacac aggatatttt gaaggcacta 1320
tctaaacacc catctgtagg ggacaataag ccagtggagc tccagcccga gaggtcctct 1380
gaagagaggc cctttgagaa аatcagtgac cagtcagaga gtagtгacct tgatgatgtc 1440
agtacaccaa ttggcagtga cctggaaaca acctcgggct ctgactgga aagtгacatt 1500
gaaagtгata аagagaaatt taaagaaat gttaaaatgt tcaaagacaa agtaaggcct 1560
cttcagaatc tggcttcaat aaataataag aaagaataca gcaatcattc cattttctca 1620
ccatcttttag aggagcagac tgcggtgtca ggagctgtga atgattctat aaaggctatt 1680
gcttctattg ctgaaaaata ctttggttca acaggactgg tggggctgca agacaaaaaa 1740
gttgгaggctt taccttacc ttccatgttt cccctcccat tttttccagc attctctcaa 1800
tcaatgtacc catttcctga tagagacttg агatcgttac ctttgaaaat ggaaccccaa 1860
tcaccaggtg aagtaaagaa actgcagaag ggcagctctg агtccccctt tgatctcacc 1920
actaagcgaa aggatgagaa gcccttgact ccagtccctt ccaagcctcc агtgacacct 1980
gccacaagcc аgaccagcc cctggatcta агtatgggca gtaggagtag агccagtgгg 2040
acaaagctga ctgagcctcg aaaaaaccac gtgtttgggg gaaaaaaagg аagcaacgtc 2100
gaatcaagac ctgcttcaga tggttccttg cagcatgcaa gaccactcc tttctttatg 2160
gaccctattt acagagtaga gaaaagaaaa ctaactgacc cacttgaagc tttaaaagag 2220
aaatacttga ggccttctcc aggattcttg tttcacccac aaatgtcagc tattgaaaac 2280
atggcagaaa агctagagag cttcagtgcc ctgaaacctg агgccagtga gctcttacag 2340
tcagtgccct ctatgttcaa cttcagggcg cctcccaatg ccctgccaga gaaccttctg 2400
cggaaggгaa агgagcgcta tacctgcaga tactgtggca агatttttcc aagggtctgca 2460
aacctaacac ggcacttgag aaccacaca ggagagcagc cttacagatg caaatactgt 2520
gacagatcat ttagcatatc ttctaacttg caaaggcatg ttcgcaacat ccacaataaa 2580
gagaagccat ttaagtgtca cttatgtgat агgtgttttg gtcaacaaac caatttagac 2640
agacacctaa agaaacatga gaatgggaac atgtccggta cagcaacatc gtcgcctcat 2700
tctgaactgg aaagtacagg tgcgattctg gatgacaaag ааgatgctta cttcacagaa 2760
attcgaaatt tcattgggaa cagcaacctt ggcagccaat ctcccaggaa tgtggaggag 2820
agaatgaatg gcagtcattt taaagatgaa аaggcttttg tgaccagtca aaattcagac 2880
ttgctggatg atgaagaagt tgaagatgag gtgttggttag atgaggagga tgaagacaat 2940
gatattactg gaaaaacagg aaaggaacca gtgacaagta atttacatga агgaaaccct 3000
gaggatgact atgaagaaac cagtgccttg gagatgagtt gcaagacatc cccagtgagg 3060
tataagaggg аagaatataa агtgгactt tctgctctag atcatataag gcacttcaca 3120
gatagcctca аaatgaggaa аatggaagat аatcaatatt ctgaagctga gctgtcttct 3180
tttagtactt cccatgtgcc агaggaactt аacagccgt tacacagaaa gtccaaatcг 3240
caggcatatg ctatgatgct gtcactgtct gacaaggagt ccctccattc tacatcccac 3300
agttcttcca acgtgtggca cagtatggcc агggctgcгg cggaatccag tgctatccag 3360

```

```

tccataagcc acgtatgacg ttatcaaggt tgaccagagt gggaccaagt ccaacagtag 3420
catggctctt tcatatagga ctatttacia gactgctgag cagaatgcct tataaacctg 3480
cagggtcact catctaaagt ctagtacact taaactgaat gatttaaaaa agaaaagaaa 3540
gaaaaaagaa actatttatt ctcgatattt tgttttgac agcaaaggca gctgctgact 3600
tctggaagat caatcaatgc gacttaaagt gattcagtga aaacaaaaaa cttgggtggc 3660
tgaaggcatc ttccagttta cccacactta gggatgggt gggtgagaag ggcagttgag 3720
atggcagcat tgatatgaat gaacactcca tagaaactga attctctttt gtacaagatc 3780
acctgacatg attgggaaca gttgctttta attacagatt taattttttt cttcgtaaaa 3840
gttttatgta atttaaccct ttgaagacag aagtagttgg atgaaatgca cagtcaatta 3900
ttatagaaac tgataacagg gagtacttgt tccccctttt gcottcttaa gtacattgtt 3960
taaaactagg gaaaaagggt atgtgtatat tgtaaaactat ggatgttaac acttcaaaga 4020
ggtaagtca gtgargtaac ctattcatca ccagtaccgc tgtaccacta ataaattgtt 4080
tgccaaatcc ttgtaataac atcttaattt tagacaatca tgtcactgtt tttaatgttt 4140
atttttttgt gtgtgttgcg tgtatcatgt atttatttgt tggcaaacta ttgtttgttg 4200
attaaaatag cactgttcca gtcagccact actttatgac gtctgaggca caccctttc 4260
cgaatttcaa ggaccaaggt gacccgacct gtgtatgaga gtgccaaatg gtgtttggct 4320
tttcttaaca ttcctttttg tttgttttgt ttgttttct tcttaatgaa ctaaatacga 4380
atagatgcaa cttagttttt gtaatactga aatncgattc aattgtataa acgattataa 4440
tttctttcat ggaagcatga ttcttctgat taaaaactgt actccatatt ttatgctgg 4500
tgtctgcaag cttgtgcat gttatgttca tgtaaatct atttgtaaaa tgaagtgtt 4560
ccaaccttat ngttaaaaga gagaangtaa ataacagact gtattcagtt atttgccct 4620
ttattgagga accagatttg ttttcttttt gtttgaatc tcattttnga aataatcagc 4680
aagttgaggt actttcttca aatgctttgt acaatataaa ctgttatgcc tttcagtgc 4740
ttactatggg aggagcaact aaaaaataaa gacttacaaa aaggagtatt tttaaagaac 4800
aaaaacttga gggggggccc ggtacccaat tcgccctata gtgagtagta ttacaattca 4860
ctggcgcgtc ttttacaacg tcgtgactgg gaaaaccctg ggttacccaa cttaatcgtc 4920
ttn 4923

```

&lt;210&gt; 83

&lt;211&gt; 1042

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 83

```

Met Lys Ser Glu Asp Tyr Pro His Glu Thr Met Ala Pro Asp Ile His
1          5          10          15
Glu Glu Arg Gln Tyr Arg Cys Glu Asp Cys Asp Gln Leu Phe Glu Ser
20          25          30
Lys Ala Glu Leu Ala Asp His Gln Lys Phe Pro Cys Ser Thr Pro His
35          40          45
Ser Ala Phe Ser Met Val Glu Glu Asp Phe Gln Gln Lys Leu Glu Ser
50          55          60
Glu Asn Asp Leu Gln Glu Ile His Thr Ile Gln Glu Cys Lys Glu Cys
65          70          75          80
Asp Gln Val Phe Pro Asp Leu Gln Ser Leu Glu Lys His Met Leu Ser
85          90          95
His Thr Glu Glu Arg Glu Tyr Lys Cys Asp Gln Cys Pro Lys Ala Phe
100         105         110
Asn Trp Lys Ser Asn Leu Ile Arg His Gln Met Ser His Asp Ser Gly
115         120         125
Lys His Tyr Glu Cys Glu Asn Cys Ala Lys Val Phe Thr Asp Pro Ser
130         135         140
Asn Leu Gln Arg His Ile Arg Ser Gln His Val Gly Ala Arg Ala His
145         150         155         160
Ala Cys Pro Glu Cys Gly Lys Thr Phe Ala Thr Ser Ser Gly Leu Lys
165         170         175
Gln His Lys His Ile His Ser Ser Val Lys Pro Phe Ile Cys Glu Val
180         185         190

```

Cys	His	Lys	Ser	Tyr	Thr	Gln	Phe	Ser	Asn	Leu	Cys	Arg	His	Lys	Arg
	195						200					205			
Met	His	Ala	Asp	Cys	Arg	Thr	Gln	Ile	Lys	Cys	Lys	Asp	Cys	Gly	Gln
	210					215					220				
Met	Phe	Ser	Thr	Thr	Ser	Ser	Leu	Asn	Lys	His	Arg	Arg	Phe	Cys	Glu
225					230					235					240
Gly	Lys	Asn	His	Phe	Ala	Ala	Gly	Gly	Phe	Phe	Gly	Gln	Gly	Ile	Ser
				245					250					255	
Leu	Pro	Gly	Thr	Pro	Ala	Met	Asp	Lys	Thr	Ser	Met	Val	Asn	Met	Ser
			260					265					270		
His	Ala	Asn	Pro	Gly	Leu	Ala	Asp	Tyr	Phe	Gly	Ala	Asn	Arg	His	Pro
	275						280					285			
Ala	Gly	Leu	Thr	Phe	Pro	Thr	Ala	Pro	Gly	Phe	Ser	Phe	Ser	Phe	Pro
	290					295					300				
Gly	Leu	Phe	Pro	Ser	Gly	Leu	Tyr	His	Arg	Pro	Pro	Leu	Ile	Pro	Ala
305					310					315					320
Ser	Ser	Pro	Val	Lys	Gly	Leu	Ser	Ser	Thr	Glu	Gln	Thr	Asn	Lys	Ser
				325					330					335	
Gln	Ser	Pro	Leu	Met	Thr	His	Pro	Gln	Ile	Leu	Pro	Ala	Thr	Gln	Asp
			340					345					350		
Ile	Leu	Lys	Ala	Leu	Ser	Lys	His	Pro	Ser	Val	Gly	Asp	Asn	Lys	Pro
	355						360					365			
Val	Glu	Leu	Gln	Pro	Glu	Arg	Ser	Ser	Glu	Glu	Arg	Pro	Phe	Glu	Lys
	370					375					380				
Ile	Ser	Asp	Gln	Ser	Glu	Ser	Ser	Asp	Leu	Asp	Asp	Val	Ser	Thr	Pro
385					390					395					400
Ser	Gly	Ser	Asp	Leu	Glu	Thr	Thr	Ser	Gly	Ser	Asp	Leu	Glu	Ser	Asp
				405					410					415	
Ile	Glu	Ser	Asp	Lys	Glu	Lys	Phe	Lys	Glu	Asn	Gly	Lys	Met	Phe	Lys
	420						425						430		
Asp	Lys	Val	Ser	Pro	Leu	Gln	Asn	Leu	Ala	Ser	Ile	Asn	Asn	Lys	Lys
	435						440					445			
Glu	Tyr	Ser	Asn	His	Ser	Ile	Phe	Ser	Pro	Ser	Leu	Glu	Glu	Gln	Thr
	450					455					460				
Ala	Val	Ser	Gly	Ala	Val	Asn	Asp	Ser	Ile	Lys	Ala	Ile	Ala	Ser	Ile
465					470					475					480
Ala	Glu	Lys	Tyr	Phe	Gly	Ser	Thr	Gly	Leu	Val	Gly	Leu	Gln	Asp	Lys
				485					490					495	
Lys	Val	Gly	Ala	Leu	Pro	Tyr	Pro	Ser	Met	Phe	Pro	Leu	Pro	Phe	Phe
	500							505					510		
Pro	Ala	Phe	Ser	Gln	Ser	Met	Tyr	Pro	Phe	Pro	Asp	Arg	Asp	Leu	Arg
	515					520						525			
Ser	Leu	Pro	Leu	Lys	Met	Glu	Pro	Gln	Ser	Pro	Gly	Glu	Val	Lys	Lys
	530					535					540				
Leu	Gln	Lys	Gly	Ser	Ser	Glu	Ser	Pro	Phe	Asp	Leu	Thr	Thr	Lys	Arg
545					550					555					560
Lys	Asp	Glu	Lys	Pro	Leu	Thr	Pro	Val	Pro	Ser	Lys	Pro	Pro	Val	Thr
				565					570					575	
Pro	Ala	Thr	Ser	Gln	Asp	Gln	Pro	Leu	Asp	Leu	Ser	Met	Gly	Ser	Arg
	580							585					590		
Ser	Arg	Ala	Ser	Gly	Thr	Lys	Leu	Thr	Glu	Pro	Arg	Lys	Asn	His	Val
	595					600						605			
Phe	Gly	Gly	Lys	Lys	Gly	Ser	Asn	Val	Glu	Ser	Arg	Pro	Ala	Ser	Asp
	610				615						620				
Gly	Ser	Leu	Gln	His	Ala	Arg	Pro	Thr	Pro	Phe	Phe	Met	Asp	Pro	Ile
625					630					635					640
Tyr	Arg	Val	Glu	Lys	Arg	Lys	Leu	Thr	Asp	Pro	Leu	Glu	Ala	Leu	Lys
				645					650					655	

Glu Lys Tyr Leu Arg Pro Ser Pro Gly Phe Leu Phe His Pro Gln Met  
 660 665 670  
 Ser Ala Ile Glu Asn Met Ala Glu Lys Leu Glu Ser Phe Ser Ala Leu  
 675 680 685  
 Lys Pro Glu Ala Ser Glu Leu Leu Gln Ser Val Pro Ser Met Phe Asn  
 690 695 700  
 Phe Arg Ala Pro Pro Asn Ala Leu Pro Glu Asn Leu Leu Arg Lys Gly  
 705 710 715 720  
 Lys Glu Arg Tyr Thr Cys Arg Tyr Cys Gly Lys Ile Phe Pro Arg Ser  
 725 730 735  
 Ala Asn Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Gln Pro Tyr  
 740 745 750  
 Arg Cys Lys Tyr Cys Asp Arg Ser Phe Ser Ile Ser Ser Asn Leu Gln  
 755 760 765  
 Arg His Val Arg Asn Ile His Asn Lys Glu Lys Pro Phe Lys Cys His  
 770 775 780  
 Leu Cys Asp Arg Cys Phe Gly Gln Gln Thr Asn Leu Asp Arg His Leu  
 785 790 795 800  
 Lys Lys His Glu Asn Gly Asn Met Ser Gly Thr Ala Thr Ser Ser Pro  
 805 810 815  
 His Ser Glu Leu Glu Ser Thr Gly Ala Ile Leu Asp Asp Lys Glu Asp  
 820 825 830  
 Ala Tyr Phe Thr Glu Ile Arg Asn Phe Ile Gly Asn Ser Asn His Gly  
 835 840 845  
 Ser Gln Ser Pro Arg Asn Val Glu Glu Arg Met Asn Gly Ser His Phe  
 850 855 860  
 Lys Asp Glu Lys Ala Leu Val Thr Ser Gln Asn Ser Asp Leu Leu Asp  
 865 870 875 880  
 Asp Glu Glu Val Glu Asp Glu Val Leu Leu Asp Glu Glu Asp Glu Asp  
 885 890 895  
 Asn Asp Ile Thr Gly Lys Thr Gly Lys Glu Pro Val Thr Ser Asn Leu  
 900 905 910  
 His Glu Gly Asn Pro Glu Asp Asp Tyr Glu Glu Thr Ser Ala Leu Glu  
 915 920 925  
 Met Ser Cys Lys Thr Ser Pro Val Arg Tyr Lys Glu Glu Glu Tyr Lys  
 930 935 940  
 Ser Gly Leu Ser Ala Leu Asp His Ile Arg His Phe Thr Asp Ser Leu  
 945 950 955 960  
 Lys Met Arg Lys Met Glu Asp Asn Gln Tyr Ser Glu Ala Glu Leu Ser  
 965 970 975  
 Ser Phe Ser Thr Ser His Val Pro Glu Glu Leu Lys Gln Pro Leu His  
 980 985 990  
 Arg Lys Ser Lys Ser Gln Ala Tyr Ala Met Met Leu Ser Leu Ser Asp  
 995 1000 1005  
 Lys Glu Ser Leu His Ser Thr Ser His Ser Ser Ser Asn Val Trp His  
 1010 1015 1020  
 Ser Met Ala Arg Ala Ala Ala Glu Ser Ser Ala Ile Gln Ser Ile Ser  
 1025 1030 1035 1040  
 His Val

&lt;210&gt; 84

&lt;211&gt; 4039

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 84

cgccatcggt ccctggctgc ttactaagtt ggatccggaa tttcttttca accgggagcc 60  
 attggtgtcg aagtgtctgc aatgaacccc gtgaatgcta ctgctctcta catctccgcg 120  
 agccgcctag tgctcaacta cgaccccgga gacccaagg cgtttactga gattaacagg 180  
 ctcttgctt acttccgaca gtccctttcg tgctgtgtt gcggacattt gctacaagat 240  
 cctattgcac ccaccaactc cacctgccaa cattatgtct gcaaaacttg taaaggcaag 300  
 aaaaatgatga tgaacacctc ctgtagctgg tgcaagact atgagcagtt tgaggaaaac 360  
 aagcagttaa gcatcctagt gaactgctac aaaaaactat gcgagtatat aacacagact 420  
 acactggcac gggatataat agaagcagtt gactgttctt ctgatatttt ggctttgctt 480  
 aatgatggat cattgttttg tgaggagaca gaaaaacct cagattcatc ctttactttg 540  
 tgtttgacac attccctttt accttcaacc tcagaaccca caactgatcc tcaagctagt 600  
 ttatctccaa tgtctgaaag caccctcagc attgtattg gcagttctgt tatcaatggt 660  
 ttgctactt ataattggct ttcaatagat agatttggta taaatattcc ttcacctgaa 720  
 cattcaata cgattgacgt atgtaatact gttgacataa aaactgagga tctgtctgac 780  
 agcctgccac ccgtttgtga cacagtagcc actgacttat gttccacagg cattgatata 840  
 tgagtttca gtgaagatat aaaacctgga gactctctgt tactgagtgt tgaggaaagta 900  
 ctccgcagct tagaaactgt ttcaaataca gaggtctgtt gccctaattt gcagccgaac 960  
 ttggaagcca ctgtatccaa tggacctttt ctgcagcttt cttcccagtc tcttagccat 1020  
 aatgttttta tgtccaccag tcttgcactt catgggttat catgtacagc agcaactccg 1080  
 aagatagcaa aattgaatag aaaacgatcc agatcagaga gtgacagtga gaaagttcag 1140  
 ccacttccaa tttctaccat tatccgaggg ccaacactgg gggcatctgc tctgtgaca 1200  
 gtgaaacggg agagcaaaaat ttctcttcaa cctatagcaa ctgttcccaa tggaggcaca 1260  
 acacctaaaa tcagcaaaac tgtactttta tctactaaaa gcatgaaaaa gactcatgaa 1320  
 catggatcca agaaatctca ctctaaaacc aagccaggta ttcttaaaaa agacaaagca 1380  
 gtaaaggaaa agattcctag tcatcatttt atgccaggaa gtcctaccaa gactgtgtac 1440  
 aaaaaacccc aggaaaagaa aggggtgtaa tgtggcggtg ctactcaaaa tccaagtgtt 1500  
 cttacatgcc gaggccaacg ctgcccttgc tactctaacc gcaaagcctg cttagattgt 1560  
 atatgtcgtg gctgccaaaa ctctatatg gccaatgggg agaagaagct ggaggcattt 1620  
 gccgtgccag aaaaggcctt ggagcagacc aggtcactt tgggcattaa cgtgactagc 1680  
 attgtgtgc gtaacgctag taccagcacc agtgaataa atgtcacagg gtccccagta 1740  
 acgacgtttt tagctgccag tacacatgat gataaaagt tggatgaagc tatagacatg 1800  
 agattcgact gttaaactcag tgggtctttt aaacctactc ctggtaggga aatagctaca 1860  
 gttttacggc agctatggtt ctgttggttt aacttgccgg agctcctgca tatagatcac 1920  
 ttgtatcaag tgttttcatt gctaagttat atgtgttagt gtcggggaaa tagtttgag 1980  
 ataattggag agtaacccta caactatatg tcttagttc ttacagaacc tcatagttt 2040  
 agaacaaagc tgatgcaact gatttataca aaatgaactt tggcaagaaa aataacatta 2100  
 acctcattgt ttatggccat gctttgtgca taatcaaagt ttatgattaa atgtaaggaa 2160  
 gtggtatcta gtcagtcctt aaagattgtg ctaatttttt tgtggaaaag tagccattag 2220  
 ttcaggaaac tcagtgctgc cttcagatgt catgtatgtt tctcctgttg gaaagctag 2280  
 gtgtccagct caacctttgt gctgacatca taccatttct gatcatgaaa tattggctac 2340  
 tgggtgatgt agcagttctt aaatcagcag tattatgaaa aaaaattccc cctcattaga 2400  
 atgtttaaga aatcttttta aaaagtaaaa ttctgtcaga ctacaaatgt ttagctgtta 2460  
 ctcatttcta gggaagaaat tctaaatccc tcttccactt tgagcagtg tctaattgga 2520  
 taaatgaagg agagtagttt tattctgaag gtaattaaat ttagactatg tagtatgtga 2580  
 cagaattttt ttaaaattat aaaaagattt tatttagtaa ttgggattta cttaaaataa 2640  
 ttttggaata atgctcccag acttgcccag atttgtgtat tgtacttatt gccactggcc 2700  
 gccactttga cttattttct ctaatagttt atttgccaca gtctttattt tgaatatgct 2760  
 cctagttttt ttttaggtg ctgttcatta tgaaggcttc tttatagagg cctaataaga 2820  
 atgccttttt ataaagcctg tgcatttagg taggttgaag ctaggaggat tttctttaga 2880  
 atgctctttt gcatgtaaag cacaaagtat gtttcagttt aaatgcactt cttccgggta 2940  
 atttttatgg ggaagacaag tgagtcacaa acattctgtt gaagggaat ctagtacgtt 3000  
 gcttgaaaga gcacagccca aataaaacaa ggactgacta ggtgtaatga aataacctgt 3060  
 gatttaaaag aagagctgca gctttgacag tgcttattta aagaaaaata ctgctggaaa 3120  
 atttccaaat tctactacgt tcaacatctc tagtaagatc tgacatatgc tgaagttatg 3180  
 ttttgatttg gcacacagca tgttcaatga tggttactcg cctagtacaa gacatggaga 3240  
 agaaaccttt ggacacagag cagatgacac ctcttctgtt tttgtagtgt atcctgggtt 3300  
 cattttctgt gaatgtgtc aggttaggtt tttttgttg ttgttgttg gctttttttt 3360  
 cttttttttt ttttggctc ttttgggtgg gtgggggtgg gctaaagcca taggaagaaa 3420  
 aatgtgatgt gtccagtatg tactattttt tttttgtttt gcaagaagag ttgaactatt 3480

```

tttgataaca agagtaaata gtggaaaatg cttcttagtt gtcttgtctt tatttgcttt 3540
ccaagatttg gaattttatt taattccttt aagtgttagc agtgtcttat gaaacatgta 3600
tttacctaac gtttgaaca gttttgtgtt gaaccagat gccctgctat ataaagttgt 3660
aaatctgttc tttattcact aatgatcact gcaaaaatga ttagaaatga gattgtacac 3720
atggatgagg atatattttg caaatcgacc aaactttcct aatattatga tcttaaaatt 3780
catagagtac tttattgctt cccaagtttg ataatcttgt gggttttttt tttttttgat 3840
gcatgggagg ttggcaatat agacaaagtg gaaatcatta gtatgtgagg gccttgattg 3900
ttatgtaata ttgccaatga tgaattcagg ttgttttttag cacaagtttc tcttttttat 3960
gctggtattc tcaactgccac atttttgga acctgtatta caccttaaat ctatcaataa 4020
atgatagttt tctaattct                                     4039

```

&lt;210&gt; 85

&lt;211&gt; 595

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 85

```

Val Gly Ser Gly Ile Ser Phe Gln Pro Gly Ala Ile Gly Val Glu Val
1      5      10      15
Ser Ala Met Asn Pro Val Asn Ala Thr Ala Leu Tyr Ile Ser Ala Ser
20      25      30
Arg Leu Val Leu Asn Tyr Asp Pro Gly Asp Pro Lys Ala Phe Thr Glu
35      40      45
Ile Asn Arg Leu Leu Pro Tyr Phe Arg Gln Ser Leu Ser Cys Cys Val
50      55      60
Cys Gly His Leu Leu Gln Asp Pro Ile Ala Pro Thr Asn Ser Thr Cys
65      70      75      80
Gln His Tyr Val Cys Lys Thr Cys Lys Gly Lys Lys Met Met Met Lys
85      90      95
Pro Ser Cys Ser Trp Cys Lys Asp Tyr Glu Gln Phe Glu Glu Asn Lys
100     105     110
Gln Leu Ser Ile Leu Val Asn Cys Tyr Lys Lys Leu Cys Glu Tyr Ile
115     120     125
Thr Gln Thr Thr Leu Ala Arg Asp Ile Ile Glu Ala Val Asp Cys Ser
130     135     140
Ser Asp Ile Leu Ala Leu Leu Asn Asp Gly Ser Leu Phe Cys Glu Glu
145     150     155     160
Thr Glu Lys Pro Ser Asp Ser Ser Phe Thr Leu Cys Leu Thr His Ser
165     170     175
Pro Leu Pro Ser Thr Ser Glu Pro Thr Thr Asp Pro Gln Ala Ser Leu
180     185     190
Ser Pro Met Ser Glu Ser Thr Leu Ser Ile Ala Ile Gly Ser Ser Val
195     200     205
Ile Asn Gly Leu Pro Thr Tyr Asn Gly Leu Ser Ile Asp Arg Phe Gly
210     215     220
Ile Asn Ile Pro Ser Pro Glu His Ser Asn Thr Ile Asp Val Cys Asn
225     230     235     240
Thr Val Asp Ile Lys Thr Glu Asp Leu Ser Asp Ser Leu Pro Pro Val
245     250     255
Cys Asp Thr Val Ala Thr Asp Leu Cys Ser Thr Gly Ile Asp Ile Cys
260     265     270
Ser Phe Ser Glu Asp Ile Lys Pro Gly Asp Ser Leu Leu Leu Ser Val
275     280     285
Glu Glu Val Leu Arg Ser Leu Glu Thr Val Ser Asn Thr Glu Val Cys
290     295     300
Cys Pro Asn Leu Gln Pro Asn Leu Glu Ala Thr Val Ser Asn Gly Pro
305     310     315     320
Phe Leu Gln Leu Ser Ser Gln Ser Leu Ser His Asn Val Phe Met Ser

```

```
<210> 86
<211> 1385 .
<212> DNA
<213> Homo sapiens
```

<400> 86							
acttagtatg	cttaccogca	gagtggagga	ctagctgtat	gccagttcc	aaaatgaagg	60	
agatgagctc	gttatttcca	gaagactgg	accaatttgt	tctaaggcag	ttggaatggt	120	
atcattcaga	agagaaggcc	tcaaatgtac	tggaagaaat	tgccaaggac	aaagttttaa	180	
aagactttta	tgttcataca	gtaatgaact	gttatttttag	tttatttggga	atagacaata	240	
tggtctctag	tcttgggtcat	atattgagag	tttacogtgg	tgtttttgctt	tggtctgttg	300	
ctttggactg	gctcacagaa	aagccagaac	gttttcaact	agcactgaaa	gcattcaggt	360	
atactctgaa	actaatgatt	gataaagcaa	gtttagggtcc	aatagaagac	tttagagaac	420	
tgattaagta	ccttgaagaa	tatgaacgtg	actggtacat	tggtttggta	tctgatgaaa	480	
agtggaagga	agcaatttta	caagaaaagc	catacttggt	ttctctgggg	tatgattcta	540	
atatgggaat	ttacactggg	agagtgttta	gccttcaaga	attattgatc	caagtgggaa	600	
agttaaatcc	tgaagctggt	agaggtcagt	gggccaatct	ttcatgggaa	ttactttatg	660	
ccacaaacga	tgatgaagaa	cgttatagta	tacaagctca	tccactactt	ttaagaaatc	720	
ttacggtaca	agcagcagaa	ccctcccctgg	gataatccgt	ttattcttca	aaacctctcc	780	
acatacatatt	gtattagagc	tcattttgac	tgtaatgtca	tcaaatgcaa	tgthttttatt	840	
ttttcatcct	aaaaaagtaa	ctgtgattct	tgtaacttga	ggacttctcc	acaccccat	900	



103

tcagatgcct gagaacagct aagctccgta aagttgggtc tcttagccat cttaatgggt 960  
 ctaaaaaaca gcaaaaacat ctttatgtct aagataaaaag aactatttgg ccaatatttg 1020  
 tgccctctgg acttttagtag gctttggtta atgtgagaaa actttttag aattatcata 1080  
 taatgaattt tgtaatgctt tcttaaatgt gttataggtg aattgccata caaagttaac 1140  
 agctatgtaa tttttacata cttaagagat aaacatatca gtgttctaag tagtgataat 1200  
 ggatcctggt gaagggttaac ataatgtgta tatatttgtt tgaaatataa tttatagtat 1260  
 tttcaaagt gctgatttat tttgacatct aatatctgaa tgtttttgta tcaagtagtt 1320  
 tgttttcata gacttcaatt cataaacttt aaaaaacttt taataaaaata ttttccttcc 1380  
 ttttc 1385

&lt;210&gt; 87

&lt;211&gt; 252

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 87

Met	Pro	Ser	Ser	Lys	Met	Lys	Glu	Met	Ser	Ser	Leu	Phe	Pro	Glu	Asp
1				5					10					15	
Trp	Tyr	Gln	Phe	Val	Leu	Arg	Gln	Leu	Glu	Cys	Tyr	His	Ser	Glu	Glu
			20					25					30		
Lys	Ala	Ser	Asn	Val	Leu	Glu	Glu	Ile	Ala	Lys	Asp	Lys	Val	Leu	Lys
		35					40					45			
Asp	Phe	Tyr	Val	His	Thr	Val	Met	Thr	Cys	Tyr	Phe	Ser	Leu	Phe	Gly
	50					55					60				
Ile	Asp	Asn	Met	Ala	Pro	Ser	Pro	Gly	His	Ile	Leu	Arg	Val	Tyr	Gly
65					70					75					80
Gly	Val	Leu	Pro	Trp	Ser	Val	Ala	Leu	Asp	Trp	Leu	Thr	Glu	Lys	Pro
				85					90					95	
Glu	Leu	Phe	Gln	Leu	Ala	Leu	Lys	Ala	Phe	Arg	Tyr	Thr	Leu	Lys	Leu
			100					105					110		
Met	Ile	Asp	Lys	Ala	Ser	Leu	Gly	Pro	Ile	Glu	Asp	Phe	Arg	Glu	Leu
			115				120					125			
Ile	Lys	Tyr	Leu	Glu	Glu	Tyr	Glu	Arg	Asp	Trp	Tyr	Ile	Gly	Leu	Val
	130					135					140				
Ser	Asp	Glu	Lys	Trp	Lys	Glu	Ala	Ile	Leu	Gln	Glu	Lys	Pro	Tyr	Leu
145					150					155					160
Phe	Ser	Leu	Gly	Tyr	Asp	Ser	Asn	Met	Gly	Ile	Tyr	Thr	Gly	Arg	Val
			165					170					175		
Leu	Ser	Leu	Gln	Glu	Leu	Leu	Ile	Gln	Val	Gly	Lys	Leu	Asn	Pro	Glu
			180					185					190		
Ala	Val	Arg	Gly	Gln	Trp	Ala	Asn	Leu	Ser	Trp	Glu	Leu	Leu	Tyr	Ala
		195					200					205			
Thr	Asn	Asp	Asp	Glu	Glu	Arg	Tyr	Ser	Ile	Gln	Ala	His	Pro	Leu	Leu
	210					215					220				
Leu	Arg	Asn	Leu	Thr	Val	Gln	Ala	Ala	Glu	Pro	Pro	Leu	Gly	Tyr	Pro
225					230					235					240
Ile	Tyr	Ser	Ser	Lys	Pro	Leu	His	Ile	His	Leu	Tyr				
				245					250						

&lt;210&gt; 88

&lt;211&gt; 4660

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 88

acaactattt ggccctgaga agtcgttctg gacgctccat catcaatggg aactgggcaa 60  
 ttgatcgacc aggaaaatac gagggcggag ggaccatgtt cacctacaag cgtccaaatg 120

agatttcgag	cactgccgga	gagtcctttt	tggcggaagg	tcccaccaac	gagatcttgg	180
atgtctacat	gatacaccag	cagccaaacc	caggcgtgca	ctacgagtag	gtgatcatgg	240
ggaccaacgc	catcagcccc	caggtgccac	cccacaggag	accaggggaa	cccttcaatg	300
gccagatggt	gacagaaggc	aggagccagg	aggagggaga	acagaaaggg	aggaacgagg	360
agaaggaaaga	cttgcggtggg	gaggcccttg	agatgttcac	ctcagaatcg	gcacagacct	420
tcccagtcag	gcattccagac	agattttctc	cccacgcacc	ggacaacttg	gtgccaccag	480
caccgcagcc	cccacggcgc	agccgggagc	acaactggaa	gcagcttggg	acaacagaat	540
gttccacgac	ctgtgggaaa	ggatcgagag	accctatttt	ccgctgtgtg	cacagaagca	600
ctcatgaaga	ggctcctgag	agttactgtg	actccagcat	gaagccgacc	cccaggaggg	660
agccctgcaa	catcttccct	tgcccagcct	tctgggacat	cggggagtgg	tctgagtcca	720
gcaagacctg	tggcctgggc	atgcagcacc	gccaggttct	gtgccgccag	gtgtacgcca	780
accgcagcct	gacgggtgcag	ccctaccgct	gccagcacct	ggagaaacct	gagaccacca	840
gcacctgcca	actcaagatc	tgcagcgagt	ggcagatccg	gaccgactgg	acctcgtgct	900
cgggtgccctg	cggcgtggga	cagaggaccc	gtgatgtgaa	gtgtgtgagc	aacattgggg	960
atgtggttga	cgatgaggaa	tgcaacatga	agctccggcc	gaatgacatt	gagaactgcg	1020
acatgggacc	ctgtgccaaag	agctggttcc	tcaccgagtg	gagcgaaagg	agctcagcgg	1080
agtgtggggc	cggagtgcgg	acacgctcgg	tgggtgtgcat	gaccaacctat	gtcagcagcc	1140
tgcccttgga	gggctgtggg	aacaaccggc	cggcagaggc	caccccatgt	gacaacggac	1200
ctgcacggg	caaggtggag	tggtttgccg	ggagctggag	tcagtgttcc	atcgagtgtg	1260
ggagcgggac	gcaacagagg	gaggtgattt	gtgttagaaa	gaatgcagac	acctttgaag	1320
tgttggaacc	ctctgaatgt	tctttcctgg	agaaaccccc	cagccagcaa	tcctgccacc	1380
tcaagccttg	cggagccaaa	tggtttagca	ccgaatggag	catgtgttcc	aagagctgcc	1440
agggtggctt	tcgggtccgg	gaagtgcggg	gtctgtctga	tgacatgact	ctaagtaacc	1500
tctgtgaccc	tcagttgaaa	ccagaagaga	gagaatcttg	taaccctcag	gactgtgtcc	1560
ctgaagtga	tgaaaactgc	aaggacaagt	actacaactg	caacgtgggtg	gtccaggcaa	1620
gactctgtgt	ctacaactac	tacaagaccg	cctgctgtgc	ctcctgcacc	cgtgtggcca	1680
acaggcagac	gggcttccctg	gggagcagat	aacactcctg	cacccccatc	agtagggcag	1740
catcactgcc	ttcccggggg	cttcagcagt	gctcctggct	ggctgtgtgt	ccaccacggg	1800
ccccctggcc	caggcgctgc	caaccaactt	agtcaccacc	cctgcctccg	gtgaatgcac	1860
cccgtagtac	ccaggggctt	tttacacaag	atgtttgaaa	gccacagtca	gtcctttaag	1920
catcaccatg	tactgatgat	cccctccttg	gacctggcat	ctgctaattg	tgccctttga	1980
aagtcaagca	gtgggaagta	catggagctc	tcagccctgc	tcccatcttg	caccttcaag	2040
tcagcagatg	ggccactgac	agagcactgc	cccatcccctg	gtgctactgg	tctttctaaa	2100
cttagcaccc	tggagagtcc	aaggaggcag	cgcccccaac	ccagcgcccc	actaagcctt	2160
gctgacacgc	gtgcatccct	ctgtgacctc	agcccagatg	tgccctgtttt	cattctcaaa	2220
gacattagac	tgttttccctg	ccctatgaca	cagatagctc	acatgaatat	tgtgctttat	2280
ttagcaggtg	tactcacaga	tactagctcc	ttagcagctc	acaacatccc	agaatgggag	2340
gcaggggggtg	actcattatc	cccattttac	tgacagggaa	actgaggctc	aacttaagta	2400
attgacctgc	cagggtatatt	cacccatcca	gtggaagagc	tgagtccccg	ccccagtcac	2460
ctaccagtat	ccagcatggg	gcctgtactt	agatgtgaaa	ggtgctgctt	cattttctgac	2520
caagagactg	agaagtttcc	cagaatgcaa	acaaagccca	ggccccctgaa	atctttccgg	2580
tcaagccttt	atcccagcac	tcagttgttt	tggatgtctg	ttcctacttg	cccttaccoc	2640
caaagttaca	gattcctagtt	acaggactct	gccagctttg	ttaaactgtc	cgtgagacaa	2700
gaaagccatt	ggggaaacca	ggtgattgcc	tgaaattctt	actccgttcc	aagtgtgtgt	2760
cctcccagga	aatcaaaggc	cagggtccct	atggccgtgg	agccttcccc	accacagagc	2820
caacttgtga	agcacacagc	tctgcagcct	gggctctgcc	ctgcctcagc	cgctcccccc	2880
acgctcttca	ccacgttccct	ggagagtccg	gccaaacctgt	cccagccaaa	acactgctgt	2940
attagaaaaa	gtctctttct	ggtctttctg	gttttgttta	tgaatttccc	tctgtggcca	3000
caaattcctc	ccctccccca	tgactcacag	tccatattgg	ccacccccag	acttgagcac	3060
caagctctgc	attaatgcag	ttggcctgcg	acaaggagct	gtggaccctt	ccccatctct	3120
tccaattcac	tttccccaac	tatccagttc	cagaggccgc	aggcctggaa	ggatgcagtg	3180
catattgaaa	ggtggaccct	ctgaaaacag	ttaagaggaa	tatatgtatg	ttttgcccac	3240
taagaaaaca	atggcaagct	aaacaaatgt	taaacttaca	gaaaattagt	cttatggtcc	3300
tgagcatatt	tcccttttag	agcaagcctg	gattcttagc	aaagtgtttc	ccccattgct	3360
cttttagctg	acaaactctgc	cactgtgatg	atggtttgca	gcttttggaa	gcagtatggc	3420
aacctggcct	gacatgctct	ttaggcttcc	actaacctgg	ggctttcaga	aattctatct	3480
ggcctttctg	tgggtagctt	tccaagcttct	cttctaggga	gccccaggca	tcatttccca	3540
aaagcatccc	catctcctga	ttctcttgga	actcctacag	ataagcatcc	tggcagaggc	3600

```

ccaggctccc aaaccgacaa agtgaaaaga gaccagagag gccaaagcata ttgactggtg 3660
ctgttcaggg cctgctcttt tccactcacc acttggtttg ctgcttgtca cgaggagagt 3720
tggtcctgta tgtggtgct ctcagatctt tccaagcaag ccagtcattt gaagaggttt 3780
tcttttcatg ctggaggcca ggctaagatc aatgagtga agagagaaag gctgttttag 3840
ctcaagttaa aggaacacct tctagccatc aaagccgccc aacagaggca agggccacca 3900
cacatgagag agcgctctgt ccttaaaggg aattctctgt tgagtgggag gtgaacaccc 3960
tggttcttcc aactcaggaa ttctcgtggc tgggctgggt cagtgatggc tttgtctctt 4020
tatgtctaaa gtgccctatg gctgctgaag gttacctaac cattctttaa aaggagaatg 4080
accctccatg ggaatggcca gcctgccaac tgtgcaattg aagaagaccc gatggatcaa 4140
ccccatgtct cccttgggga gaaagtgcac aaaccagggg tctctttttt tttttttcaa 4200
caaaccattg agctgttctt ggagttcatc tctggagagg ttatacatta ttagaagttt 4260
gattattatt atagtttgat caatttattt gtcttagaga tccaattttt actaattccc 4320
tagtttttta tttcagcatc tgaatgtctt tctccctagc acagtgcata caatcagggc 4380
cttgggtatt tccagtgata actttccttg gagaggatct aagaaaagcc cagatttcgg 4440
tagccatctc cctccaaata tgtctcttct tgccttctta gtgccatta tttccccttc 4500
tcttttcttc tgtcaactgcc atctccttct gtggtcttcc cattgttctt taactggccg 4560
taatgtggaa ttgatattta cattttgata cggttttttt ctgggcctgt gtacgggatg 4620
gcctcatttc ctgctctgaa ttttaaaatt agatatttaa 4660

```

&lt;210&gt; 89

&lt;211&gt; 538

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 89

```

Met Phe Thr Tyr Lys Arg Pro Asn Glu Ile Ser Ser Thr Ala Gly Glu
 1           5           10           15
Ser Phe Leu Ala Glu Gly Pro Thr Asn Glu Ile Leu Asp Val Tyr Met
           20           25           30
Ile His Gln Gln Pro Asn Pro Gly Val His Tyr Glu Tyr Val Ile Met
           35           40           45
Gly Thr Asn Ala Ile Ser Pro Gln Val Pro Pro His Arg Arg Pro Gly
           50           55           60
Glu Pro Phe Asn Gly Gln Met Val Thr Glu Gly Arg Ser Gln Glu Glu
           65           70           75           80
Gly Glu Gln Lys Gly Arg Asn Glu Glu Lys Glu Asp Leu Arg Gly Glu
           85           90           95
Ala Pro Glu Met Phe Thr Ser Glu Ser Ala Gln Thr Phe Pro Val Arg
           100          105          110
His Pro Asp Arg Phe Ser Pro His Arg Pro Asp Asn Leu Val Pro Pro
           115          120          125
Ala Pro Gln Pro Pro Arg Arg Ser Arg Asp His Asn Trp Lys Gln Leu
           130          135          140
Gly Thr Thr Glu Cys Ser Thr Thr Cys Gly Lys Gly Ser Gln Tyr Pro
           145          150          155          160
Ile Phe Arg Cys Val His Arg Ser Thr His Glu Glu Ala Pro Glu Ser
           165          170          175
Tyr Cys Asp Ser Ser Met Lys Pro Thr Pro Glu Glu Glu Pro Cys Asn
           180          185          190
Ile Phe Pro Cys Pro Ala Phe Trp Asp Ile Gly Glu Trp Ser Glu Cys
           195          200          205
Ser Lys Thr Cys Gly Leu Gly Met Gln His Arg Gln Val Leu Cys Arg
           210          215          220
Gln Val Tyr Ala Asn Arg Ser Leu Thr Val Gln Pro Tyr Arg Cys Gln
           225          230          235          240
His Leu Glu Lys Pro Glu Thr Thr Ser Thr Cys Gln Leu Lys Ile Cys
           245          250          255
Ser Glu Trp Gln Ile Arg Thr Asp Trp Thr Ser Cys Ser Val Pro Cys

```

	260		265		270
Gly Val	Gly Gln Arg Thr Arg Asp	Val Lys Cys	Val Ser Asn Ile Gly		
	275	280	285		
Asp Val	Val Asp Asp Glu Glu Cys	Asn Met Lys	Leu Arg Pro Asn Asp		
	290	295	300		
Ile Glu	Asn Cys Asp Met Gly Pro	Cys Ala Lys	Ser Trp Phe Leu Thr		
305	310	315	320		
Glu Trp	Ser Glu Arg Ser Ser Ala	Glu Cys Gly	Ala Gly Val Arg Thr		
	325	330	335		
Arg Ser	Val Val Cys Met Thr Asn	His Val Ser	Ser Leu Pro Leu Glu		
	340	345	350		
Gly Cys	Gly Asn Asn Arg Pro Ala	Glu Ala Thr	Pro Cys Asp Asn Gly		
	355	360	365		
Pro Cys	Thr Gly Lys Val Glu Trp	Phe Ala Gly	Ser Trp Ser Gln Cys		
	370	375	380		
Ser Ile	Glu Cys Gly Ser Gly Thr	Gln Gln Arg	Glu Val Ile Cys Val		
385	390	395	400		
Arg Lys	Asn Ala Asp Thr Phe Glu	Val Leu Asp	Pro Ser Glu Cys Ser		
	405	410	415		
Phe Leu	Glu Lys Pro Pro Ser Gln	Gln Ser Cys	His Leu Lys Pro Cys		
	420	425	430		
Gly Ala	Lys Trp Phe Ser Thr Glu	Trp Ser Met	Cys Ser Lys Ser Cys		
	435	440	445		
Gln Gly	Gly Phe Arg Val Arg Glu	Val Arg Cys	Leu Ser Asp Asp Met		
	450	455	460		
Thr Leu	Ser Asn Leu Cys Asp Pro	Gln Leu Lys	Pro Glu Glu Arg Glu		
465	470	475	480		
Ser Cys	Asn Pro Gln Asp Cys Val	Pro Glu Val	Asp Glu Asn Cys Lys		
	485	490	495		
Asp Lys	Tyr Tyr Asn Cys Asn Val	Val Val Gln	Ala Arg Leu Cys Val		
	500	505	510		
Tyr Asn	Tyr Tyr Lys Thr Ala Cys	Cys Ala Ser	Cys Thr Arg Val Ala		
	515	520	525		
Asn Arg	Gln Thr Gly Phe Leu Gly	Ser Arg			
	530	535			

&lt;210&gt; 90

&lt;211&gt; 4793

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 90

```

attggatcaa acatgtcaca agagtcggac aataataaaa gactagtggc cttagtgcc 60
atgcccagtg accctccatt caatacccga agagcctaca ccagtgagga tgaagcctgg 120
aagtcatact tggagaatcc cctgacagca gccaccaagg ccatgatgat cattaatgg 180
gatgaggaca gtgctgctgc cctcggcctg ctctatgact actacaaggt tcctcgagac 240
aagaggctgc tgtctgtaag caaagcaagt gacagccaag aagaccagga gaaaagaaac 300
tgccttggca ccagtgaagc ccagagtaat ttgagtggag gagaaaaccg agtgcaagtc 360
ctaaagactg ttccagtga cctttcccta aatcaagatc acctggagaa ttccaagcgg 420
gaacagtaca gcatcagctt ccccgagagc tctgccatca tcccgggtgtc gggaatcacg 480
gtggtgaaag ctgaagattt cacaccagtt ttcattggccc cacctgtgca ctatccccgg 540
ggagatgggg aagagcaacg agtggttatc tttgaacaga ctacgtatga cgtgccctcg 600
ctggccaccc acagcgccta tctcaaagac gaccagcgca gcaactccga cagcacatac 660
agcgagagct tcaaggagcg agccacagag aaatttcgga gtgcttcagt tggggctgag 720
gagtacatgt atgatcagac atcaagtggc acatttcagt acaccctgga agccacaaa 780
tctctccgtc agaagcaggg ggagggcccc atgacctacc tcaacaaagg acagtctat 840
gccataacac tcagcgagac cgagagacaac aaatgcttcc gacaccccat cagcaaagtc 900

```

```

aggagtgtgg  t gatgggtgt  cttcagttaa  gacaaaaaca  gagatgaaca  gctcaaatac  960
tgaaataact  ggcactctcg  gcagcatacg  gcgaagcaga  gggtccttga  cattgccgat  1020
tacaaggaga  gctttaatac  gattggaaac  attgaagaga  ttgcatataa  tgctgtttcc  1080
tttacctggg  acgtgaatga  agaggcgaag  attttcatca  cctggaattg  cttgagcaca  1140
gatttctcct  cccaaaaagg  ggtgaaagga  cttcctttga  tgattcagat  tgacacatac  1200
agttataaca  atcgtagcaa  taaaccatt  catagagctt  attgccagat  caaggtcttc  1260
tgtgacaaag  gagcagaaag  aaaaatccga  gatgaagagc  agaagcagaa  caggaagaac  1320
gggaaaggcc  aggctccca  aactcaatgc  aacagctcct  ctgatgggaa  gttggctgcc  1380
atacctttac  agaagaagag  tgacatcacc  tacttcaaaa  ccatgcctga  tctccactca  1440
cagccagttc  tcttcatacc  tgatgttcac  tttgcaaac  tgcagaggac  cggacaggtg  1500
tattacaaca  cggatgatga  acgagaaggt  ggcagtgctc  ttgttaaacy  gatgttccgg  1560
cccatggaag  aggagtttgg  tccggtgcct  tcaaagcaga  tgaagaaga  agggacaaa  1620
cgagtgtctc  tgtacgtgag  gaaggagact  gacgatgtgt  tcgatgcatt  gatgttgaag  1680
tctcccacag  tgatgggct  gatggaagcg  atatctgaga  aatatgggct  gccctgggag  1740
aagatagcaa  agctttacaa  gaaaagcaa  aaaggcatct  tggtgaacat  ggatgacaac  1800
atcatcgagc  actactcgaa  cgaggacacc  ttcactcctc  acatggagag  catggtggag  1860
ggcttcaagg  tcacgctcat  ggaaatctag  cctggggtt  ggcacccgt  ttggctggag  1920
ctctcagtc  gttcctccct  gagagagaca  gaagccccag  cccagaacc  tggagacca  1980
tctccccat  ctcaactg  ctgttacaag  accgtgctgg  ggagtggggc  aaggacagg  2040
ccccagtc  ggtgtgctt  gccatccac  tggcacctac  caggagcog  aagcctgagc  2100
cctcaggaa  ggtgccttag  gcctgttga  ttcctattta  ttgccacct  tttcctggag  2160
cccaggtcca  ggcccgccag  gactctgcag  gtcactgcta  gctccagatg  agaccgtcca  2220
gcgttcccc  ttcaagagaa  aactcatcc  cgaacagcct  aaaaaattcc  catcccttct  2280
ttctacccc  tccatatcta  tatctccga  gtggctggac  aaaatgagct  acgtctgggt  2340
gcagtagtta  taggtggggc  aagaggtgga  tgcccacttt  ctggtcagac  acctttaggt  2400
tgctctggg  aaggtgtct  tgctaaatac  ctccagggtt  cccagcaagt  ggccaccagg  2460
ccttgtacag  gaagacattc  agtcaccgtg  taattagtaa  cacagaaagt  ctgctgtct  2520
gcattgtaca  tagtgtttat  aatattgtaa  taatatattt  tacctgtggt  atgtgggat  2580
gtttactgcc  actggcctag  aggagacaca  gacctggaga  ccgttttaat  ggggttttt  2640
gcctctgtgc  ctgttcaaga  gacttgagg  gctaggtaga  gggcctttgg  gatgttaagg  2700
tgactgcagc  tgatgccaag  atggactctg  caatgggcat  acctgggggc  tcgttccctg  2760
tcccagagg  aagccccctc  tcttctcca  tgggcatgac  tctccttoga  ggccaccacg  2820
tttatctcac  aatgatgtgt  tttgcctgac  tttccctttg  cgtgtctcg  tgggaaaggt  2880
cattctgtct  gagaccccag  ctcttctcc  agctttggct  gcgggcatgg  cctgagcttt  2940
ctggagagcc  tctgcagggg  gtttgccatc  agggccctgt  ggctgggtct  gctgcagagc  3000
tcttggtca  tcaggagaat  cctggacact  gtactgtgcc  tcccagttta  caaacacgcc  3060
cttcatctca  agtggccctt  taaaaggcct  gctgccatgt  gagagctgtg  aacagctcag  3120
ctctgagtcg  gcagactggg  gcttctcct  gggccaccag  atggaaaggg  ggtattgttt  3180
gcctcactcc  tggatgctgc  gttttaagga  agtgagttag  aaagaatgtg  ccaagatacc  3240
tggtcctgt  gaaaccagcc  tcaggaggga  aactgggaga  gagaagctgt  ggtctcctgc  3300
tacatgccct  gggagctgga  agagaaaaac  actcccctaa  acaatcgcaa  aatgatgaac  3360
catcatgggc  cactgttctc  tttgagggga  caggtttagg  ggtttgctt  cgcccttgtg  3420
ggctgaagca  ctacttttt  ggtagctaga  cacatcctgc  acccaaaggt  tctctacaaa  3480
ggcccagatt  tgtttgtaaa  gcactttgac  tcttacctgg  agggccgctc  tctaagggt  3540
tctgcgctc  ccacctcatc  tgccttgag  atgcagagca  ggatggaggg  tctgcttcta  3600
gctcagctgt  ttctccttga  ggttgaggag  gaattgaatt  gaatgggaca  gagggcaggt  3660
gctgtggcca  agaagatctc  cgagcagcag  tgacggggca  ccttgctgtg  tgtcctctgg  3720
gcatgttaac  ccttctgtgg  ggccaaaggt  ttgcatcgtg  gatccagctg  tgctccagtc  3780
tgtccctcc  tctccactc  tgactgccac  gcccggacc  agcagcttgg  ggaccctcca  3840
gggtactaat  ggggctctgt  tctgagatgg  acaaattcag  tgttgaaat  acatgttcta  3900
ctatgcactt  cccatgctcc  taggttagg  aatagtttca  aacatgattg  gcagacataa  3960
caacggcaaa  tactcggaat  ggggcatagg  actccagagt  aggaaaaaga  caaaagattt  4020
ggcagctga  cacaggcaac  ctaccctct  ctctccagcc  tctttatgaa  actgtttgtt  4080
tgccagtcct  gccctaaggc  agaagatgaa  ttgaagatgc  tgtgcattgt  tcctaagtcc  4140
ttgagcaatc  atggtggtga  caattgccac  aagggatatg  agggcagtg  caccagagg  4200
tggtgccaag  tgccacatcc  cttccgatcc  attccctct  gtatcctcg  agcaccacag  4260
tttgcccttg  atgtgtccgc  tgtgtatgtt  agctgaactt  tgatgagcaa  aatttctga  4320
gcgaaacact  ccaaagagat  aggaaaactt  gccgcctctt  cttttttgtc  ccttaatcaa  4380

```

```

actcaataa gcttaaaaaa aatccatgga agatcatgga catgtgaaat gagcattttt 4440
ttctttttt tttttttttt tttttttaac aaagtctgaa ctgaacagaa caagactttt 4500
tcctcataca tctccaaatt gtttaaaactt actttatgag tgtttgttta gaagttcgga 4560
ccaacagaaa aatgcagtca gatgtcatct tggaattggt ttctaaaaga gtaaggcatg 4620
tccctgcca gaaacttagg aagcatgaaa taaatcaaatt gtttattttt cttcttattt 4680
aaaaatcatgc taatgcaaca gaaatagagg gtttgtgcca aatgctatga acggcccttt 4740
cttaagaca agcaaggag attgatatat gtacaatttg ctctcatgtt ttt 4793

```

&lt;210&gt; 91

&lt;211&gt; 625

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 91

```

Met Ser Gln Glu Ser Asp Asn Asn Lys Arg Leu Val Ala Leu Val Pro
 1          5          10          15
Met Pro Ser Asp Pro Pro Phe Asn Thr Arg Arg Ala Tyr Thr Ser Glu
          20          25          30
Asp Glu Ala Trp Lys Ser Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr
          35          40          45
Lys Ala Met Met Ile Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu
          50          55          60
Gly Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Asp Lys Arg Leu Leu
          65          70          75          80
Ser Val Ser Lys Ala Ser Asp Ser Gln Glu Asp Gln Glu Lys Arg Asn
          85          90          95
Cys Leu Gly Thr Ser Glu Ala Gln Ser Asn Leu Ser Gly Gly Glu Asn
          100          105          110
Arg Val Gln Val Leu Lys Thr Val Pro Val Asn Leu Ser Leu Asn Gln
          115          120          125
Asp His Leu Glu Asn Ser Lys Arg Glu Gln Tyr Ser Ile Ser Phe Pro
          130          135          140
Glu Ser Ser Ala Ile Ile Pro Val Ser Gly Ile Thr Val Val Lys Ala
          145          150          155          160
Glu Asp Phe Thr Pro Val Phe Met Ala Pro Pro Val His Tyr Pro Arg
          165          170          175
Gly Asp Gly Glu Gln Arg Val Val Ile Phe Glu Gln Thr Gln Tyr
          180          185          190
Asp Val Pro Ser Leu Ala Thr His Ser Ala Tyr Leu Lys Asp Asp Gln
          195          200          205
Arg Ser Thr Pro Asp Ser Thr Tyr Ser Glu Ser Phe Lys Asp Ala Ala
          210          215          220
Thr Glu Lys Phe Arg Ser Ala Ser Val Gly Ala Glu Glu Tyr Met Tyr
          225          230          235          240
Asp Gln Thr Ser Ser Gly Thr Phe Gln Tyr Thr Leu Glu Ala Thr Lys
          245          250          255
Ser Leu Arg Gln Lys Gln Gly Glu Gly Pro Met Thr Tyr Leu Asn Lys
          260          265          270
Gly Gln Phe Tyr Ala Ile Thr Leu Ser Glu Thr Gly Asp Asn Lys Cys
          275          280          285
Phe Arg His Pro Ile Ser Lys Val Arg Ser Val Val Met Val Val Phe
          290          295          300
Ser Glu Asp Lys Asn Arg Asp Glu Gln Leu Lys Tyr Trp Lys Tyr Trp
          305          310          315          320
His Ser Arg Gln His Thr Ala Lys Gln Arg Val Leu Asp Ile Ala Asp
          325          330          335
Tyr Lys Glu Ser Phe Asn Thr Ile Gly Asn Ile Glu Glu Ile Ala Tyr
          340          345          350

```

Asn Ala Val Ser Phe Thr Trp Asp Val Asn Glu Glu Ala Lys Ile Phe  
 355 360 365  
 Ile Thr Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val  
 370 375 380  
 Lys Gly Leu Pro Leu Met Ile Gln Ile Asp Thr Tyr Ser Tyr Asn Asn  
 385 390 395 400  
 Arg Ser Asn Lys Pro Ile His Arg Ala Tyr Cys Gln Ile Lys Val Phe  
 405 410 415  
 Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Gln Lys Gln  
 420 425 430  
 Asn Arg Lys Asn Gly Lys Gly Gln Ala Ser Gln Thr Gln Cys Asn Ser  
 435 440 445  
 Ser Ser Asp Gly Lys Leu Ala Ala Ile Pro Leu Gln Lys Lys Ser Asp  
 450 455 460  
 Ile Thr Tyr Phe Lys Thr Met Pro Asp Leu His Ser Gln Pro Val Leu  
 465 470 475 480  
 Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg Thr Gly Gln Val  
 485 490 495  
 Tyr Tyr Asn Thr Asp Asp Glu Arg Glu Gly Gly Ser Val Leu Val Lys  
 500 505 510  
 Arg Met Phe Arg Pro Met Glu Glu Glu Phe Gly Pro Val Pro Ser Lys  
 515 520 525  
 Gln Met Lys Glu Glu Gly Thr Lys Arg Val Leu Leu Tyr Val Arg Lys  
 530 535 540  
 Glu Thr Asp Asp Val Phe Asp Ala Leu Met Leu Lys Ser Pro Thr Val  
 545 550 555 560  
 Met Gly Leu Met Glu Ala Ile Ser Glu Lys Tyr Gly Leu Pro Val Glu  
 565 570 575  
 Lys Ile Ala Lys Leu Tyr Lys Lys Ser Lys Lys Gly Ile Leu Val Asn  
 580 585 590  
 Met Asp Asp Asn Ile Ile Glu His Tyr Ser Asn Glu Asp Thr Phe Ile  
 595 600 605  
 Leu Asn Met Glu Ser Met Val Glu Gly Phe Lys Val Thr Leu Met Glu  
 610 615 620  
 Ile  
 625

&lt;210&gt; 92

&lt;211&gt; 2085

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 92

ggctgcagtt acagagtgtt gccatcacca agtatgtggc ggacgtcctg ccggggaaga 60  
 atcaaagagc agagagcatg gccagtgcag cgagggaact ggttatccag cggttgagtc 120  
 tgggtgaggag tctttgcgag agcgaggagc agcggttact ggaacagggtg catggcgaag 180  
 aggagcgggc ccaccagagc atcctgacac agcgggtgca ctgggcccag gcgctgcaga 240  
 aacttgacac catccgcaact ggcctggttg gcatgcttac tcacctggat gacctccagc 300  
 tgattcagaa ggagcaagag attttcgaga ggaccgaaga agcagagggc attttgatc 360  
 cccaggagtc ggaatgtta aactttaatg agaagtgcac tcggagccca ctactgacct 420  
 aactctgggc aacggcggtt cttgggtctc tctcaggcac agaggacata cggatcgatg 480  
 agaggacagt cagccccttc ctgcaattgt cagatgatcg aaagaccctg accttcagca 540  
 ccaagaagtc aaaggcctgt gcagatggcc cggaagcgtt cgaccactgg ccaatgccc 600  
 tggctgccac ctcttcocag aatgggctcc atgcctggat ggtgaatgtc cagaacagtt 660  
 gtgcctataa ggtgggcgtg gcttcaggcc acctgccccg caagggttct ggcagtact 720  
 gccgtctggg ccacaatgcc ttctcctggg tcttctctcg ctatgatcag gagtttcgtt 780  
 tctcacacaa tgggcagcac gagcccctgg ggctgctgcg gggcccagcc cagctgggtg 840

```

tagtgctgga cttgcaggtt caggagctgc tcttctatga gccagcctcc ggcatagtgc 900
tctgtgcccc tcatgtgtcc ttcccggggc ccctcttccc agtctttgct gtggccgatc 960
agaccatttc tatcgtccgc tgacctctgg ccacaggaag ccagggtccac cgcccaccac 1020
cctttcaggc catgtttcta ctcagtgtgc ttttcccaaa tgatgtgtgt ggtgtttcta 1080
agagaaacag ggcccataac cagtgggcag ctttaggagg gatggggatc tgtttcagat 1140
ctaggcataa cctgtaaatc acagggtgtcc aaacttttgg cttccctggg ccacatttga 1200
agaagaattt tcttgggcca cataaaatac actaacgata gctgatgagc taaaaaaaaa 1260
aaaaaaaaagc tgtgtataat ttttgtgata tctgccacca cagataagca aaaaagtcct 1320
tgcatcctaaa gggttggaga ttgctgcttt gagtgtctggg tacctgtggg gaacctacta 1380
ctccctgggc cttagtctcc caaatccacc atgcatctgc ccctctgagg gtgtcttcac 1440
tttgtctctg gcatctagca tgggtgcctgg tgcatagtga gcatgcaata aatatttggc 1500
agggtgagtgg atggatagat ggataggtga atgtaggtgg acagggtgact ggggtggagt 1560
tgtggtctct ggagaagcac tgccattcag cctcctgtctc cagctgttca catgcagaaa 1620
tgctctcttc acaggcagag aagcctgtgg ctaaagtttc cacatcccat taactcagt 1680
cttttgtctt tttcatgaca tggcacatag agaaaatatt ttttctagc acacaagagc 1740
aacctgaaag gctgtcctctg gctaggggac tctgtcccgg gggaccgtgt cctcccccat 1800
gtcctgccta ggccctcaga ggaccagggg atcatgtctc caggtaaccc gactgtagcc 1860
cctgtctggc gagctccagc ctgtgcccac tgataatagc agggacggcc tttctcttag 1920
agcagctgat aagtttccct acctgatggc cccctctgac ataaactgca cacctggggt 1980
gatggcttaa agccagaaa agctgagggg gttaagaggg ccaaccttag ggcacgtggg 2040
cattattaaa ggtcttaaaa gcattaaaaa aaaaaaaaaa aaaaaa 2085

```

&lt;210&gt; 93

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 93

```

Met Ala Ser Ala Ala Arg Glu Leu Val Ile Gln Arg Leu Ser Leu Val
 1           5           10           15
Arg Ser Leu Cys Glu Ser Glu Glu Gln Arg Leu Leu Glu Gln Val His
          20           25           30
Gly Glu Glu Glu Arg Ala His Gln Ser Ile Leu Thr Gln Arg Val His
          35           40           45
Trp Ala Glu Ala Leu Gln Lys Leu Asp Thr Ile Arg Thr Gly Leu Val
          50           55           60
Gly Met Leu Thr His Leu Asp Asp Leu Gln Leu Ile Gln Lys Glu Gln
          65           70           75           80
Glu Ile Phe Glu Arg Thr Glu Glu Ala Glu Gly Ile Leu Asp Pro Gln
          85           90           95
Glu Ser Glu Met Leu Asn Phe Asn Glu Lys Cys Thr Arg Ser Pro Leu
          100          105          110
Leu Thr Gln Leu Trp Ala Thr Ala Val Leu Gly Ser Leu Ser Gly Thr
          115          120          125
Glu Asp Ile Arg Ile Asp Glu Arg Thr Val Ser Pro Phe Leu Gln Leu
          130          135          140
Ser Asp Asp Arg Lys Thr Leu Thr Phe Ser Thr Lys Lys Ser Lys Ala
          145          150          155          160
Cys Ala Asp Gly Pro Glu Arg Phe Asp His Trp Pro Asn Ala Leu Ala
          165          170          175
Ala Thr Ser Phe Gln Asn Gly Leu His Ala Trp Met Val Asn Val Gln
          180          185          190
Asn Ser Cys Ala Tyr Lys Val Gly Val Ala Ser Gly His Leu Pro Arg
          195          200          205
Lys Gly Ser Gly Ser Asp Cys Arg Leu Gly His Asn Ala Phe Ser Trp
          210          215          220
Val Phe Ser Arg Tyr Asp Gln Glu Phe Arg Phe Ser His Asn Gly Gln
          225          230          235          240

```



111

His	Glu	Pro	Leu	Gly	Leu	Leu	Arg	Gly	Pro	Ala	Gln	Leu	Gly	Val	Val
			245						250					255	
Leu	Asp	Leu	Gln	Val	Gln	Glu	Leu	Leu	Phe	Tyr	Glu	Pro	Ala	Ser	Gly
			260						265				270		
Ile	Val	Leu	Cys	Ala	His	His	Val	Ser	Phe	Pro	Gly	Pro	Leu	Phe	Pro
			275				280					285			
Val	Phe	Ala	Val	Ala	Asp	Gln	Thr	Ile	Ser	Ile	Val	Arg			
			290				295					300			

&lt;210&gt; 94

&lt;211&gt; 2317

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 94

```

aaaactccag gaggcggagg aggctagtgg cagtacctgg gcaccctgac cctccccaca 60
ggccagagcc caccctcctg ctcatgaggg cagacaggcc tttccaggga cacagtcctt 120
cttctcccca ggaccccagg gccaaactccc cctgccggcc ctctgccatc aaattggcag 180
tggtccagg ggagtcacct ggggatgggg gaccactgtt ggggacctct ctgcgtgcac 240
ccctgtagt gggaagcag gacaggggcc tggggagacg gaagggcgcc aggggttgag 300
agaggatgg ggacgttgt ggacttgaag gggaaacagg ccctcgggga agcccctggc 360
caggcctgcc tctccctccc ctggtggggc cagcgccctt gctcacttgt ctctgccac 420
agtgcctgtc tgtggaggac gccctggggc tgggcgagcc tgaggggtca gggctgcccc 480
cgggcccggt cctggaggcc aggtacgtcg cccgcctcag tgccgccgcc gtcctgtacc 540
tcagcaaccc cgagggcacc tgtgaggacg ctcgggctgg cctctggggc tctcatgcag 600
accacctcct ggccctgctc gagagcccca aggccctgac cccgggcctg agctggctgc 660
tgagaggat ggaggcccg gctgccggcc agaccccaa gacggcctgc gtagatatcc 720
ctcagctgt ctagaggcg gtggggcgcg gggctccggg cagtgtggc ggcgtcctgg 780
ctgccctgt ggaccatgtc aggagcgggt cttgttcca cgcttgccg agccctcagt 840
acttcgtgga ctttgtgttc cagcagcaca gcagcgaggt ccctatgacg ctggccgagc 900
tgtcagcctt gatgcagcgc ctgggggtgg gcaggaggcc ccacagtgc cacagtcac 960
ggcacagggg agccagcagc cgggaccctg tgccctcat cagctccagc aacagctcca 1020
gtgtgtggga cacggtatgc ctgagtcca gggacgtgat ggctgcata ggactgtcgg 1080
aacaggctgg ggtgaccccg gaggcctggg cccaactgag ccctgccctg ctccaacagc 1140
agctgagtgg agcctacacc tcccagcca ggccccctg ccaggaccag ctccagccagt 1200
cagagagata tctgtacggc tccctggcca cgctgtcat ctgcctctgc gcggtctttg 1260
gcctcctgct gctgacctgc actggctgca ggggggtcgc ccactacatc ctgcagacct 1320
tcttgagcct ggcagtgggt gcaactcact gggacgtgt cctgcatact acgcccagg 1380
tgctggggct gcatacacac agcgaagagg gcctcagccc acagcccacc tggcgccctc 1440
tggtatgct ggccgggctc tacgccttct tctgtttga gaacctctt aatctcctgc 1500
tgccagggga cccggaggac ctggaggacg ggccctgcgg ccacagcagc catagccacg 1560
ggggccacag ccacggtgtg tccctgcagc tggcaccag cgagctccgg cagcccagc 1620
ccccccacga gggctccgcg gcagacctgg tggcggagga gagcccgagg ctgctgaacc 1680
ctgagcccag gagactgagc ccagagtga ggctactgcc ctatatgatc actctgggcg 1740
acgccgtgca caacttcgac gacgggctgg ccgtggcgcg cgccttcgcg tctcctgga 1800
agaccgggct ggccacctcg ctggccgtgt tctgccacga gttgccacac gagctggggg 1860
acttcgccc cttgtgtcac gcgggctgt ccgtgcgcca agcactgctg ctgaacctgg 1920
cctccgctg caccgcttc gctggtctta cgtggcactc gcggttgagg tcagcgagga 1980
gagcgaggcc tggatcctgg cagtggccac cggcctgttc cttacgtagc actctgcgac 2040
atgctccgg cgatgttgaa agtacgggac ccgcggcccc tggctcctct tctgtgtgca 2100
caacgtgggc ctgctgggcg gctggaccgt cctgctgctg ctgtccctgt acgaggatga 2160
catcacctt tgataccctg ccctagtccc ccaccttga cttaagatcc cacacctcac 2220
aaacctacag ccagaaacc cagaagcccc tatagaggcc ccagtcctaa ctccagtaaa 2280
gacactcttg tcccttgga aaaaaaaaa aaaaaaa 2317

```

&lt;210&gt; 95

&lt;211&gt; 626

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 95

```

Met Val Asp Val Val Gly Leu Glu Arg Glu Thr Gly Pro Arg Gly Ser
 1          5          10          15
Pro Trp Pro Gly Leu Pro Leu Pro Ser Leu Val Gly Pro Ala Pro Leu
 20          25          30
Leu Thr Cys Leu Cys Pro Gln Cys Leu Ser Val Glu Asp Ala Leu Gly
 35          40          45
Leu Gly Glu Pro Glu Gly Ser Gly Leu Pro Pro Gly Pro Val Leu Glu
 50          55          60
Ala Arg Tyr Val Ala Arg Leu Ser Ala Ala Ala Val Leu Tyr Leu Ser
 65          70          75          80
Asn Pro Glu Gly Thr Cys Glu Asp Ala Arg Ala Gly Leu Trp Ala Ser
 85          90          95
His Ala Asp His Leu Leu Ala Leu Leu Glu Ser Pro Lys Ala Leu Thr
 100         105         110
Pro Gly Leu Ser Trp Leu Leu Gln Arg Met Gln Ala Arg Ala Ala Gly
 115         120         125
Gln Thr Pro Lys Thr Ala Cys Val Asp Ile Pro Gln Leu Leu Glu Glu
 130         135         140
Ala Val Gly Ala Gly Ala Pro Gly Ser Ala Gly Gly Val Leu Ala Ala
 145         150         155         160
Leu Leu Asp His Val Arg Ser Gly Ser Cys Phe His Ala Leu Pro Ser
 165         170         175
Pro Gln Tyr Phe Val Asp Phe Val Phe Gln Gln His Ser Ser Glu Val
 180         185         190
Pro Met Thr Leu Ala Glu Leu Ser Ala Leu Met Gln Arg Leu Gly Val
 195         200         205
Gly Arg Glu Ala His Ser Asp His Ser His Arg His Arg Gly Ala Ser
 210         215         220
Ser Arg Asp Pro Val Pro Leu Ile Ser Ser Ser Asn Ser Ser Ser Val
 225         230         235         240
Trp Asp Thr Val Cys Leu Ser Ala Arg Asp Val Met Ala Ala Tyr Gly
 245         250         255
Leu Ser Glu Gln Ala Gly Val Thr Pro Glu Ala Trp Ala Gln Leu Ser
 260         265         270
Pro Ala Leu Leu Gln Gln Gln Leu Ser Gly Ala Tyr Thr Ser Gln Ser
 275         280         285
Arg Pro Pro Val Gln Asp Gln Leu Ser Gln Ser Glu Arg Tyr Leu Tyr
 290         295         300
Gly Ser Leu Ala Thr Leu Leu Ile Cys Leu Cys Ala Val Phe Gly Leu
 305         310         315         320
Leu Leu Leu Thr Cys Thr Gly Cys Arg Gly Val Ala His Tyr Ile Leu
 325         330         335
Gln Thr Phe Leu Ser Leu Ala Val Gly Ala Leu Thr Gly Asp Ala Val
 340         345         350
Leu His Leu Thr Pro Lys Val Leu Gly Leu His Thr His Ser Glu Glu
 355         360         365
Gly Leu Ser Pro Gln Pro Thr Trp Arg Leu Leu Ala Met Leu Ala Gly
 370         375         380
Leu Tyr Ala Phe Phe Leu Phe Glu Asn Leu Phe Asn Leu Leu Leu Pro
 385         390         395         400
Arg Asp Pro Glu Asp Leu Glu Asp Gly Pro Cys Gly His Ser Ser His
 405         410         415
Ser His Gly Gly His Ser His Gly Val Ser Leu Gln Leu Ala Pro Ser
 420         425         430

```

Glu Leu Arg Gln Pro Lys Pro Pro His Glu Gly Ser Arg Ala Asp Leu  
 435 440 445  
 Val Ala Glu Glu Ser Pro Glu Leu Leu Asn Pro Glu Pro Arg Arg Leu  
 450 455 460  
 Ser Pro Glu Leu Arg Leu Leu Pro Tyr Met Ile Thr Leu Gly Asp Ala  
 465 470 475 480  
 Val His Asn Phe Ala Asp Gly Leu Ala Val Gly Ala Ala Phe Ala Ser  
 485 490 495  
 Ser Trp Lys Thr Gly Leu Ala Thr Ser Leu Ala Val Phe Cys His Glu  
 500 505 510  
 Leu Pro His Glu Leu Gly Asp Phe Ala Ala Leu Leu His Ala Gly Leu  
 515 520 525  
 Ser Val Arg Gln Ala Leu Leu Leu Asn Leu Ala Ser Ala Leu Thr Ala  
 530 535 540  
 Phe Ala Gly Leu Thr Trp His Ser Arg Leu Glu Ser Ala Arg Arg Ala  
 545 550 555 560  
 Arg Pro Gly Ser Trp Gln Trp Pro Pro Ala Cys Ser Leu Arg Ser Thr  
 565 570 575  
 Leu Arg His Ala Pro Gly Asp Val Glu Ser Thr Gly Pro Ala Ala Pro  
 580 585 590  
 Gly Ser Ser Ser Cys Cys Thr Thr Trp Ala Cys Trp Ala Ala Gly Pro  
 595 600 605  
 Ser Cys Cys Cys Cys Pro Cys Thr Arg Met Thr Ser Pro Ser Asp Thr  
 610 615 620  
 Leu Pro  
 625

&lt;210&gt; 96

&lt;211&gt; 2761

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 96

agcgggctct gcagagaaat caaagatggc ggttgatatct gctgttcgct ggctgggcct 60  
 ccgcagcagg cttggccagc cgctgacggg tcggcgggcg ggtttgtgtg aacaggcacg 120  
 cagctgcaga ttttattctg gtagtgcaac cctctcaaag gttgaaggaa ctgatgtaac 180  
 agggattgaa gaagtagtaa ttccaaaaaa gaaaacttgg gataaagtag ccgttcttca 240  
 ggcacttgca tccacagtaa acagggatac cacagctgtg ccttatgtgt ttcaagatga 300  
 tccttacctt atgccagcat catctttgga atctcgttca tttttactgg caaagaaatc 360  
 cggggagaat gtggccaagt ttattattaa ttcatacccc aaatatattc agaaggacat 420  
 agctgaacct catataccgt gtttaatgcc tgagtacttt gaacctcaga tcaaagacat 480  
 aagtgaagcc gccctgaagg aacgaattga gtcagaaaa gtcaaagcct ctgtggacat 540  
 gtttgatcag cttttgcaag caggaaccac tgtgtctctt gaaacaacaa atagtctctt 600  
 ggatttattg tgttactatg gtgaccagga gccctcaact gattaccatt ttcaacaac 660  
 tggacagtca gaagcattgg aagaggaaaa tgaatgagaca tctaggagga aagctgttca 720  
 tcagtttggg gttacatggc gagcaaaaaa caacgctgag agaattcttt ctctaattgc 780  
 agagaaaaat gaacattcct attgcacaat gatccgagga atgggtgaagc accgagctta 840  
 tgagcaggca ttaaacttgt aactgagtt actaaacaac agactccatg ctgatgtata 900  
 cacatttaat gcattgattg aagcaacagt atgtgcgata aatgagaaat ttgaggaaaa 960  
 atggagtaaa atactggagc tgctaagaca catggttgca cagaaggatga aaccaaactc 1020  
 tcagactttt aataccattc tgaaatgtct ccgaagattt catgtgtttg caagatcgcc 1080  
 agccttacag gttttacgtg aaatgaaagc cattggaata gaacctcgc ttgcaacata 1140  
 tcaccatatt attgcctgt ttgatcaacc tggagaccct ttaaagagat catccttc 1200  
 ctttatgat ataataatg aattaatggg aaagagattt tctccaaagg acccgatga 1260  
 tggcatataa gttttttcag tcagccatgg ccatatgctc atctctcaga gatctagaac 1320  
 ttgcctacca agtacatggc cttttaaaaa ccggagacaa ctggaaattc attggacctg 1380  
 atcaacatcg taatttctat tattccaagt tcttcgattt gatttgtcta atggaacaaa 1440

```

ttgatgttac cttgaagtgg tatgaggacc tgataccttc agcctacttt cccactccc 1500
aaacaatgat acatcttctc caagcattgg atgtggccaa tcggctagaa gtgattccta 1560
aaatttggaag agatagtaaa gaatatggtc atactttccg cagtgcactg agagaagaga 1620
tcctgatgct catggcaagg gacaagcacc caccagagct tcagggtggca tttgctgact 1680
gtgctgctga tatcaaactc gcgtatgaaa gccaacccat cagacagact gctcaggatt 1740
ggccagccac ctctctcaac tgtatagcta tcctcttttt aagggtctggg agaactcagg 1800
aagcctggaa aatgttgggg cttttcagga agcataataa gattcctaga agtgagttgc 1860
tgaatgagct tatggacagt gcaaaagtgt ctaacagccc ttcccaggcc attgaagtag 1920
tagagctggc aagtgccttc agcttaccta tttgtgaggg cctcaccagc agagtaatga 1980
gtgattttgc aatcaaccag gaacaaaagg aagccctaag taatctaact gcattgacca 2040
gtgacagtga tactgacagc agcagtgaca gcgacagtga caccagtga ggcaaatgaa 2100
agtggagatt caggagcagc aatggtctca ccatagctgc tggaatcaca cctgagaact 2160
gagatatacc aatattttaac attgttacaa agaagaaaag atacagattt ggtgaatttg 2220
ttactgtgag gtacagtcag tacacagctg acttatgtag atttaagctg ctaatatgct 2280
acttaacat ctattaatgc accattaaag gcttagcatt taagtagcaa cattgcggtt 2340
ttcagacaca tgggtgaggtc catggctctt gtcacagga taagcctgca cacctagagt 2400
gtcgggtgagc tgacctcagc atgctgtcct cgtgcgattg cctctcctg ctgctggact 2460
tctgcctttg ttggcctgat gtgctgctgt gatgctggtc cttcatctta ggtgttcatt 2520
cagttctaac acagttgggg ttgggtcaat agtttcccaa ttccaggata ttccgatgtc 2580
agaaataacg catcttagga atgactaaac aagataatgg cagtttaggc tgcacaaactg 2640
gtaaaatgac tgtagataaa tgttgaatt agtgtacacg tttgtatttt tgttaataata 2700
gccgctgcc tagttttcta acttgaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2760
a 2761

```

&lt;210&gt; 97

&lt;211&gt; 422

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 97

```

Ala Gly Ser Ala Glu Lys Ser Lys Met Ala Val Val Ser Ala Val Arg
 1          5          10          15
Trp Leu Gly Leu Arg Ser Arg Leu Gly Gln Pro Leu Thr Gly Arg Arg
 20          25          30
Ala Gly Leu Cys Glu Gln Ala Arg Ser Cys Arg Phe Tyr Ser Gly Ser
 35          40          45
Ala Thr Leu Ser Lys Val Glu Gly Thr Asp Val Thr Gly Ile Glu Glu
 50          55          60
Val Val Ile Pro Lys Lys Lys Thr Trp Asp Lys Val Ala Val Leu Gln
 65          70          75          80
Ala Leu Ala Ser Thr Val Asn Arg Asp Thr Thr Ala Val Pro Tyr Val
 85          90          95
Phe Gln Asp Asp Pro Tyr Leu Met Pro Ala Ser Ser Leu Glu Ser Arg
100          105          110
Ser Phe Leu Leu Ala Lys Lys Ser Gly Glu Asn Val Ala Lys Phe Ile
115          120          125
Ile Asn Ser Tyr Pro Lys Tyr Phe Gln Lys Asp Ile Ala Glu Pro His
130          135          140
Ile Pro Cys Leu Met Pro Glu Tyr Phe Glu Pro Gln Ile Lys Asp Ile
145          150          155          160
Ser Glu Ala Ala Leu Lys Glu Arg Ile Glu Leu Arg Lys Val Lys Ala
165          170          175
Ser Val Asp Met Phe Asp Gln Leu Leu Glu Ala Gly Thr Thr Val Ser
180          185          190
Leu Glu Thr Thr Asn Ser Leu Leu Asp Leu Leu Cys Tyr Tyr Gly Asp
195          200          205
Gln Glu Pro Ser Thr Asp Tyr His Phe Gln Gln Thr Gly Gln Ser Glu
210          215          220

```

115

Ala Leu Glu Glu Glu Asn Asp Glu Thr Ser Arg Arg Lys Ala Gly His  
 225 230 235 240  
 Gln Phe Gly Val Thr Trp Arg Ala Lys Asn Asn Ala Glu Arg Ile Phe  
 245 250 255  
 Ser Leu Met Pro Glu Lys Asn Glu His Ser Tyr Cys Thr Met Ile Arg  
 260 265 270  
 Gly Met Val Lys His Arg Ala Tyr Glu Gln Ala Leu Asn Leu Tyr Thr  
 275 280 285  
 Glu Leu Leu Asn Asn Arg Leu His Ala Asp Val Tyr Thr Phe Asn Ala  
 290 295 300  
 Leu Ile Glu Ala Thr Val Cys Ala Ile Asn Glu Lys Phe Glu Glu Lys  
 305 310 315 320  
 Trp Ser Lys Ile Leu Glu Leu Leu Arg His Met Val Ala Gln Lys Val  
 325 330 335  
 Lys Pro Asn Leu Gln Thr Phe Asn Thr Ile Leu Lys Cys Leu Arg Arg  
 340 345 350  
 Phe His Val Phe Ala Arg Ser Pro Ala Leu Gln Val Leu Arg Glu Met  
 355 360 365  
 Lys Ala Ile Gly Ile Glu Pro Ser Leu Ala Thr Tyr His His Ile Ile  
 370 375 380  
 Arg Leu Phe Asp Gln Pro Gly Asp Pro Leu Lys Arg Ser Ser Phe Ile  
 385 390 395 400  
 Ile Tyr Asp Ile Met Asn Glu Leu Met Gly Lys Arg Phe Ser Pro Lys  
 405 410 415  
 Asp Pro Asp Asp Gly Ile  
 420

&lt;210&gt; 98

&lt;211&gt; 2757

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 98

agcgggctct gcagagaaat caaagatggc ggttgatct gctgttcgct ggctgggcct 60  
 ccgcagcagg cttggccagc cgctgacggg tcggcgggcg ggtttgtgtg aacaggcacg 120  
 cagctgcaga ttttattctg gtagtgcaac cctctcaaag gttgaaggaa ctgatgtaac 180  
 agggattgaa gaagtagtaa ttccaaaaaa gaaaacttgg gataaagtag ccgttcttca 240  
 ggcacttgca tccacagtaa acagggatac cacagctgtg ccttatgtgt ttcaagatga 300  
 tccttacctt atgccagcat catctttgga atctcgttca tttttactgg caaagaaatc 360  
 cggggagaat gtggccaagt ttattattaa ttcatacccc aaatattttc agaaggacat 420  
 agctgaacct catataccgt gtttaatgcc tgagtacttt gaacctcaga tcaaagacat 480  
 aagtgaagcc gccctgaagg aacgaattga gctcagaaaa gtcaaagcct ctgtggacat 540  
 gtttgatcag cttttgcaag caggaaccac tgtgtctctt gaaacaacaa atagtctctt 600  
 ggatttattg tggtactatg gtgaccagga gccctcaact gattaccatt ttcaacaaac 660  
 tggacagtca gaagcattgg aagaggaaaa tgatgagaca tctaggagga aagctggtca 720  
 tcagtttgga gttacatggc gagcaaaaaa caacgctgag agaatctttt ctctaattgcc 780  
 agagaaaaat gaacattcct attgcacaat gatccgagga atggtgaagc accgagctta 840  
 tgagcaggca ttaaacttgt aactgagtt actaaacaac agactccatg ctgatgtata 900  
 cacatttaat gcattgattg aagcaacagt atgtgcgata aatgagaaat ttgaggaaaa 960  
 atggagtaaa atactggagc tgctaagaca catggttgca cagaaggtga aaccaaatct 1020  
 tcagactttt aataccattc tgaaatgtct ccgaagattt catgtgtttg caagatcgcc 1080  
 agccttacag gttttacgtg aaatgaaagc cattggaata gaaccctcgc ttgcaacata 1140  
 tcaccatatt attgcctgt ttgatcaacc tggagaccct ttaaagagat catccttcat 1200  
 catttatgat ataataatg aattaatggg aaagagattt tctccaaagg acccgatga 1260  
 tgataagttt tttcagtcag ccatgagcat atgctcatct ctcaagatc tagaacttgc 1320  
 ctaccaagta catggccttt taaaaaccgg agacaactgg aaattcattg gacctgatca 1380  
 acatcgtaat ttctattatt ccaagttctt cgatttgatt tgtctaattg aacaaattga 1440

```

tggtaccttg aagtgggatg aggacctgat accttcagcc tactttcccc actcccaaac 1500
aatgatacat cttctccaag cattggatgt ggccaatcgg ctagaagtga ttcctaaaat 1560
ttggaaagat agtaaagaat atggtcatac tttccgcagt gacctgagag aagagatcct 1620
gatgctcatg gcaagggaca agcaccacc agagcttcag gtggcatttg ctgactgtgc 1680
tgctgatatc aaatctgcgt atgaaagcca acccatcaga cagactgctc aggattggcc 1740
agccacctct ctcaactgta tagctatcct ctttttaagg gctgggagaa ctcaggaagc 1800
ctggaaaatg ttggggcttt tcaggaagca taataagatt cctagaagtg agttgctgaa 1860
tgagcttatg gacagtgcaa aagtgtctaa cagcccttcc caggccattg aagtagtaga 1920
gctggcaagt gccttcagct tacctatttg tgagggcctc acccagagag taatgagtga 1980
ttttgcaatc aaccaggaac aaaaggaagc cctaagtaat ctaactgcat tgaccagtga 2040
cagtatact gacagcagca gtgacagcga cagtgcaccc agtgaaggca aatgaaagtg 2100
gagattcagg agcagcaatg gtctcaccat agctgctgga atcacacctg agaactgaga 2160
tataccaata tttaacattg ttacaaagaa gaaaagatac agatttggtg aatttggtac 2220
tgtgaggtac agtcagtaca cagctgactt atgtagattt aagctgctaa tatgctactt 2280
aaccatctat taatgcacca ttaaaggctt agcatttaag tagcaacatt gcggttttca 2340
gacacatggt gaggtccatg gctcttgtca tcaggataag cctgcacacc tagagtgtcg 2400
gtgagctgac ctcacgatgc tgcctcgtg cgattgccct ctctgctgc tggacttctg 2460
cctttgttgg cctgatgtgc tgctgtgatg ctggctcttc atcttaggtg ttcatgcagt 2520
tctaacacag ttgggggttg gtcaatagtt tccaatttc aggatatttc gatgtcagaa 2580
ataacgcatac ttagggaatga ctaaacaaga taatggcagt ttaggctgca caactggtaa 2640
aatgactgta gataaatgtt gtaattagtg tacacgtttg tatttttgtt aatatagccg 2700
ctgccatagt tttctaactt gaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaa 2757

```

&lt;210&gt; 99

&lt;211&gt; 697

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 99

```

Ala Gly Ser Ala Glu Lys Ser Lys Met Ala Val Val Ser Ala Val Arg
 1          5          10          15
Trp Leu Gly Leu Arg Ser Arg Leu Gly Gln Pro Leu Thr Gly Arg Arg
 20          25          30
Ala Gly Leu Cys Glu Gln Ala Arg Ser Cys Arg Phe Tyr Ser Gly Ser
 35          40          45
Ala Thr Leu Ser Lys Val Glu Gly Thr Asp Val Thr Gly Ile Glu Glu
 50          55          60
Val Val Ile Pro Lys Lys Lys Thr Trp Asp Lys Val Ala Val Leu Gln
 65          70          75          80
Ala Leu Ala Ser Thr Val Asn Arg Asp Thr Thr Ala Val Pro Tyr Val
 85          90          95
Phe Gln Asp Asp Pro Tyr Leu Met Pro Ala Ser Ser Leu Glu Ser Arg
100          105          110
Ser Phe Leu Leu Ala Lys Lys Ser Gly Glu Asn Val Ala Lys Phe Ile
115          120          125
Ile Asn Ser Tyr Pro Lys Tyr Phe Gln Lys Asp Ile Ala Glu Pro His
130          135          140
Ile Pro Cys Leu Met Pro Glu Tyr Phe Glu Pro Gln Ile Lys Asp Ile
145          150          155          160
Ser Glu Ala Ala Leu Lys Glu Arg Ile Glu Leu Arg Lys Val Lys Ala
165          170          175
Ser Val Asp Met Phe Asp Gln Leu Leu Gln Ala Gly Thr Thr Val Ser
180          185          190
Leu Glu Thr Thr Asn Ser Leu Leu Asp Leu Leu Cys Tyr Tyr Gly Asp
195          200          205
Gln Glu Pro Ser Thr Asp Tyr His Phe Gln Gln Thr Gly Gln Ser Glu
210          215          220
Ala Leu Glu Glu Glu Asn Asp Glu Thr Ser Arg Arg Lys Ala Gly His

```

225		230		235		240
Gln Phe Gly Val Thr	Trp Arg Ala Lys Asn	Asn Ala Glu Arg Ile Phe				
	245	250		255		
Ser Leu Met Pro Glu	Lys Asn Glu His Ser	Tyr Cys Thr Met Ile Arg				
	260	265		270		
Gly Met Val Lys His	Arg Ala Tyr Glu Gln	Ala Leu Asn Leu Tyr Thr				
	275	280		285		
Glu Leu Leu Asn Asn	Arg Leu His Ala Asp	Val Tyr Thr Phe Asn Ala				
	290	295		300		
Leu Ile Glu Ala Thr	Val Cys Ala Ile Asn	Glu Lys Phe Glu Glu Lys				
305	310	315		320		
Trp Ser Lys Ile Leu	Glu Leu Leu Arg His	Met Val Ala Gln Lys Val				
	325	330		335		
Lys Pro Asn Leu Gln	Thr Phe Asn Thr Ile	Leu Lys Cys Leu Arg Arg				
	340	345		350		
Phe His Val Phe Ala	Arg Ser Pro Ala Leu	Gln Val Leu Arg Glu Met				
	355	360		365		
Lys Ala Ile Gly Ile	Glu Pro Ser Leu Ala	Thr Tyr His His Ile Ile				
	370	375		380		
Arg Leu Phe Asp Gln	Pro Gly Asp Pro Leu	Lys Arg Ser Ser Phe Ile				
385	390	395		400		
Ile Tyr Asp Ile Met	Asn Glu Leu Met Gly	Lys Arg Phe Ser Pro Lys				
	405	410		415		
Asp Pro Asp Asp Asp	Lys Phe Phe Gln Ser	Ala Met Ser Ile Cys Ser				
	420	425		430		
Ser Leu Arg Asp Leu	Glu Leu Ala Tyr Gln	Val His Gly Leu Leu Lys				
	435	440		445		
Thr Gly Asp Asn Trp	Lys Phe Ile Gly Pro	Asp Gln His Arg Asn Phe				
	450	455		460		
Tyr Tyr Ser Lys Phe	Phe Asp Leu Ile Cys	Leu Met Glu Gln Ile Asp				
465	470	475		480		
Val Thr Leu Lys Trp	Tyr Glu Asp Leu Ile	Pro Ser Ala Tyr Phe Pro				
	485	490		495		
His Ser Gln Thr Met	Ile His Leu Leu Gln	Ala Leu Asp Val Ala Asn				
	500	505		510		
Arg Leu Glu Val Ile	Pro Lys Ile Trp Lys	Asp Ser Lys Glu Tyr Gly				
	515	520		525		
His Thr Phe Arg Ser	Asp Leu Arg Glu Glu	Ile Leu Met Leu Met Ala				
	530	535		540		
Arg Asp Lys His Pro	Pro Glu Leu Gln Val	Ala Phe Ala Asp Cys Ala				
545	550	555		560		
Ala Asp Ile Lys Ser	Ala Tyr Glu Ser Gln	Pro Ile Arg Gln Thr Ala				
	565	570		575		
Gln Asp Trp Pro Ala	Thr Ser Leu Asn Cys	Ile Ala Ile Leu Phe Leu				
	580	585		590		
Arg Ala Gly Arg Thr	Gln Glu Ala Trp Lys	Met Leu Gly Leu Phe Arg				
	595	600		605		
Lys His Asn Lys Ile	Pro Arg Ser Glu Leu	Leu Asn Glu Leu Met Asp				
	610	615		620		
Ser Ala Lys Val Ser	Asn Ser Pro Ser Gln	Ala Ile Glu Val Val Glu				
625	630	635		640		
Leu Ala Ser Ala Phe	Ser Leu Pro Ile Cys	Glu Gly Leu Thr Gln Arg				
	645	650		655		
Val Met Ser Asp Phe	Ala Ile Asn Gln Glu	Gln Lys Glu Ala Leu Ser				
	660	665		670		
Asn Leu Thr Ala Leu	Thr Ser Asp Ser Asp	Thr Asp Ser Ser Ser Asp				
	675	680		685		
Ser Asp Ser Asp Thr	Ser Glu Gly Lys					

690

695

&lt;210&gt; 100

&lt;211&gt; 1940

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 100

```

tacatggcga gcaaaaaaac aacgctgaga gaatcttttc tctaatagcc gagaaaaatg 60
aacattccta ttgcacaatg atccgaggaa tggatgaagct gatgtataca catttaatgc 120
attgattgaa gcaacagtat gtgcgataaa tgagaaatgt gaggaaaaat ggagtaaaat 180
actggagctg ctaagacaca tgggtgcaca gaaggtgaaa ccaaactctc agacttttaa 240
taccattctg aaatgtctcc gaagatttca tgtgtttgca agatcgccag ccttacaggt 300
tttacgtgaa atgaaagcca ttggaataga accctcgctt gcaacatata accatattat 360
tcgcctgttt gatcaacctg gagacccttt aaagagatca tccttcatca tttatgatat 420
aatgaatgaa ttaatgggaa agagattttc tccaaaggac ccggatgatg gcatataagt 480
tttttcagtc agccatgagc atatgctcat ctctcagaga tctagaactt gcctaccaag 540
tacatggcct tttaaaaacc ggagacaact ggaaattcat tggacctgat caacatcgta 600
atttctatta ttccaagttc ttcgatttga tttgtctaata ggaacaaatt gatgttacct 660
tgaagtggta tgaggacctg ataccttcag cctactttcc ccactcccaa acaatgatag 720
atcttctcca agcattggat gtggccaatc ggctagaagt gattcctaaa atttgaaaag 780
atagtaaaga atatggtcat actttccgca gtgacctgag agaagagatc ctgatgctca 840
tggcaaggga caagcaccca ccagagcttc aggtggcatt tgctgactgt gctgctgata 900
tcaaactctg gtatgaaagc caaccatca gacagactgc tcaggattgg ccagccacct 960
ctctcaactg tatagctatc ctctttttta gggctgggag aactcaggaa gcctggaaaa 1020
tggtggggct tttcaggaag cataataaga ttctagaag tgagttgctg aatgagctta 1080
tggacagtgc aaaagtgtct aacagccctt cccaggccat tgaagtagta gagctggcaa 1140
gtgccttcag cttacctatt tgtgagggcc tcaccagag agtaatgagt gattttgcaa 1200
tcaaccagga acaaaaggaa gccctaagta atctaactgc attgaccagt gacagtgata 1260
ctgacagcag cagtgcagac gacagtgaac ccagtgaagg caaatgaaag tggagattca 1320
ggagcagcaa tggctctacc atagctgctg gaatcacacc tgagaactga gatataccaa 1380
tatttaacat tgttacaaag aagaaaagat acagatttgg tgaatttggt actgtgaggt 1440
acagtcagta cacagctgac ttatgtagat ttaagctgct aatatgctac ttaaccatct 1500
attaatgcac cattaaaggc ttagcattta agtagcaaca ttgctggttt cagacacatg 1560
gtgaggtcca tggctcttgt catcaggata agcctgcaca cctagagtgt cggtgagctg 1620
acctcacgat gctgtcctcg tgcgattgcc ctctcctgct gctggacttc tgccttttgt 1680
ggcctgatgt gctgtgtgta tgcgtgtcct tcacttagg tgttcattga gttctaacac 1740
agttggggtt ggggtcaatag tttcccaatt tcaggatatt tcgatgtcag aaataacgca 1800
tcttaggaat gactaaacaa gataatggca gtttaggctg cacaactggt aaaatgactg 1860
tagataaatg ttgtaattag tgtacacggt tgtatttttg ttaatatagc cgctgccata 1920
gttttctaac ttgaacagcc

```

&lt;210&gt; 101

&lt;211&gt; 280

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 101

```

Met Met Ala Tyr Lys Phe Phe Gln Ser Ala Met Ser Ile Cys Ser Ser
1           5           10           15
Leu Arg Asp Leu Glu Leu Ala Tyr Gln Val His Gly Leu Leu Lys Thr
20           25           30
Gly Asp Asn Trp Lys Phe Ile Gly Pro Asp Gln His Arg Asn Phe Tyr
35           40           45
Tyr Ser Lys Phe Phe Asp Leu Ile Cys Leu Met Glu Gln Ile Asp Val
50           55           60
Thr Leu Lys Trp Tyr Glu Asp Leu Ile Pro Ser Ala Tyr Phe Pro His

```



65		70		75		80
Ser Gln Thr Met	Ile His Leu Leu Gln Ala Leu Asp Val Ala Asn Arg					
	85		90		95	
Leu Glu Val Ile	Pro Lys Ile Trp Lys Asp Ser Lys Glu Tyr Gly His					
	100		105		110	
Thr Phe Arg Ser	Asp Leu Arg Glu Glu Ile Leu Met Leu Met Ala Arg					
	115		120		125	
Asp Lys His Pro	Pro Glu Leu Gln Val Ala Phe Ala Asp Cys Ala Ala					
	130		135		140	
Asp Ile Lys Ser	Ala Tyr Glu Ser Gln Pro Ile Arg Gln Thr Ala Gln					
	145		150		155	
Asp Trp Pro Ala	Thr Ser Leu Asn Cys Ile Ala Ile Leu Phe Leu Arg					
	165		170		175	
Ala Gly Arg Thr	Gln Glu Ala Trp Lys Met Leu Gly Leu Phe Arg Lys					
	180		185		190	
His Asn Lys Ile	Pro Arg Ser Glu Leu Leu Asn Glu Leu Met Asp Ser					
	195		200		205	
Ala Lys Val Ser	Asn Ser Pro Ser Gln Ala Ile Glu Val Val Glu Leu					
	210		215		220	
Ala Ser Ala Phe	Ser Leu Pro Ile Cys Glu Gly Leu Thr Gln Arg Val					
	225		230		235	
Met Ser Asp Phe	Ala Ile Asn Gln Glu Gln Lys Glu Ala Leu Ser Asn					
	245		250		255	
Leu Thr Ala Leu	Thr Ser Asp Ser Asp Thr Asp Ser Ser Ser Asp Ser					
	260		265		270	
Asp Ser Asp Thr	Ser Glu Gly Lys					
	275		280			

&lt;210&gt; 102

&lt;211&gt; 1853

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 102

```

gcagtgtcac taggccggct gggggccctg ggtacgctgt agaccagacc gcgacaggcc 60
agaacacggg cggcggcttc gggccgggag acccgcgag ccctcggggc atctcagtg 120
ctcattcccc accccctccc ccgggtcggg ggaggcggcg cgtccggcgg agggttgagg 180
ggagcggggc aggcctggag cgccatgagc agcccgatg cgggatacgc cagtgcagac 240
cagagccaga cccagagcgc gctgcccgcg gtgatggccg ggctggggcc ctgcccctgg 300
gccgagtcgc tgagccccat cggggacatg aaggtgaagg gcgaggcgcc ggcgaacagc 360
ggagcaccgg ccggggcgcg gggccgagcc aagggcgagt cccgtatccg gcggccgatg 420
aacgctttca tgggtgtggg taaggacgag cgcaagcggc tggcgagca gaatccagac 480
ctgcacaacg ccgagttgag caagatgctg ggcaagtcgt ggaaggcgct gacgctggcg 540
gagaagcggc ccttcgtgga ggaggcagag cggctgcgcg tgcagcacat gcaggaccac 600
cccaactaca agtaccggcc gcggcgcgcg aagcaggtga agcggctgaa gcgggtggag 660
ggcggttcc tgcacggcct ggctgagccg caggcgcccg cgtggggccc cgaggggcgc 720
cgcggtggca tggacggcct gggcctccag ttccccgagc agggcttccc cgccggcccc 780
ccgctgctgc ctccgcacat gggcggccac taccgcgact gccagagtct gggcgcgcc 840
ccgctcgacg gctaccggtt gccacgccc gacacgtccc cgtgggacgg cgtggacccc 900
gacccggtt tcttcgccc cccgatgccc ggggactgcc cgcgggccgg cacctacagc 960
tacgcgcagg tctcggacta cgctggcccc ccggagcctc ccgccggtcc catgcacccc 1020
cgactcggcc cagagccccg ggtccctcg attccggg ccctggcgcc acccagcgcc 1080
cttcacgtgt actacggcgc gatgggctcg cccggggcgg gcggcgggcg cggcttccag 1140
atgcagcgc aacaccagca ccagcacc caccagacc accccccggg ccccgagac 1200
ccgtcgcccc ctccggaggc actgccctgc cgggacggca cggaacccag tcagccccgc 1260
gagctcctcg gggagggtga ccgcacgga tttgaacagt atctgcactt cgtgtgcaag 1320
cctgagatgg gcctccccta ccaggggcat gactccggtg tgaatctccc cgacagccac 1380

```

120

```

ggggccattt cctcgggtgt gtccgacgcc agctccgcgg tatattactg caactatcct 1440
gacgtgtgac aggtccctga tccgccccag cctgcaggcc agaagcagtg ttacacactt 1500
cctggaggag ctaaggaaat cctcagactc ctgggttttt gttgttgctg ttgttgtttt 1560
ttaaaggtg tggtggcata taatttatgg taatttatgt tgtctgccac ttgaacagtt 1620
tggtgggggtg aggtttcatt taaaatttgt tcagagattt gtttcccaca gttggattgt 1680
caaaacccta tttccaagtt caagttaact agctttgaat gtgtcccaaa acagcttcct 1740
ccatttcctg aaagtttatt gatcaaagaa atgttgcctt ggggtgtgtt tttcaatcct 1800
ctaaaaaata aaatctggaa tcctgaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1853

```

&lt;210&gt; 103

&lt;211&gt; 414

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 103

```

Met Ser Ser Pro Asp Ala Gly Tyr Ala Ser Asp Asp Gln Ser Gln Thr
 1          5          10          15
Gln Ser Ala Leu Pro Ala Val Met Ala Gly Leu Gly Pro Cys Pro Trp
 20          25          30
Ala Glu Ser Leu Ser Pro Ile Gly Asp Met Lys Val Lys Gly Glu Ala
 35          40          45
Pro Ala Asn Ser Gly Ala Pro Ala Gly Ala Ala Gly Arg Ala Lys Gly
 50          55          60
Glu Ser Arg Ile Arg Arg Pro Met Asn Ala Phe Met Val Trp Ala Lys
 65          70          75          80
Asp Glu Arg Lys Arg Leu Ala Gln Gln Asn Pro Asp Leu His Asn Ala
 85          90          95
Glu Leu Ser Lys Met Leu Gly Lys Ser Trp Lys Ala Leu Thr Leu Ala
100          105          110
Glu Lys Arg Pro Phe Val Glu Glu Ala Glu Arg Leu Arg Val Gln His
115          120          125
Met Gln Asp His Pro Asn Tyr Lys Tyr Arg Pro Arg Arg Arg Lys Gln
130          135          140
Val Lys Arg Leu Lys Arg Val Glu Gly Gly Phe Leu His Gly Leu Ala
145          150          155          160
Glu Pro Gln Ala Ala Ala Leu Gly Pro Glu Gly Gly Arg Val Ala Met
165          170          175
Asp Gly Leu Gly Leu Gln Phe Pro Glu Gln Gly Phe Pro Ala Gly Pro
180          185          190
Pro Leu Leu Pro Pro His Met Gly Gly His Tyr Arg Asp Cys Gln Ser
195          200          205
Leu Gly Ala Pro Pro Leu Asp Gly Tyr Pro Leu Pro Thr Pro Asp Thr
210          215          220
Ser Pro Leu Asp Gly Val Asp Pro Asp Pro Ala Phe Phe Ala Ala Pro
225          230          235          240
Met Pro Gly Asp Cys Pro Ala Ala Gly Thr Tyr Ser Tyr Ala Gln Val
245          250          255
Ser Asp Tyr Ala Gly Pro Pro Glu Pro Pro Ala Gly Pro Met His Pro
260          265          270
Arg Leu Gly Pro Glu Pro Ala Gly Pro Ser Ile Pro Gly Leu Leu Ala
275          280          285
Pro Pro Ser Ala Leu His Val Tyr Tyr Gly Ala Met Gly Ser Pro Gly
290          295          300
Ala Gly Gly Gly Arg Gly Phe Gln Met Gln Pro Gln His Gln His Gln
305          310          315          320
His Gln His Gln His His Pro Pro Gly Pro Gly Gln Pro Ser Pro Pro
325          330          335
Pro Glu Ala Leu Pro Cys Arg Asp Gly Thr Asp Pro Ser Gln Pro Ala

```

	340		345		350										
Glu	Leu	Leu	Gly	Glu	Val	Asp	Arg	Thr	Glu	Phe	Glu	Gln	Tyr	Leu	His
	355						360					365			
Phe	Val	Cys	Lys	Pro	Glu	Met	Gly	Leu	Pro	Tyr	Gln	Gly	His	Asp	Ser
	370						375					380			
Gly	Val	Asn	Leu	Pro	Asp	Ser	His	Gly	Ala	Ile	Ser	Ser	Val	Val	Ser
	385						390					395			400
Asp	Ala	Ser	Ser	Ala	Val	Tyr	Tyr	Cys	Asn	Tyr	Pro	Asp	Val		
			405					410							

&lt;210&gt; 104

&lt;211&gt; 2398

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

```

ttacttactt gcttgccctgc ttgcttagag acagggtctc cctttgtctc ccaggctgga 60
gtgcagtggc atgatcatag ctccactgcag gttcaaaactt ctgggctcaa gtaatcctac 120
cgcctcagcc tcatgagtag ctgggactac aggtgtgggt gtccacgccc agctaatttt 180
ttttttcttt agtagagatg aggtcttgct atgttgccca ggctggtctt gaacttctag 240
actcaagcaa tctcttgcc tcggcctccc aaagtgtctg gattacaggc atgagccact 300
gcacaggccc ctttctttt ttctccattt tctttctttt ttctccccct tttctgggag 360
gcaggccagc ctccacagcca gacaccagct gtgggagttg tcttacgcat atgctctgcc 420
ccttagaagg attcagtctg tgccctggag gggcctacgg tcccgcctgg ttgtgggtct 480
gtcttgaaca caaatggtga gggtgaaatg gatgctagta tcatggatgg aaaagacctg 540
tctgcaggag cagtgtccgc agtccagtgt atagcaaact ccattaaact tgctcggtt 600
gtcatggaaa agacacctca ttgctttctg actgaccaag gcgcagcgca gtttgcagca 660
gctatggggg ttccagagat tcctggagaa aaactggtga cagagagaaa caaaaagcgc 720
ctggaaaaag agaagcatga aaaagggtgct cagaaaaacag attgtcaaaa aaacttggga 780
accgtgggtg ctgttgccct ggactgcaaa gggaatgtag cctacgcaac ctccacaggc 840
ggtatcgtaa ataaaatggt cggccgcggt ggggactcac cgtgtctagg agctggaggt 900
tatgccgaca atgacatcgg agccgtctca accacagggc atggggaaag catcctgaag 960
gtgaacctgg ctgactcac cctgttccac atagaacaag gaaagacggt agaagagggt 1020
gcggacctat cgttgggtta tatgaagtca aggtttaaag gtttaggtgg cctcatcggt 1080
gttagcaaaa caggagactg ggtggcaaa tggacctcca cctccatgcc ctgggcagcc 1140
gccaaggacg gcaagctgca cttcggaatt gatcctgacg atactactat caccgacctt 1200
ccctaagccg ctggaagatt gtattccaga tgctagctta gaggtcaagt acagtctcct 1260
catgagacat agcctaatac attagatcta gaattggaaa aattgtcccg tctgtcaact 1320
gttttgttgc cttaataaag atctgaatgt ttggttgtgg ggcgggttct gaagcratga 1380
gagaaatgcc cgtattagga ggattacttg agccctggag gtcaaagctg aggtgagcca 1440
tgattactcc actgactcc agcctgggca acagagccag gccctgtwkc mmawrawwam 1500
wmamwrmam wmcagcctgg gcaacagagc caggccctgt atcaaaaaaa aaagaaaagg 1560
gaaaaaagaa agaaagcagc agcatgatcc tgacatgaca gatgtgggag acccacagcc 1620
tgcagacact gtgggctgga aggtgggaag ggaggggccg gtggaggtgg agctgtttga 1680
aagtgcaca gcagcagtag aagcagtggg gggcgaagcc caggtgacct tcagaacggt 1740
gcacaagaac atcagggaaa agaaccagaa tcctttaagg aaaatgttct tcatgtatga 1800
gagactaaag tgatttttct aagaaagtcc agcccttctc tgacttacct ggacatttct 1860
agatacttcc aaaggaccct ctgggaatcc atagcttctt aatctggaga tgggaggtca 1920
taaggagac gctgtggggt tcttgaagt ttcttgggtt cacagaggag cccctcact 1980
tggtgttctc ccgtgagcca gcctccacct gccaaagaca ctctggtcct cgtatagtga 2040
gtaatggggc tcagggcctc tccaacaaca gagaggagct gatgctgtag ggctgacccc 2100
gtgacttctt gactcctcac cctgtccagt gctttgagat tcttcccacc tccccatcct 2160
caccagccgg atcgggcgct gtgcagtgtg gtcagcatgg tgaagaaagt catttcttgg 2220
gtggacagta ttctcttcta tctctcatta cactggaaat gttatttctg ctgtatcatc 2280
cgtgctcaac gttttagtct gtcaggctca cttctctctt ggaaagaatt tgcttaactt 2340
gacattccat gtgccgctaa taaaatatat tttgaaagaa aaaaaaaaaa aaaaaaaa 2398

```

<210> 105  
 <211> 232  
 <212> PRT  
 <213> Homo sapiens

<400> 105

```

Met Asp Ala Ser Ile Met Asp Gly Lys Asp Leu Ser Ala Gly Ala Val
 1           5           10           15
Ser Ala Val Gln Cys Ile Ala Asn Pro Ile Lys Leu Ala Arg Leu Val
          20           25           30
Met Glu Lys Thr Pro His Cys Phe Leu Thr Asp Gln Gly Ala Ala Gln
      35           40           45
Phe Ala Ala Ala Met Gly Val Pro Glu Ile Pro Gly Glu Lys Leu Val
      50           55           60
Thr Glu Arg Asn Lys Lys Arg Leu Glu Lys Glu Lys His Glu Lys Gly
 65           70           75           80
Ala Gln Lys Thr Asp Cys Gln Lys Asn Leu Gly Thr Val Gly Ala Val
          85           90           95
Ala Leu Asp Cys Lys Gly Asn Val Ala Tyr Ala Thr Ser Thr Gly Gly
      100           105           110
Ile Val Asn Lys Met Val Gly Arg Val Gly Asp Ser Pro Cys Leu Gly
      115           120           125
Ala Gly Gly Tyr Ala Asp Asn Asp Ile Gly Ala Val Ser Thr Thr Gly
      130           135           140
His Gly Glu Ser Ile Leu Lys Val Asn Leu Ala Arg Leu Thr Leu Phe
 145           150           155           160
His Ile Glu Gln Gly Lys Thr Val Glu Glu Ala Ala Asp Leu Ser Leu
      165           170           175
Gly Tyr Met Lys Ser Arg Val Lys Gly Leu Gly Gly Leu Ile Val Val
      180           185           190
Ser Lys Thr Gly Asp Trp Val Ala Lys Trp Thr Ser Thr Ser Met Pro
      195           200           205
Trp Ala Ala Ala Lys Asp Gly Lys Leu His Phe Gly Ile Asp Pro Asp
      210           215           220
Asp Thr Thr Ile Thr Asp Leu Pro
225           230

```

<210> 106  
 <211> 1811  
 <212> DNA  
 <213> Homo sapiens

<400> 106

```

gagtcaccaa ggaaggcagc ggcagctcca ctcagccagt acccagatac gctgggaacc 60
ttccccagcc atggcttccc tggggcagat cctcttctgg agcataatta gcatcatcat 120
tattctggct ggagcaattg cactcatcat tggctttggt atttcaggga gacactccat 180
cacagtcact actgtgcct cagctgggaa cattggggag gatggaatcc agagctgcac 240
ttttgaacct gacatcaaac tttctgatat cgtgatataa tggctgaagg aaggtgtttt 300
aggcttggtc catgagttca aagaaggcaa agatgagctg tcggagcagg atgaaatgtt 360
cagaggccgg acagcagtggt ttgctgatca agtgatagtt ggcaatgcct ctttgcggct 420
gaaaaacgtg caactcacag atgctggcac ctacaaatgt tatatcatca cttctaaagg 480
caaggggaat gctaaccttg agtataaaac tggagccttc agcatgccgg aagtgaatgt 540
ggactataat gccagctcag agaccttgcg gtgtgaggct ccccgatggt tccccagcc 600
cacagtggtc tgggcatccc aagttgacca gggagccaac ttctcggaag tctccaatac 660
cagctttgag ctgaactctg agaatgtgac catgaagggt gtgtctgtgc tctacaatgt 720
tacgatcaac aacacatact cctgtatgat tgaatatgac attgccaaag caacagggga 780
tatcaaagtg acagaatcgg agatcaaaag gcggagtcac ctacagctgc taaactcaaa 840

```

```

ggcttctctg tgtgtctctt ctttctttgc catcagctgg gcacttctgc ctctcagccc 900
ttacctgatg ctaaaataat gtgcctcggc cacaaaaaag catgcaaagt cattgttaca 960
acagggatct acagaactat ttcaccacca gatatgacct agttttatat ttctgggagg 1020
aaatgaattc atatctagaa gtctggagtg agcaaacaag agcaagaaac aaaaagaagc 1080
caaaagcaga aggtccaat atgaacaaga taaatctatc ttcaaagaca tattagaagt 1140
tgggaaaata attcatgtga actagagtca actgtgtcag ggctaagaaa ccctggtttt 1200
gagtagaaaa gggcctggaa agagggggagc caacaaatct gtctgcttcc tcacattagt 1260
cattggcaaa taagcattct gtctctttgg ctgctgcctc agcacagaga gccagaactc 1320
tatcgggcac caggataaca tctctcagtg aacagagttg acaaggccta tgggaaatgc 1380
ctgatgggat tatcttcagc ttgttgagct tctaagtctc ttcccttca ttctaccctg 1440
caagccaagt tctgtaagag aaatgcctga gttctagctc aggttttctt actctgaatt 1500
tagatctcca gaccctgcct ggccacaatt caaatgaagg caacaaacat ataccttcca 1560
tgaagcacac acagactttt gaaagcaagg acaatgactg cttgaattga ggccttgagg 1620
aatgaagctt tgaaggaaaa gaatactttg tttccagccc ccttccaca ctcttcatgt 1680
gttaaccact gccttcctgg accttgagc caccgtgact gtattacatg ttgttataga 1740
aaactgattt tagagttctg atcgttcaag agaatgatta aatatacatt tcctaaaaaa 1800
aaaaaaaaa a 1811

```

&lt;210&gt; 107

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 107

```

Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile
1      5      10      15
Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser
20     25     30
Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly Asn Ile
35     40     45
Gly Glu Asp Gly Ile Gln Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
50     55     60
Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val
65     70     75     80
His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met
85     90     95
Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Ile Val Gly Asn
100    105    110
Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
115    120    125
Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
130    135    140
Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn
145    150    155    160
Ala Ser Ser Glu Thr Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
165    170    175
Pro Thr Val Val Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
180    185    190
Glu Val Ser Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met
195    200    205
Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser
210    215    220
Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val
225    230    235    240
Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser
245    250    255
Lys Ala Ser Leu Cys Val Ser Ser Phe Phe Ala Ile Ser Trp Ala Leu
260    265    270

```

Leu Pro Leu Ser Pro Tyr Leu Met Leu Lys  
275 280

<210> 108  
<211> 2611  
<212> DNA  
<213> Homo sapiens

<400> 108  
ctttttttcac ctctgtctgaa atgggtgcct cccagtgtct ctgctgctca aaattttctct 60  
tccagagaca gaacctcgcc tgttttctca caaaccacaca ctgtggcagc cttgttaatg 120  
cagatggcca tgggtgaagtg tggacagact ggaataatat gtccaagttt ttccagtatg 180  
gatggcgatg caccactaat gagaatacct attcaaaccg taccctgatg ggcaactgga 240  
accaggaaaag atatgacctg aggaatatcg tgcagcccaa acccttgcct tcccagtttg 300  
gacactactt tgaaacaaca tatgatacaa gctacaacaa caaaatgcc a tttcaaacac 360  
atagattttaa gcgagagcct cactgggttc caggacatca acctgaactg gatcctcccc 420  
gatacaaatg cacagaaaag tcaacttaca tgaatagcta ttcaaagcct taaattgggc 480  
atcactcagg atgtgtataa gatcttaata ttgatagttt cacatccagg tttctaagaa 540  
atgataagat acttcaacttt tccagagtga aatgtaggag ggagcacatt ctaagtacag 600  
ctaaaaat t agctcactgt aacacagttt cactctctga ataaataaag caaaaaacac 660  
agtaaatatt ctttatccct ttttttgttg ttgttttaac caagatttaa atgtcaaat 720  
taatacagca actcagttct acatttgggg tgtttagtaa gggccttaaa aagaattatt 780  
ttaggccagg cacggtggct catgcctgta atcccagcac tttgggaggc cgaggcaggt 840  
ggatcacgtg aggtcaggag ttcgagacca gcctgaccaa catggtgaaa cactgtctct 900  
actaaaaaca caaaaattag ctgagcatgg tggctcacgc ctgtaatccc agctactcag 960  
gaggctgagg caggggaatc gcttgaacct gagaagtga ggttgtggtg agctgagatc 1020  
atgccactgc actttagcct gggtagacaga gcgagactct gtctcaaaaa aaaaaaaaaa 1080  
aaaagaatta tttctctgaa gtctacaacc actgtggtct tcccttcctt ctgtcgtagc 1140  
aagacctcag aatctagcat aacttaggct aggtttggct agatgctttc tgggtataag 1200  
ccagagtcgt atagtgaac tttgctgtga ccttagtgaa catcccctct tggaggactac 1260  
aaaaacaaac gtaacttttt aaaattatta tggagaattt tacgtaaaac aaaagtagac 1320  
aggctagtct aatgaactcc catgtatcat taccagcat caactattta tgactaatct 1380  
tacctacttc tactttgtct tattgaatta attttggagc agatcttaga aatagaattt 1440  
aatctataaa aatcttggtg ggctgggtac ggtggctcat gcctgtaatc ccagcacttt 1500  
gggaggctga ggtgggtgga tcacctgagg tcaggagtcc aagaccagcc tggccaatgt 1560  
ggtgaaaactc catctcttct aaaaatacaa aaattagctg gtcttggtgg cgggcgcctg 1620  
taatcccagc tacttgggag gctgaggcag gagaattgct tgaaccagc aagcagaggt 1680  
tgcagtgagc tgagacggtg ccattgctct ccagcctggg cgacaagagc gaaactccgt 1740  
ctcaaaaaaa aaaaagaaaa gaaaaagaaa aaaaaaatct tggatatactg gctgggcaca 1800  
gtggctcaca cctaattcca gcaacttggg aggtgaggc agaggatag cttgaggctg 1860  
ggagttcaaa accagcctgg gcaacatagc aagaccccat ctctaccaaa aaaaattttt 1920  
ttaaagattt caggtatatt tctcaaaaag ataaggactg tcaattgtct actccccccc 1980  
aacaagggtc actaaggaaa cctgttgact aaacaaagct cattaacact attgtagtgt 2040  
agcaaaggag accatcaact tgacacagag tcttggtaat gattcaaagg gaggatgta 2100  
gagtaaggta tttataagga tttgagataa ggtccaact ggtttaaaat gagtcaaaat 2160  
agggaactag tagagactga gaaagggttg tgaatagctt aggtttggta aacttaggaa 2220  
atcaacagtt ttaattttta tatggttaaa ctgattagta tttcctattt ttttatctac 2280  
tgtgtaagaa gacctataa tatatgggca ttactgagag atactgcca tatgttgtcc 2340  
tcgtaagcaa ggagatattt tttatctccc atatattacc tttcaaacct ttgttacttt 2400  
agtttcgaga tatagatcca gtttatgttg ttactcagta gtgaggaagt ttcttttttt 2460  
tttttaaatg gctatcaagt tgtccccca ttagttattg aaaagaccat aattttttca 2520  
ctcctattca atgccattt tattgtaaat aaactatgta catgtaaaaa aaaaaaaaaa 2580  
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2611

<210> 109  
<211> 150  
<212> PRT

125

&lt;213&gt; Homo sapiens

&lt;400&gt; 109

```

Met Ala Ala Ser Gln Cys Leu Cys Cys Ser Lys Phe Leu Phe Gln Arg
 1           5           10           15
Gln Asn Leu Ala Cys Phe Leu Thr Asn Pro His Cys Gly Ser Leu Val
      20           25           30
Asn Ala Asp Gly His Gly Glu Val Trp Thr Asp Trp Asn Asn Met Ser
 35           40           45
Lys Phe Phe Gln Tyr Gly Trp Arg Cys Thr Thr Asn Glu Asn Thr Tyr
 50           55           60
Ser Asn Arg Thr Leu Met Gly Asn Trp Asn Gln Glu Arg Tyr Asp Leu
 65           70           75           80
Arg Asn Ile Val Gln Pro Lys Pro Leu Pro Ser Gln Phe Gly His Tyr
      85           90           95
Phe Glu Thr Thr Tyr Asp Thr Ser Tyr Asn Asn Lys Met Pro Leu Ser
      100           105           110
Thr His Arg Phe Lys Arg Glu Pro His Trp Phe Pro Gly His Gln Pro
      115           120           125
Glu Leu Asp Pro Pro Arg Tyr Lys Cys Thr Glu Lys Ser Thr Tyr Met
      130           135           140
Asn Ser Tyr Ser Lys Pro
145           150

```

&lt;210&gt; 110

&lt;211&gt; 1032

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 110

```

ggcaaggggg agtgtagagc agagcagaag cctgagccag acggagagacc acctcctctc 60
ccaggaactg aacccaaagg atcacctggt attccctgag agtacagatt tctccggcgt 120
ggccctcaag ggacagacat ggctcagcgg atgacaacac agctgctgct ccttctagtg 180
tgggtggctg tagtagggga ggctcagaca aggattgcat gggccaggac tgagcttctc 240
aatgtctgca tgaacgccaa gcaccacaag gaaaagccag gccccgagga caagttgcat 300
gagcagtgtc gaccctggag gaagaatgcc tgctgttcta ccaacaccag ccaggaagcc 360
cataaggatg tttcctacct atatagattc aactggaacc actgtggaga gatggcacct 420
gctgcaaac ggcatthcat ccaggacacc tgcctctacg agtgctcccc caacttgggg 480
ccctggatcc agcaggtgga tcagagctgg cgcaaagagc gggactgaa cgtgcccctg 540
tgcaaagagg actgtgagca atggtgggaa gattgtcgca cctcctacac ctgcaagagc 600
aactggcaca agggctggaa ctggacttca gggtttaaca agtgcgagc gggagctgcc 660
tgccaacctt tccatttcta cttccccaca cccactgttc tgtgcaatga aatctggact 720
cactcctaca aggtcagcaa ctacagccga gggagtggcc gctgcatcca gatgtggttc 780
gaccagccc agggcaaccc caatgaggag gtggcgaggt tctatgctgc agccatgagt 840
ggggtgggc cctgggcagc ctggccttcc ctgcttagcc tggccctaag gctgctgtgg 900
ctgctcagct gacctcctt taccttctga tacctggaaa tccctgccct gttcagcccc 960
acagctocca actatttggg tcctgctcca tggctgggcc tctgacagcc actttgaata 1020
aaccagacac cg                                     1032

```

&lt;210&gt; 111

&lt;211&gt; 257

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 111

```

Met Ala Gln Arg Met Thr Thr Gln Leu Leu Leu Leu Val Trp Val
 1           5           10           15

```

126.

Ala Val Val Gly Glu Ala Gln Thr Arg Ile Ala Trp Ala Arg Thr Glu  
 20 25 30  
 Leu Leu Asn Val Cys Met Asn Ala Lys His His Lys Glu Lys Pro Gly  
 35 40 45  
 Pro Glu Asp Lys Leu His Glu Gln Cys Arg Pro Trp Arg Lys Asn Ala  
 50 55 60  
 Cys Cys Ser Thr Asn Thr Ser Gln Glu Ala His Lys Asp Val Ser Tyr  
 65 70 75 80  
 Leu Tyr Arg Phe Asn Trp Asn His Cys Gly Glu Met Ala Pro Ala Cys  
 85 90 95  
 Lys Arg His Phe Ile Gln Asp Thr Cys Leu Tyr Glu Cys Ser Pro Asn  
 100 105 110  
 Leu Gly Pro Trp Ile Gln Gln Val Asp Gln Ser Trp Arg Lys Glu Arg  
 115 120 125  
 Val Leu Asn Val Pro Leu Cys Lys Glu Asp Cys Glu Gln Trp Trp Glu  
 130 135 140  
 Asp Cys Arg Thr Ser Tyr Thr Cys Lys Ser Asn Trp His Lys Gly Trp  
 145 150 155 160  
 Asn Trp Thr Ser Gly Phe Asn Lys Cys Ala Val Gly Ala Ala Cys Gln  
 165 170 175  
 Pro Phe His Phe Tyr Phe Pro Thr Pro Thr Val Leu Cys Asn Glu Ile  
 180 185 190  
 Trp Thr His Ser Tyr Lys Val Ser Asn Tyr Ser Arg Gly Ser Gly Arg  
 195 200 205  
 Cys Ile Gln Met Trp Phe Asp Pro Ala Gln Gly Asn Pro Asn Glu Glu  
 210 215 220  
 Val Ala Arg Phe Tyr Ala Ala Ala Met Ser Gly Ala Gly Pro Trp Ala  
 225 230 235 240  
 Ala Trp Pro Phe Leu Leu Ser Leu Ala Leu Met Leu Leu Trp Leu Leu  
 245 250 255  
 Ser

&lt;210&gt; 112

&lt;211&gt; 1104

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 112

tggaggcctg gctgggtgctc acatacaata attaaactgct gagtggcctt cgcccaatcc 60  
 caggctccac tcctgggctc cattcccaact ccctgcctgt ctctaggcc actaaaccac 120  
 agctgtcccc tgggaataagg caagggggag tgtagagcag agcagaagcc tgagccagac 180  
 ggagagccac ctccctctccc agggacagac atggctcagc ggatgacaac acagctgctg 240  
 ctccctctag tgtgggtggc tgtagtaggg gaggctcaga caaggattgc atggggccagg 300  
 actgagcttc tcaatgtctg catgaacgcc aagcaccaca aggaaaagcc aggccccgag 360  
 gacaagttgc atgagcagtg tcgaccctgg aggaagaatg cctgctgttc taccaacacc 420  
 agccaggaag cccataagga tgtttctac ctatatagat tcaactggaa ccaactgtga 480  
 gagatggcac ctgcctgcaa acggcatttc atccaggaca cctgcctcta cgagtgtcc 540  
 cccaacttgg ggccctggat ccagcaggtg gatcagagct ggcgcaaaga gcgggtactg 600  
 aacgtgcccc tgtgcaaaga ggactgtgag caatgggtgg aagattgtcg cacctcctac 660  
 acctgcaaga gcaactggca caagggctgg aactggactt cagggtttaa caagtgcgca 720  
 gtgggagctg cctgcccaacc ttccatttc tacttcccca caccactgt tctgtgcaat 780  
 gaaatctgga ctcaactcta caaggtcagc aactacagcc gagggagtgg ccgctgcatc 840  
 cagatgtggt tcgaccagc ccagggcaac cccaatgagg aggtggcgag gttctatgct 900  
 gcagccatga gtggggctgg gccctgggca gctggcctt tcctgcttag cctggcccta 960  
 atgctgctgt ggctgctcag ctgacctcct ttaccttct gatacctgga aatccctgcc 1020  
 ctgttcagcc ccacagctcc caactatttg gttcctgctc catggtcggg cctctgacag 1080



ccactttgaa taaaccagac accg

1104

&lt;210&gt; 113

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 113

cattccttgg	tgccactgac	cacagctctt	tcttcagggg	cagacatggc	tcagcggatg	60
acaacacagc	tgctgctcct	tctagtgtgg	gtggctgtag	taggggaggc	tcagacaagg	120
attgcatggg	ccaggactga	gcttctcaat	gtctgcatga	acgccaagca	ccacaaggaa	180
aagccaggcc	ccgaggacaa	gttgcacgac	cagtgtcgac	cctggaggaa	gaatgcctgc	240
tggtctacca	acaccagcca	ggaagcccat	aaggatgttt	cctacctata	tagattcaac	300
tggaaccact	gtggagagat	ggcacctgcc	tgcaaacggc	atttcatcca	ggacacctgc	360
ctctacagat	gtccccccaa	cttggggccc	tggatccagc	aggtggatca	gagctggcgc	420
aaagagcggg	tactgaacgt	gcccctgtgc	aaagaggact	gtgagcaatg	gtgggaagat	480
tgctgcacct	cctacacctg	caagagcaac	tggcacaagg	gctggaactg	gacttcaggg	540
tttaacaagt	gcgcagtggg	agctgcctgc	caacctttcc	atttctactt	ccccacaccc	600
actgttctgt	gcaatgaaat	ctggactcac	tcctacaagg	tcagcaacta	cagccgaggg	660
agtggccgct	gcatccagat	gtggttcgac	ccagcccagg	gcaaccccaa	tgaggaggtg	720
gcgaggttct	atgctgcagc	catgagtggg	gctgggccct	gggcagcctg	gcctttcctg	780
cttagcctgg	ccctaattgt	gctgtggctg	ctcagctgac	ctccttttac	cttctgatac	840
ctggaatatc	ctgccctgtt	cagccccaca	gctcccaact	atttggttcc	tgctccatgg	900
tcgggcctct	gacagccact	ttgaataaac	cagacaccg			939

&lt;210&gt; 114

&lt;211&gt; 1331

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 114

ggaaaggatt	ttctcagccc	ccatccccag	caactgtgtg	tggccgcacc	catgagagcc	60
tcagcactct	gaagggtcag	ggggcaaagg	ccaaaagagc	tctggcctga	acttgggtgg	120
tccctactgt	gtgacttggg	gcatggccct	catctgtgct	gaaatgattc	cacaaagatt	180
aaactggcta	tcatttgttg	atttccccct	tcttacattt	aatccttgca	ggagaaagct	240
aagcctcaag	atagtttgct	tctctttccc	ccaaggccaa	ggagaagggt	gagtgagggc	300
tggggctcgg	acaggttgaa	cggaaccctt	gtgctctaaa	cagttagggt	ttgttcccgc	360
aggaactgaa	cccaaaggat	cacctggtat	tccttgagag	tacagatttc	tcgggcgtgg	420
ccctcaaggg	acagacatgg	ctcagcggat	gacaacacag	ctgctgctcc	ttctagtgtg	480
ggtggctgta	gtaggggagg	ctcagacaag	gattgcatgg	gccaggactg	agcttctcaa	540
tgtctgcatg	aacgccaagc	accacaagga	aaagccaggc	cccaggagca	agttgcatga	600
gcagtgtcga	ccctggagga	agaatgcctg	ctgttctacc	aacaccagcc	aggaagccca	660
taaggatgtt	tcctacctat	atagattcaa	ctggaaccac	tgtggagaga	tggcacctgc	720
ctgcaaaccg	catttcatcc	aggacacctg	cctctacgag	tgctccccca	acttggggcc	780
ctggatccag	caggtggatc	agagctggcg	caaagagcgg	gtactgaacg	tgcccctgtg	840
caaagaggac	tgtgagcaat	ggtgggaaga	ttgtcgcacc	tcctacacct	gcaagagcaa	900
ctggcacaag	ggctggaact	ggacttcagg	gtttaacaag	tgcgagtggt	gagctgcctg	960
ccaacctttc	catttctact	tccccacacc	caactgttct	tgcaatgaaa	tctggactca	1020
ctcctacaag	gtcagcaact	acagccgagg	gagtggccgc	tgcatccaga	tgtggttcga	1080
cccagcccag	ggcaacccca	atgaggaggt	ggcgagggtt	tatgctgcag	ccatgagtgg	1140
ggctgggccc	tgggcagcct	ggcctttcct	gcttagcctg	gccctaatac	tgctgtggct	1200
gctcagctga	cctcctttta	ccttctgata	cctggaaatc	cctgccctgt	tcagccccac	1260
agctcccaac	tatttgggtc	ctgctccatg	gtcgggcctc	tgacagccac	tttgaataaa	1320
ccagacaccg	c					1331

&lt;210&gt; 115

&lt;211&gt; 929

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 115

```

aggacagac atggctcagc ggatgacaac acagctgctg ctccttctag tgtgggtggc 60
tgtagtaggg gaggtcaga caaggattgc atgggccagg actgagcttc tcaatgtctg 120
catgaacgcc aagcaccaca aggaaaagcc agggcccgag gacaagttgc atgagcagtg 180
tcgaccctgg aggaagaatg cctgctgttc taccaacacc agccaggaag cccataagga 240
tgtttcctac ctatatagat tcaactggaa ccaactgtga gagatggcac ctgcctgcaa 300
acggcatttc atccaggaca cctgcctcta cgagtgtccc cccaacttgg ggccctggat 360
ccagcaggtg gatcagagct ggcgcaaaga gcgggtactg aacgtgcccc tgtgcaaaga 420
ggactgtgag caatgggtggg aagattgtcg cacctcctac acctgcaaga gcaactggca 480
caagggtctg aactggactt cagggtttaa caagtgcgca gtgggagctg cctgcccaacc 540
tttccatttc tacttcccc caccactgt tctgtgcaat gaaatctgga ctcaactcta 600
caaggtcagc aactacagcc gagggagtgg ccgctgcac cagatgtggt tcgaccagc 660
ccagggcaac cccaatgagg aggtggcgag gttctatgct gcagccatga gtggggctgg 720
gccctgggca gcctggcctt tcctgcttag cctggcccta atgctgctgt ggctgctcag 780
ctgacctctt ttaccttct gatacctgga aatccctgcc ctgttcagcc ccacagctcc 840
caactatttg gttcctgctc catggtcggg cctctgacag ccactttgaa taaaccagac 900
accgcacatg tgtcttgaga attatttgg 929

```

&lt;210&gt; 116

&lt;211&gt; 858

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 116

```

agagcctgga cctacagcgc tgttggtgga ggtcctgcct ccaggaatag atggacatgg 60
cctggcagat gatgcagctg ctgcttctgg ctttggtgac tgctgcgggg agtgcccagc 120
ccaggagtgc gcgggccagg acggacctgc tcaatgtctg catgaacgcc aagcaccaca 180
agacacagcc cagccccgag gacgagctgt atggccagtg cagtccctgg aagaagaatg 240
cctgctgcac ggccagcacc agccaggagc tgcacaagga cacctccgc ctgtacaact 300
ttaactggga tcaactgtgt aagatggaac ccacctgcaa gcgccacttt atccaggaca 360
gctgtctcta tgagtgtctc cccaacctgg ggccctggat ccggcaggtc aaccagagct 420
ggcgcaaaga gcgcattctg aacgtgcccc tgtgcaaaga ggactgtgag cgctgggtggg 480
aggactgtcg cacctcctac acctgcaaaa gcaactggca caaaggctgg aattggacct 540
cagggattaa tgagtgtcgc gccggggccc tctgcagcac ctttgagtcc tacttcccc 600
ctccagccgc cctttgtgaa ggcctctgga gccactcctt caaggtcagc aactatagtc 660
gagggagcgg ccgctgcac cagatgtggt ttgactcagc ccagggcaac cccaatgagg 720
aggtggccaa gttctatgct gcggccatga atgctggggc cccgtctcgt gggattattg 780
attcctgatc caagaagggt cctctggggg tcttccaaca acctattcta atagacaaat 840
ccacatgaaa aaaaaaaaa 858

```

&lt;210&gt; 117

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 117

```

Met Ala Trp Gln Met Met Gln Leu Leu Leu Leu Ala Leu Val Thr Ala
1           5           10          15
Ala Gly Ser Ala Gln Pro Arg Ser Ala Arg Ala Arg Thr Asp Leu Leu
20          25          30
Asn Val Cys Met Asn Ala Lys His His Lys Thr Gln Pro Ser Pro Glu
35          40          45
Asp Glu Leu Tyr Gly Gln Cys Ser Pro Trp Lys Lys Asn Ala Cys Cys
50          55          60
Thr Ala Ser Thr Ser Gln Glu Leu His Lys Asp Thr Ser Arg Leu Tyr
65          70          75          80

```

129

Asn	Phe	Asn	Trp	Asp	His	Cys	Gly	Lys	Met	Glu	Pro	Thr	Cys	Lys	Arg
			85						90					95	
His	Phe	Ile	Gln	Asp	Ser	Cys	Leu	Tyr	Glu	Cys	Ser	Pro	Asn	Leu	Gly
		100						105					110		
Pro	Trp	Ile	Arg	Gln	Val	Asn	Gln	Ser	Trp	Arg	Lys	Glu	Arg	Ile	Leu
		115					120					125			
Asn	Val	Pro	Leu	Cys	Lys	Glu	Asp	Cys	Glu	Arg	Trp	Trp	Glu	Asp	Cys
	130					135					140				
Arg	Thr	Ser	Tyr	Thr	Cys	Lys	Ser	Asn	Trp	His	Lys	Gly	Trp	Asn	Trp
	145				150				155					160	
Thr	Ser	Gly	Ile	Asn	Glu	Cys	Pro	Ala	Gly	Ala	Leu	Cys	Ser	Thr	Phe
			165						170					175	
Glu	Ser	Tyr	Phe	Pro	Thr	Pro	Ala	Ala	Leu	Cys	Glu	Gly	Leu	Trp	Ser
			180					185					190		
His	Ser	Phe	Lys	Val	Ser	Asn	Tyr	Ser	Arg	Gly	Ser	Gly	Arg	Cys	Ile
	195					200					205				
Gln	Met	Trp	Phe	Asp	Ser	Ala	Gln	Gly	Asn	Pro	Asn	Glu	Glu	Val	Ala
	210					215				220					
Lys	Phe	Tyr	Ala	Ala	Ala	Met	Asn	Ala	Gly	Ala	Pro	Ser	Arg	Gly	Ile
	225				230				235					240	
Ile	Asp	Ser													

&lt;210&gt; 118

&lt;211&gt; 1362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 118

```

atggcttcac ccagcctccc gggcagtgac tgcctccaaa tcattgatca cagtcattgtc 60
cccgagtttg aggtggccac ctggatcaaa atcaccctta ttctgggtgta cctgatcatc 120
ttcgtgatgg gccttctggg gaacagcgcc accattcggg tcacccaggt gctgcagaag 180
aaaggatact tgcagaagga ggtgacagac cacatgggtga gtttggcttg ctcggacatc 240
ttgggtgttc tcatcggtcat gcccatggag ttctacagca tcatctggaa tcccctgacc 300
acgtccagct acaccctgtc ctgcaagctg cacactttcc tcttcgagggc ctgcagctac 360
gctacgctgc tgcacgtgct gacactcagc tttgagcgct acatcgocat ctgtcacccc 420
ttcaggtaca aggtgtgtgc gggaccttgc caggtgaagc tgctgattgg cttcgtctgg 480
gtcacctccg ccctgggtggc actgcccttg ctgtttgcca tgggtactga gtacccctg 540
gtgaacgtgc ccagccaccg ggtctcact tgcaaccgct ccagcaccgc ccaccacgag 600
cagcccagaga cctccaatat gtccatctgt accaacctct ccagccgctg gaccgtgttc 660
cagtcacagca tcttcggcgc cttcgtggtc tacctcgtgg tcttgccttc cgtagccttc 720
atgtgctgga acatgatgca ggtgctcatg aaaagccaga agggctcgtg ggccgggggc 780
acgcggcctc cgcagctgag gaagtccgag agcgaagaga gcaggaccgc caggaggcag 840
accatcatct tctgaggct gattgttgtg acattggccg tatgctggat gcccaaccag 900
attcggagga tcatggctgc ggccaaaccc aagcacgact ggacgaggtc ctacttccgg 960
gcgtacatga tctctctccc cttctcggag acgtttttct acctcagctc ggtcatcaac 1020
ccgtcctgtg acaagggtgtc ctgcgagcag tttcggcggg tggtcgtgca ggtgctgtgc 1080
tgccgcctgt cgctgcagca cgccaaccac gagaagcgcc tgcgcgtaca tgcgcactcc 1140
accaccgaca gcgcccgctt tgtgcagcgc ccgttgctct tcgcgtcccg gcgccagtcc 1200
tctgcaagga gaactgagaa gattttctta agcacttttc agagcgaggc cgagccccag 1260
tctaagtccc agtcattgag tctcgagtca ctagagccca actcaggcgc gaaaccagcc 1320
aattctgctg cagagaatgg ttttcaggag catgaagttt ga 1362

```

&lt;210&gt; 119

&lt;211&gt; 453

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 119

```

Met Ala Ser Pro Ser Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp
 1          5          10          15
His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr
      20          25          30
Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn
      35          40          45
Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
 50          55          60
Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile
65          70          75          80
Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
      85          90          95
Asn Pro Leu Thr Thr Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr
      100          105          110
Phe Leu Phe Glu Ala Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
      115          120          125
Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys
130          135          140
Ala Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp
145          150          155          160
Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr
      165          170          175
Glu Tyr Pro Leu Val Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn
      180          185          190
Arg Ser Ser Thr Arg His His Glu Gln Pro Glu Thr Ser Asn Met Ser
      195          200          205
Ile Cys Thr Asn Leu Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile
210          215          220
Phe Gly Ala Phe Val Val Tyr Leu Val Val Leu Leu Ser Val Ala Phe
225          230          235          240
Met Cys Trp Asn Met Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser
      245          250          255
Leu Ala Gly Gly Thr Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu
260          265          270
Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile
275          280          285
Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile
290          295          300
Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg
305          310          315          320
Ala Tyr Met Ile Leu Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser
      325          330          335
Ser Val Ile Asn Pro Leu Leu Tyr Thr Val Ser Ser Gln Gln Phe Arg
340          345          350
Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala
355          360          365
Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr Asp Ser
370          375          380
Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser
385          390          395          400
Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu
      405          410          415
Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu
420          425          430
Pro Asn Ser Gly Ala Lys Pro Ala Asn Ser Ala Ala Glu Asn Gly Phe
435          440          445

```

Gln Glu His Glu Val  
450

<210> 120  
<211> 2870  
<212> DNA  
<213> Homo sapiens

<400> 120

```
aggtcgaggg cgggcgtgag tggagcgggg gccgcggcgg cggcgagag atgtgactcg 60
ggccgaaggc cagctggagc gtcggcgctg cggggcgcg ggggtcgaat gttcgtggca 120
tcagagagaa agatgagagc tcaccagggt ctcaaccttc tcctgctctt cgtgatcacc 180
tcgggtggcct ctgaaaacgc cagcacatcc cgaggctgtg ggctggacct cctccctcag 240
tacgtgtccc tgtgcgacct ggacgccatc tggggcattg tgggtggaggc ggtggccggg 300
gcgggcgccc tgatcacact gctcctgatg ctcaatctcc tgggtcgggt gcccttcac 360
aaggagaagg agaagaagag ccctgtgggc ctccactttc tgttctcctt ggggaccttg 420
ggcctctttg ggctgacgtt tgccttcac atccaggagg acgagaccat ctgctctgtc 480
cgccgcttcc tctggggcgt cctctttgcg ctctgcttct cctgcctgct gagccaggca 540
tggcgctgac ggaggctggt gcggcatggc acgggccccg cgggctggca gctgggtggc 600
ctggcgctgt gctgatgct ggtgcaagtc atcatcgctg tggagtggct ggtgctcacc 660
gtgctgctgt acacaaggcc agcctgcgcc tacgagccca tggactttgt gatggccctc 720
atctacgaca tggtagctgt tgtggtcacc ctggggctgg cctcttcac tctgtgcggc 780
aagttcaaga ggtggaagct gaacggggcc ttctctctca tcacagcctt cctctctgtg 840
ctcatctggg tggcctggat gaccatgtac ctcttcggca atgtcaagct gcagcagggg 900
gatgcctgga acgacccac ctgggccatc acgctggcgg ccagcggtcg ggtcttcgtc 960
atcttcacag ccacccctga gatccactgc acccttctgc cagccctgca ggagaacacg 1020
cccaactact tcgacacgtc gcagcccagg atgcgggaga cggccttcga ggaggacgtg 1080
cagctgccgc gggcctatat ggagaacaag gccttctcca tggatgaaca caatgcagct 1140
ctccgaacag caggatttcc caacggcagc ttgggaaaaa gaccagtggt cagcttgggg 1200
aaaagaccca gcgtccggt tagaagcaac gtgtatcagc caactgagat ggccgtcgtg 1260
ctcaacgggt ggaccatccc aactgctccg ccaagtcaca caggaagaca cctttggtga 1320
aagactttaa gttccagaga atcagaattt ctcttaccga tttgcctccc tggctgtgtc 1380
tttcttgagg gagaaatcgg taacagttgc cgaaccaggc cgcctcacag ccaggaaatt 1440
tggaaatcct agccaagggg atttctgtga aatgtgaaca ctgacgaact gaaaagctaa 1500
caccgactgc ccgcccctcc cctgccacac acacagacac gtaataccag accaactca 1560
atcccgcgaa actaaagcaa agctaattgc aaatagtatt aggtcactg gaaaatgtg 1620
ctgggaagac tgtttcatcc tctgggggta gaacagaacc aaattcacag ctgggtggcc 1680
agactggtgt tggttggagg tggggggctc cactcttat cactctccc cagcaagtgc 1740
tggaccccag gtagcctctt ggagatgacc gttgcgttga ggacaaatgg ggactttgcc 1800
accggttgc ctggtggttt gcacatttca ggggggtcag gagagttaag gaggttgtg 1860
gtgggattcc aaggtagggc ccaactgaat cgtggggtga gctttatagc cagtagaggt 1920
ggagggaccc tggcatgtgc caaagaagag gccctctggg tgatgaagtg accatcacat 1980
ttggaaagt atcaaccact gttccttcta tggggctctt gctctaattg ctatggtgag 2040
aacacaggcc ccgccccttc cctttagtag ccatagaat attctggctt ggggcagcag 2100
tcccttcttc ccttgatcat ctgcctgt tctacactt acgggtgtat ctccaaatcc 2160
tctcccaatt ttattccctt attcatttca agagctccaa tggggtctcc agctgaaagc 2220
ccctccggga ggaggttg aaggcaggca ccacggcagg ttttccgga tgatgtcacc 2280
tagcagggtc tcagggttcc ccactaggat gcagagatga cctctcgctg cctcacaagc 2340
agtgcacct cgggtccttt ccgttgctat ggtgaaaatt cctggatgga atggatcaca 2400
tgagggtttc ttgttgcttt tggagggtgt gggggatatt ttgttttgg ttttctgcag 2460
gttccatgaa aacagccctt ttccaagccc attgtttctg tcatggtttc catctgtcct 2520
gagcaagtca ttcttttgtt atttagcatt tcgaacatct cggccattca aagcccccat 2580
gttctctgca ctgtttggcc agcataacct ctagcatcga ttcaaagcag agttttaacc 2640
tgacggcatg ataggtataa atgaggtggt gtccttctgc agatactcta atcactacat 2700
tgctttttct ataaaactac ccataagcct ttaaccttta aagaaaaatg aaaaaggtta 2760
gtgtttgggg gccgggggag gactgaccgc ttcataagcc agtacgtctg agctgagtat 2820
gtttcaataa accttttgat atttctcaaa aaaaaaaaaa aaaaaaaaaa 2870
```

```
<210> 121
<211> 403
<212> PRT
<213> Homo sapiens
```

<400> 121

Met	Phe	Val	Ala	Ser	Glu	Arg	Lys	Met	Arg	Ala	His	Gln	Val	Leu	Thr
1				5					10					15	
Phe	Leu	Leu	Leu	Phe	Val	Ile	Thr	Ser	Val	Ala	Ser	Glu	Asn	Ala	Ser
			20					25					30		
Thr	Ser	Arg	Gly	Cys	Gly	Leu	Asp	Leu	Leu	Pro	Gln	Tyr	Val	Ser	Leu
		35					40					45			
Cys	Asp	Leu	Asp	Ala	Ile	Trp	Gly	Ile	Val	Val	Glu	Ala	Val	Ala	Gly
	50					55					60				
Ala	Gly	Ala	Leu	Ile	Thr	Leu	Leu	Leu	Met	Leu	Ile	Leu	Leu	Val	Arg
65					70					75					80
Leu	Pro	Phe	Ile	Lys	Glu	Lys	Glu	Lys	Lys	Ser	Pro	Val	Gly	Leu	His
				85					90					95	
Phe	Leu	Phe	Leu	Leu	Gly	Thr	Leu	Gly	Leu	Phe	Gly	Leu	Thr	Phe	Ala
			100					105					110		
Phe	Ile	Ile	Gln	Glu	Asp	Glu	Thr	Ile	Cys	Ser	Val	Arg	Arg	Phe	Leu
		115					120					125			
Trp	Gly	Val	Leu	Phe	Ala	Leu	Cys	Phe	Ser	Cys	Leu	Leu	Ser	Gln	Ala
	130				135						140				
Trp	Arg	Val	Arg	Arg	Leu	Val	Arg	His	Gly	Thr	Gly	Pro	Ala	Gly	Trp
145					150					155					160
Gln	Leu	Val	Gly	Leu	Ala	Leu	Cys	Leu	Met	Leu	Val	Gln	Val	Ile	Ile
				165					170					175	
Ala	Val	Glu	Trp	Leu	Val	Leu	Thr	Val	Leu	Arg	Asp	Thr	Arg	Pro	Ala
			180					185					190		
Cys	Ala	Tyr	Glu	Pro	Met	Asp	Phe	Val	Met	Ala	Leu	Ile	Tyr	Asp	Met
		195					200					205			
Val	Leu	Leu	Val	Val	Thr	Leu	Gly	Leu	Ala	Leu	Phe	Thr	Leu	Cys	Gly
		210				215					220				
Lys	Phe	Lys	Arg	Trp	Lys	Leu	Asn	Gly	Ala	Phe	Leu	Leu	Ile	Thr	Ala
225					230					235					240
Phe	Leu	Ser	Val	Leu	Ile	Trp	Val	Ala	Trp	Met	Thr	Met	Tyr	Leu	Phe
				245					250					255	
Gly	Asn	Val	Lys	Leu	Gln	Gln	Gly	Asp	Ala	Trp	Asn	Asp	Pro	Thr	Leu
			260					265					270		
Ala	Ile	Thr	Leu	Ala	Ala	Ser	Gly	Trp	Val	Phe	Val	Ile	Phe	His	Ala
		275					280					285			
Ile	Pro	Glu	Ile	His	Cys	Thr	Leu	Leu	Pro	Ala	Leu	Gln	Glu	Asn	Thr
		290				295					300				
Pro	Asn	Tyr	Phe	Asp	Thr	Ser	Gln	Pro	Arg	Met	Arg	Glu	Thr	Ala	Phe
305					310					315					320
Glu	Glu	Asp	Val	Gln	Leu	Pro	Arg	Ala	Tyr	Met	Glu	Asn	Lys	Ala	Phe
				325					330					335	
Ser	Met	Asp	Glu	His	Asn	Ala	Ala	Leu	Arg	Thr	Ala	Gly	Phe	Pro	Asn
			340					345					350		
Gly	Ser</														

<210> 122  
 <211> 1474  
 <212> DNA  
 <213> Homo sapiens

<400> 122  
 ccatgctgcc ttccgggcag taccatccat ctccacaccc tggaagacac agtgagttag 60  
 caccaccacc aggtaattgg ccttatcagc tctgtgcctg tctccagtcg ggctggaata 120  
 agtctcctca tatgtgcaag ctcgccctc ccctggaatc taaagcctcc tcagccttct 180  
 gagtcagcct gaaaggaaca ggccgaactg ctgtatgggc tctactgccg gtgtgacctc 240  
 accctctcca gtcaccctc ctgagttcca gctatgagtt cctgcaactt cacacatgcc 300  
 acctgtgtgc ttattgggtat cccaggatta gagaaagccc atttctgggt tggcttcccc 360  
 ctcctttcca tgtatgtagt ggcaatgtgt ggaaactgca tctgtgtctt catcgtaagg 420  
 acggaacgca gcctgcacgc tccgatgtac ctctttctct gcatgcttgc agccattgac 480  
 ctggccttat ccacatccac catgcctaag atccttgccc ttttctgggt tgattcccga 540  
 gagattagca ttgaggcctg tcttaccagc atgttcttta ttcatgccct ctcagccatt 600  
 gaatccacca tctgtctggc catggccttt gaccgttatg tggccatctg ccaccactg 660  
 cgccatgctg cagtgtctca caatacagta acagcccaga ttggcatcgt ggctgtgggtc 720  
 cgcggtatccc tctttttttt cccactgcct ctgctgatca agcggtctggc cttctgccac 780  
 tccaatgtcc tctcgcactc ctattgtgtc caccaggatg taatgaagtt ggcctatgca 840  
 gacactttgc ccaatgtggt atatggtctt actgccattc tctgtgtcat gggcgtggac 900  
 gtaatgttca tctccttgct ctattttctg ataatacga cggttctgca actgccttcc 960  
 aagtcagagc gggccaaggc ctttggaaac tgtgtgtcac acattggtgt ggtactcgcc 1020  
 ttctatgtgc cacttattgg cctctcagtt gtacaccgct ttggaacag cttcatccc 1080  
 attgtgcgtg ttgtcatggg tgacatctac ctgctgtgct ctcctgtcat caatcccat 1140  
 atctatggtg ccaaaaccaa acagatcaga acacgggtgc tggctatggt caagatcagc 1200  
 tgtgacaagg acttgcaggc tgtgggaggc aagtgaccct taacactaca cttctcctta 1260  
 tctttattgg cttgataaac ataattattt ctaacactag cttatttcca gttgcccata 1320  
 agcacatcag tacttttctc tggctggaat agtaaactaa agtatggtac atctaccta 1380  
 aggactatta tgtggaataa tacatactaa tgaagtatta catgatttaa agactacaat 1440  
 aaaaccaaac atgcttataa cattaaaaaa aaaa 1474

<210> 123  
 <211> 320  
 <212> PRT  
 <213> Homo sapiens

<400> 123  
 Met Ser Ser Cys Asn Phe Thr His Ala Thr Cys Val Leu Ile Gly Ile  
 1 5 10 15  
 Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser  
 20 25 30  
 Met Tyr Val Val Ala Met Cys Gly Asn Cys Ile Val Val Phe Ile Val  
 35 40 45  
 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met  
 50 55 60  
 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile  
 65 70 75 80  
 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Ile Glu Ala Cys  
 85 90 95  
 Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr  
 100 105 110  
 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro  
 115 120 125  
 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly

134

130	135	140
Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu		
145	150	155
Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser		160
	165	170
Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu		175
	180	185
Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val		190
	195	200
Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val		205
	210	215
Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys		220
225	230	235
Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly		240
	245	250
Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg		255
	260	265
Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro		270
	275	280
Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala		285
	290	295
Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln Ala Val Gly Gly Lys		300
305	310	315
		320

&lt;210&gt; 124

&lt;211&gt; 2205

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 124

```

cacagggctc ccccccgcct ctgacttctc tgtccgaagt cgggacaccc tcctaccacc 60
tgtagagaag cgggagtgga tctgaaataa aatccaggaa tctggggggtt cctagacgga 120
gccagacttc ggaacgggtg tcctgctact cctgctgggg ctccctccagg acaagggcac 180
acaactgggt ccgttaagcc cctctctcgc tcagacgcca tggagctgga tctgtctcca 240
cctcatctta gcagctctcc ggaagacctt tggccagccc ctgggacccc tcctgggact 300
ccocggcccc ctgatacccc tctgcctgag gaggtaaaga ggtcccagcc tctcctcatc 360
ccaaccaccg gcaggaaact tcgagaggag gagaggcgtg ccacctccct cccctctatc 420
cccaaccctt tccctgagct ctgcagtcct ccctcacaga gcccaattct cgggggcccc 480
tccagtgaac gggggctgct ccccgcgat gccagccgcc cccatgtagt aaaggtgtac 540
agtgaggatg gggcctgcag gtctgtggag gtggcagcag gtgccacagc tcgccacgtg 600
tgtgaaatgc tgggtgcagcg agctcacgcc ttgagcgacg agacctgggg gctggtggag 660
tgccaccccc acctagcact ggagcggggt ttggaggacc acgagtcctg ggtggaagtg 720
caggctgcct ggcccggtgg cggagatagc cgcttcgtct tccggaaaaa cttcgccaag 780
tacgaactgt tcaagagctc cccacactcc ctggtccag aaaaaatggt ctccagctgt 840
ctcgatgcac acaactggtat atcccatgaa gacctcatcc agaacttcct gaatgctggc 900
agctttcctg agatccaggg ctttctgcag ctgcgggggt caggacggaa gctttggaaa 960
cgctttttct gtttcttgcg ccgatctggc ctctattact ccaccaaggg cacctctaag 1020
gatccgaggc acctgcagta cgtggcagat gtgaacagat ccaacgtgta cgtggtgacg 1080
cagggccgca agctctacgg gatgccact gacttcggtt tctgtgtcaa gcccaacaag 1140
cttcgaaatg gacacaaggg gcttcggatc ttctgcagtg aagatgagca gagccgcacc 1200
tgctggctgg ctgccttcg cctcttcaag tacggggtgc agctgtacaa gaattaccag 1260
caggcacagt cctgccatct gcatccatct tgtttggtt cccaccctt gagaagtgcc 1320
tcagataata ccctggtggc catggacttc tctggccatg ctgggcgtgt cattgagaac 1380
ccccgggagg ctctgagtgt ggccctggag gaggccagg cctggaggaa gaagacaaac 1440
caccgcctca gcctgccat gccagcctcc ggcacgagcc tcagtgcagc catccaccgc 1500
acccaactct gggtccacgg gcgcatttcc cgtgaggaga gccagcggct tattggacag 1560
cagggcttgg tagacggcct gttcctggtc cgggagagtc agcggaaacc ccagggtttt 1620

```



135

```

gtcctctctt tgtgccacct gcagaaagtg aagcattatc tcattcctgcc gagcgaggag 1680
gagggtcgcc tgtacttcag catggatgat ggccagaccc gcttactga cctgctgcag 1740
ctcgtggagt tccaccagct gaaccgcggc atcctgccgt gcttgctgcg ccattgctgc 1800
acgcggttg ccctctgacc aggccgtgga ctggctcatg cctcagcccg ccttcaggct 1860
gcccgcggcc cctccacca tccagtggac tctggggcgc ggccacaggg gacgggatga 1920
ggagcgggag ggttccgcca ctccagtttt ctctctgct tctttgcctc cctcagatag 1980
aaaacagccc cactccagt cactctctga cccctctcct caagggaagg ccttgggttg 2040
ccccctctcc ttctcctagc tctggagggtg ctgctctagg gcagggaatt atgggagaag 2100
tgggggcagc ccaggcggtt tcacgccccca cactttgtac agaccgagag gccagttgat 2160
ctgctctggt ttatactagt gacaataaaag attatttttt gatac 2205

```

&lt;210&gt; 125

&lt;211&gt; 532

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 125

```

Met Glu Leu Asp Leu Ser Pro Pro His Leu Ser Ser Ser Pro Glu Asp
1      5      10      15
Leu Trp Pro Ala Pro Gly Thr Pro Pro Gly Thr Pro Arg Pro Pro Asp
20     25     30
Thr Pro Leu Pro Glu Glu Val Lys Arg Ser Gln Pro Leu Leu Ile Pro
35     40     45
Thr Thr Gly Arg Lys Leu Arg Glu Glu Glu Arg Arg Ala Thr Ser Leu
50     55     60
Pro Ser Ile Pro Asn Pro Phe Pro Glu Leu Cys Ser Pro Pro Ser Gln
65     70     75     80
Ser Pro Ile Leu Gly Gly Pro Ser Ser Ala Arg Gly Leu Leu Pro Arg
85     90     95
Asp Ala Ser Arg Pro His Val Val Lys Val Tyr Ser Glu Asp Gly Ala
100    105    110
Cys Arg Ser Val Glu Val Ala Ala Gly Ala Thr Ala Arg His Val Cys
115    120    125
Glu Met Leu Val Gln Arg Ala His Ala Leu Ser Asp Glu Thr Trp Gly
130    135    140
Leu Val Glu Cys His Pro His Leu Ala Leu Glu Arg Gly Leu Glu Asp
145    150    155    160
His Glu Ser Val Val Glu Val Gln Ala Ala Trp Pro Val Gly Gly Asp
165    170    175
Ser Arg Phe Val Phe Arg Lys Asn Phe Ala Lys Tyr Glu Leu Phe Lys
180    185    190
Ser Ser Pro His Ser Leu Phe Pro Glu Lys Met Val Ser Ser Cys Leu
195    200    205
Asp Ala His Thr Gly Ile Ser His Glu Asp Leu Ile Gln Asn Phe Leu
210    215    220
Asn Ala Gly Ser Phe Pro Glu Ile Gln Gly Phe Leu Gln Leu Arg Gly
225    230    235    240
Ser Gly Arg Lys Leu Trp Lys Arg Phe Phe Cys Phe Leu Arg Arg Ser
245    250    255
Gly Leu Tyr Tyr Ser Thr Lys Gly Thr Ser Lys Asp Pro Arg His Leu
260    265    270
Gln Tyr Val Ala Asp Val Asn Glu Ser Asn Val Tyr Val Val Thr Gln
275    280    285
Gly Arg Lys Leu Tyr Gly Met Pro Thr Asp Phe Gly Phe Cys Val Lys
290    295    300
Pro Asn Lys Leu Arg Asn Gly His Lys Gly Leu Arg Ile Phe Cys Ser
305    310    315    320
Glu Asp Glu Gln Ser Arg Thr Cys Trp Leu Ala Ala Phe Arg Leu Phe

```

```
<210> 126
<211> 1619
<212> DNA
<213> Homo sapiens
```

<400>	126					
agttctgcg	tgccaggag	tggagcagag	ctcagcccg	tcccaaacac	agatgggacc	60
atgaactccg	gacacagctt	cagccagacc	ccctcggcct	ccttccatgg	cgccggaggt	120
ggctggggcc	ggcccaggag	cttccccagg	gtctccaccg	tccatggcgg	tgcgggggga	180
gcccgcatt	ccctgtcctt	caccacgcgg	agctgccac	cccctggagg	gtcttggggt	240
tctggaagaa	gcagccccc	actaggcgga	aatgggaagg	ccaccatgca	gaattctaac	300
gaccgcctgg	ccctcctacct	ggagaaggtt	cgcgccctgg	aggaggccaa	catgaagctg	360
gaaagccgca	tcctgaaatg	gcaccagcag	agagatcctg	gcagtaagaa	agattattcc	420
cagtatgagg	aaaacatcac	acacctgcag	gagcagatag	tggatggtaa	gatgaccaat	480
gctcagatta	ttcttctcat	tgacaatgcc	aggatggcag	tggatgactt	caacctcaag	540
tatgaaaatg	aacactcctt	taagaaagac	ttggaaattg	aagtcgaggg	cctccgaagg	600
accttagaca	acctgaccat	tgtcacaaca	gacctagaac	aggaggtgga	aggaatgagg	660
aaagagctca	ttctcatgaa	ggagcaccat	gagcaggaaa	tggaggagca	tcattgtcca	720
agtgaactta	atgtcaattg	gaaggtggat	acaggtccca	gggaagatct	gattaagggtc	780
ctggaggata	tgagaacaag	atatgcagctt	ataattaaga	agaagcatcg	agacttggac	840
acttggtata	aagaacagtc	tgcagccatg	tccaggagg	gaccagtc	agccattgtg	900
cagagcagac	aaggtgacat	ccacgaactg	aagcgcacat	tccaggccct	ggagattgac	960
ctgcaggcac	agtacagcac	gaaatctgct	ttggaaaaca	tgttatccga	gaccagtcct	1020
cggtactcct	gcaagctcca	ggacatgcaa	gagatcatct	ccactatga	ggaggaactg	1080
acgcagctac	gccacgaact	ggagcggcag	aacaatgaat	accaagtgt	gctgggcatc	1140
aaaaccacc	tggagaagaa	aatcaccacg	taccgacggc	tcctcgaggg	agagattgaa	1200
gggacacggg	agaatacaga	gtcgagcatg	aaagtgtctg	caactccaaa	gatcaaggcc	1260
ataaccgag	agaccatcaa	cggaaagatta	gttctttgtc	aagtgaatga	aatccaaaag	1320
cacgcatgag	accaatgaaa	gtttccgcct	gttgtaaagt	ctattttccc	ccaagggaaag	1380

137

tccttgacaca gacaccagtg agtgagttct aaaagataacc cttggaatta tcagactcag 1440  
 aaacttttat tttttttttt ctgtaacagt ctcaccagac ttctcataat gctcttaata 1500  
 tattgcactt ttctaataca agtgcgagtt tatgagggta aagctctact ttctactgc 1560  
 agccttcaga ttctcatcat tttgcatcta tttttagacc aataaaaactc cgcactagc 1619

&lt;210&gt; 127

&lt;211&gt; 422

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 127

Met	Asn	Ser	Gly	His	Ser	Phe	Ser	Gln	Thr	Pro	Ser	Ala	Ser	Phe	His
1				5					10					15	
Gly	Ala	Gly	Gly	Gly	Trp	Gly	Arg	Pro	Arg	Ser	Phe	Pro	Arg	Ala	Pro
		20						25					30		
Thr	Val	His	Gly	Gly	Ala	Gly	Gly	Ala	Arg	Ile	Ser	Leu	Ser	Phe	Thr
		35					40					45			
Thr	Arg	Ser	Cys	Pro	Pro	Pro	Gly	Gly	Ser	Trp	Gly	Ser	Gly	Arg	Ser
	50					55					60				
Ser	Pro	Leu	Leu	Gly	Gly	Asn	Gly	Lys	Ala	Thr	Met	Gln	Asn	Leu	Asn
65				70				75						80	
Asp	Arg	Leu	Ala	Ser	Tyr	Leu	Glu	Lys	Val	Arg	Ala	Leu	Glu	Glu	Ala
			85					90					95		
Asn	Met	Lys	Leu	Glu	Ser	Arg	Ile	Leu	Lys	Trp	His	Gln	Gln	Arg	Asp
		100						105					110		
Pro	Gly	Ser	Lys	Lys	Asp	Tyr	Ser	Gln	Tyr	Glu	Glu	Asn	Ile	Thr	His
		115						120				125			
Leu	Gln	Glu	Gln	Ile	Val	Asp	Gly	Lys	Met	Thr	Asn	Ala	Gln	Ile	Ile
	130					135					140				
Leu	Leu	Ile	Asp	Asn	Ala	Arg	Met	Ala	Val	Asp	Asp	Phe	Asn	Leu	Lys
145				150						155					160
Tyr	Glu	Asn	Glu	His	Ser	Phe	Lys	Lys	Asp	Leu	Glu	Ile	Glu	Val	Glu
			165						170					175	
Gly	Leu	Arg	Arg	Thr	Leu	Asp	Asn	Leu	Thr	Ile	Val	Thr	Thr	Asp	Leu
		180						185					190		
Glu	Gln	Glu	Val	Glu	Gly	Met	Arg	Lys	Glu	Leu	Ile	Leu	Met	Lys	Glu
		195					200					205			
His	His	Glu	Gln	Glu	Met	Glu	Glu	His	His	Val	Pro	Ser	Asp	Phe	Asn
	210					215					220				
Val	Asn	Val	Lys	Val	Asp	Thr	Gly	Pro	Arg	Glu	Asp	Leu	Ile	Lys	Val
225				230						235					240
Leu	Glu	Asp	Met	Arg	Gln	Glu	Tyr	Glu	Leu	Ile	Ile	Lys	Lys	Lys	His
			245						250					255	
Arg	Asp	Leu	Asp	Thr	Trp	Tyr	Lys	Glu	Gln	Ser	Ala	Ala	Met	Ser	Gln
		260						265					270		
Glu	Ala	Ala	Ser	Pro	Ala	Thr	Val	Gln	Ser	Arg	Gln	Gly	Asp	Ile	His
		275					280					285			
Glu	Leu	Lys	Arg	Thr	Phe	Gln	Ala	Leu	Glu	Ile	Asp	Leu	Gln	Ala	Gln
	290					295					300				
Tyr	Ser	Thr	Lys	Ser	Ala	Leu	Glu	Asn	Met	Leu	Ser	Glu	Thr	Gln	Ser
305				310						315					320
Arg	Tyr	Ser	Cys	Lys	Leu	Gln	Asp	Met	Gln	Glu	Ile	Ile	Ser	His	Tyr
			325						330					335	
Glu	Glu	Glu	Leu	Thr	Gln	Leu	Arg	His	Glu	Leu	Glu	Arg	Gln	Asn	Asn
		340						345					350		
Glu	Tyr	Gln	Val	Leu	Leu	Gly	Ile	Lys	Thr	His	Leu	Glu	Lys	Glu	Ile
	355					360						365			
Thr	Thr	Tyr	Arg	Arg	Leu	Leu	Glu	Gly	Glu	Ser	Glu	Gly	Thr	Arg	Glu

138

370	375	380
Glu Ser Lys Ser Ser Met Lys Val Ser Ala Thr	Pro Lys Ile Lys Ala	
385	390	395
Ile Thr Gln Glu Thr Ile Asn Gly Arg Leu Val	Leu Cys Gln Val Asn	
	405	410
Glu Ile Gln Lys His Ala		
420		

<210> 128  
 <211> 1359  
 <212> DNA  
 <213> Homo sapiens

<400> 128  
 ctttttggtg taaatctgga ctctaattct gtaatatatc aaggaatctc gtaaaaccga 60  
 cactaaaacg tccctgccta caaatcatcc ggccaaatta tgagttcatt gtattatgcg 120  
 aatgctttat tttctaaata tccagcctca agttcggttt tcgctaccgg agccttceca 180  
 gaacaaactt cttgtgcgtt tgctccaac cccagcgcc cgggctatgg agcgggttcg 240  
 ggcgcttcct tcgccgctc gatgcaggc ttgtaacccg gcgggggggg catggcgggc 300  
 cagagcgcg cggcggtcta cgccgcccgc tatgggctcg agccgagttc cttcaacatg 360  
 cactgcgcgc cctttgagca gaacctctcc ggggtgtgtc ccggcgactc cgccaaggcg 420  
 gcggggcgca aggagcagag ggactcggac ttggcggccg agagtaactt ccggatctac 480  
 ccctcgatgc gaagctcagg aactgaccgc aaacgaggcc gccagaccta caccgctac 540  
 cagaccctgg agctggagaa ggaatttcac tacaatcgct acctgacgcg gcggcgcgcg 600  
 atcgagatcg cgacgcgct ctgcctcacg gaaagacaga tcaagatttg gtttcagaac 660  
 cggcgcatga agtggaaaaa ggagaacaag accgcgggcc cggggaccac cgccaagac 720  
 agggctgaag cagaggagga agaggaagag tgagggatgg agaaagggca gaggaagaga 780  
 catgagaaaag ggagacgaag agaagcccag ctctgggaac tgaatcagga aactcaaatc 840  
 gaatagggaa gtaaaaaaac aaaaacaaaa acaaaaaaaa accctattta 900  
 aatgaaagga gtttaaaaaac attttttaag gagggagaaa ggagaaattt tggtttttca 960  
 aactgaaaa aatagtacct ataggaaagt ctgtcaggtt tggttttttt gtacaatatg 1020  
 aaaaggacat tatctacctg ttctgtagct ttctggaatt tacctcccct tttctatggt 1080  
 gctattgtaa ggtctttgta aaatcttgca gttttgtaag ccctctttta tgctgtcttt 1140  
 gtggactgtg ggtctggact aacctgtgg ttgcctgcc tctgtgcct ccgcttccc 1200  
 agcagcgga ccaaggggccc ttagggagcc ccaaaaccta ccaactcgct gttcccgaag 1260  
 cgccttgctg ctgctgcttg cttcccgtcc ccagcccca tgctcccttt acattctgtg 1320  
 tgtatctaaa ggatggaaaa ataaacgcga attaaaaat 1359

<210> 129  
 <211> 217  
 <212> PRT  
 <213> Homo sapiens

<400> 129  
 Met Ser Ser Leu Tyr Tyr Ala Asn Ala Leu Phe Ser Lys Tyr Pro Ala  
 1 5 10 15  
 Ser Ser Ser Val Phe Ala Thr Gly Ala Phe Pro Glu Gln Thr Ser Cys  
 20 25 30  
 Ala Phe Ala Ser Asn Pro Gln Arg Pro Gly Tyr Gly Ala Gly Ser Gly  
 35 40 45  
 Ala Ser Phe Ala Gly Ser Met Gln Gly Leu Tyr Pro Gly Gly Gly Gly  
 50 55 60  
 Met Ala Gly Gln Ser Ala Ala Gly Val Tyr Ala Ala Gly Tyr Gly Leu  
 65 70 75 80  
 Glu Pro Ser Ser Phe Asn Met His Cys Ala Pro Phe Glu Gln Asn Leu  
 85 90 95  
 Ser Gly Val Cys Pro Gly Asp Ser Ala Lys Ala Ala Gly Ala Lys Glu

139

100	105	110
Gln Arg Asp Ser Asp Leu Ala Ala Glu Ser Asn Phe Arg Ile Tyr Pro		
115	120	125
Ser Met Arg Ser Ser Gly Thr Asp Arg Lys Arg Gly Arg Gln Thr Tyr		
130	135	140
Thr Arg Tyr Gln Thr Leu Glu Leu Glu Lys Glu Phe His Tyr Asn Arg		
145	150	155
Tyr Leu Thr Arg Arg Arg Arg Ile Glu Ile Ala His Ala Leu Cys Leu		
165	170	175
Thr Glu Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp		
180	185	190
Lys Lys Glu Asn Lys Thr Ala Gly Pro Gly Thr Thr Gly Gln Asp Arg		
195	200	205
Ala Glu Ala Glu Glu Glu Glu Glu Glu		
210	215	

&lt;210&gt; 130

&lt;211&gt; 1257

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 130

```

gaggcgcgcg ggtgaaaggc gcattgatgc agcctgcggc ggcctcggag cgcgcgaggag 60
cagacgctga ccacgttcct ctccctcggc tcctccgcct ccagctccgc gctgcccggc 120
agccgggagc catgcgaccc caggcccccg ccgcctcccc gcagcggtcc cgcgcgctcc 180
tgctgctcct gctgctgcag ctgcccgcgc cgtcgagcgc ctctgagatc cccaagggga 240
agcaaaaggc gcagctccgg cagagggagg tggtagacct gtataatgga atgtgcttac 300
aagggccagc aggagtgcct ggtcgagacg ggagccctgg ggccaatggc attccgggta 360
cacctgggat ccaggtcgg gatggattca aaggagaaaa gggggaatgt ctgagggaaa 420
gctttgagga gtcctggaca cccaactaca agcagtgttc atggagttca ttgaattatg 480
gcatagatct tgggaaaatt gcggagtgtta catttacaaa gatgcgttca aatagtgttc 540
taagagtttt gttcagtggc tcacttcggc taaaatgcag aaatgcatgc tgtcagcgtt 600
ggtatttcac attcaatgga gctgaatgtt caggacctct tcccattgaa gctataattt 660
atttggaacca aggaagccct gaaatgaatt caacaattaa tattcatcgc acttcttctg 720
tggaaggact ttgtgaagga attggtgctg gattagtgtg tgttgctatc tgggttgga 780
cttggtcaga ttacccaaaa ggagatgctt ctactggatg gaattcagtt tctcgcatca 840
ttattgaaga actacccaaaa taaatgcttt aattttcatt tgctacctct ttttttatta 900
tgccttgga tggttcactt aaatgacatt ttaaataagt ttatgtatac atctgaatga 960
aaagcaaagc taaatatgtt tacagaccaa agtgtgtatt cacactgttt ttaaattctag 1020
cattattcat tttgcttcaa tcaaaagtgg tttcaatatt ttttttagtt ggtagaata 1080
ctttcttcat agtcacattc tctcaaccta taatttgaa tattgttgtg gtcttttggt 1140
ttttctctta gtatagcatt tttaaaaaaa tataaaagct accaatcttt gtacaatttg 1200
taaagtgtta gaattttttt tatatctgtt aaataaaaat tatttccaac aacctta 1257

```

&lt;210&gt; 131

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 131

Met	Gln	Pro	Ala	Ala	Ala	Ser	Glu	Arg	Gly	Gly	Ala	Asp	Ala	Asp	His
1			5						10				15		
Val	Pro	Leu	Leu	Gly	Leu	Leu	Arg	Leu	Gln	Leu	Arg	Ala	Ala	Arg	Gln
		20						25				30			
Pro	Gly	Ala	Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu
		35					40					45			
Arg	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	

140

50	55	60
Ala Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg		
65	70	75
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly		80
	85	90
Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr		95
	100	105
Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys		110
	115	120
Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys		125
	130	135
Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu		140
	145	150
Cys Thr Phe Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe		155
	160	165
Ser Gly Ser Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp		170
	175	180
Tyr Phe Thr Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu		185
	190	195
Ala Ile Ile Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile		200
	205	210
Asn Ile His Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly		215
	220	225
Ala Gly Leu Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr		230
	235	240
Pro Lys Gly Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile		245
	250	255
Ile Glu Glu Leu Pro Lys		260
	265	270
	275	

&lt;210&gt; 132

&lt;211&gt; 1177

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 132

cacgcgtccg	aatttacttt	gttggacaac	cacagctggg	gctaggaatg	gttcagaagg	60
tttaaggccg	gaaaggga	tgaagggcc	cggcgctaac	cctctaagga	cctgttttgc	120
ttctgtttta	accaaaggg	cagtctgtca	ttacacacac	cctgggtctt	catatgtggc	180
cgccagtata	atggaatgtg	cttacaaggg	ccagcaggag	tgccctggcg	agacgggagc	240
cctggggcca	atggcattcc	gggtacacct	gggatcccag	gtcgggatgg	attcaaagga	300
gaaaaggggg	aatgtctgag	ggaaagcttt	gaggagtcct	ggacacccaa	ctacaagcag	360
tggtcatgga	gttcattgaa	ttatggcata	gatcttggga	aaattgcgga	gtgtacattt	420
acaaagatgc	gttcaaatag	tgctctaaga	gttttgttca	gtggctcact	tcggctaata	480
tgacagaaatg	catgctgtca	gcgttggtat	ttcacattca	atggagctga	atgttcagga	540
cctcttccca	ttgaagctat	aatttatattg	gaccaaggaa	gccctgaaat	gaattcaaca	600
attaatatcc	atcgcaacttc	ttctgtggaa	ggactttgtg	aaggaattgg	tgctggatta	660
gtggatgttg	ctatctgggt	tggcacttgt	tcagattacc	caaaaggaga	tgcttctact	720
ggatggaatt	cagtttctcg	catcattatt	gaagaactac	caaaataaat	gctttaattt	780
tcatttgcta	cctctttttt	tattatgcct	tggaatgggt	cacttaaata	acatttttaa	840
taagtttatg	tatacatctg	aatgaaaagc	aaagctaaat	atgtttacag	accaaagtgt	900
gatttcacac	tgtttttaaa	tctagcatta	ttcattttgc	ttcaatcaaa	agtggtttca	960
atattttttt	tagttgggta	gaatactttc	ttcatagtca	cattctctca	acctataatt	1020
tggaatattg	ttgtgggtctt	ttgttttttc	tcttagtata	gcatttttaa	aaaaataata	1080
aagctaccaa	tccttggtaca	atttgtaaat	gttaagaatt	ttttttatat	ctgttaataa	1140
aaaattattt	ccaacaaccw	waaaaaaaaa	aaaaagg			1177

141

<210> 133  
 <211> 210  
 <212> PRT  
 <213> Homo sapiens

<400> 133

```

Met Gly Ser Leu Ser Leu His Thr Pro Trp Val Phe Ile Cys Gly Arg
 1           5           10           15
Gln Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val Pro Gly Arg
      20           25           30
Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr Pro Gly Ile Pro
      35           40           45
Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu Arg Glu Ser
      50           55           60
Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser Trp Ser Ser
      65           70           75           80
Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys Thr Phe Thr
      85           90           95
Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser Gly Ser Leu
      100          105          110
Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe
      115          120          125
Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr
      130          135          140
Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg
      145          150          155          160
Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val
      165          170          175
Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
      180          185          190
Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu Leu
      195          200          205
Pro Lys
      210

```

<210> 134  
 <211> 1340  
 <212> DNA  
 <213> Homo sapiens

<400> 134

```

agggagtcga cccacgcgtc cggaagctcc ggggtgtcgcg ggggcgggag gaattaaggg 60
agggagagag gcgcgcgggt gaaaggcgca ttgatgcagc ctgcggcggc ctcgagcgc 120
ggcggagcca gacgctgacc acgttcctct cctcgggtctc ctccgcctcc agctccgcgc 180
tgcccggcag ccgggagcca tgcgaccca gggccccgcc gcctccccgc agcggctccg 240
cggcctcctg ctgctcctgc tgctgcagct gccgcgcgcg tcgagcgccct ctgagatccc 300
caaggggaag caaaaggcgc agctccggca gagggaggtg gtggacctgt ataatggaat 360
gtgcttacaa gggccagcag gaggtcctgg tcgagacggg agccctgggg ccaatggcat 420
tccgggtaca cctgggatcc caggtcggga tggattcaaa ggagaaaagg gggatgtct 480
gagggaaagc tttgaggagt cctggacacc caactacaag cagtgttcatt ggagttcatt 540
gaattatggc atagatcttg ggaaaattgc ggagtgtaca ttacaaaaga tgcgttcaaa 600
tagtgctcta agagttttgt tcagtggctc acttcggcta aaatgcagaa atgcatgctg 660
tcagcgttgg tatttcacat tcaatggagc tgaatgttca ggacctcttc ccattgaagc 720
tataatttat ttggaccaag gaagccctga aatgaattca acaattaata ttcacgcac 780
ttcttctgtg gaaggacttt gtgaagggaat tggtgctgga ttagtggatg ttgctatctg 840
ggttggcact tggtcagatt acccaaaagg agatgcttct actggatgga attcagtttc 900
tcgcatcatt attgaagaac taccaaaaata aatgctttaa ttttcatttg ctacctcttt 960

```

```

ttttattatg ccttggaatg gttcacttaa atgacatttt aaataagttt atgtatacat 1020
ctgaatgaaa agcaaagcta aatatgttta cagaccaaag tgtgatttca cactgttttt 1080
aaatctagca ttattcattt tgcttcaatc aaaagtgggt tcaatatttt ttttagttgg 1140
ttagaataact ttcttcatag tcacattctc tcaacctata atttggaata ttgttggtgg 1200
cttttgtttt ttcttctagt atagcatttt taaaaaata taaaagctac caatctttgt 1260
acaatttgta aatgttaaga atttttttta tatctgttaa ataaaaatta tttccaacaa 1320
ccwwaaaaaa aaaaaaaagg                                     1340

```

&lt;210&gt; 135

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 135

```

Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly Leu
 1          5          10          15
Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala Ser Glu
      20          25          30
Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg Glu Val Val
      35          40          45
Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala Gly Val Pro Gly
      50          55          60
Arg Asp Gly Ser Pro Gly Ala Asn Gly Ile Pro Gly Thr Pro Gly Ile
      65          70          75          80
Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys Gly Glu Cys Leu Arg Glu
      85          90          95
Ser Phe Glu Glu Ser Trp Thr Pro Asn Tyr Lys Gln Cys Ser Trp Ser
      100          105          110
Ser Leu Asn Tyr Gly Ile Asp Leu Gly Lys Ile Ala Glu Cys Thr Phe
      115          120          125
Thr Lys Met Arg Ser Asn Ser Ala Leu Arg Val Leu Phe Ser Gly Ser
      130          135          140
Leu Arg Leu Lys Cys Arg Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr
      145          150          155          160
Phe Asn Gly Ala Glu Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile
      165          170          175
Tyr Leu Asp Gln Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His
      180          185          190
Arg Thr Ser Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu
      195          200          205
Val Asp Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly
      210          215          220
Asp Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
      225          230          235          240
Leu Pro Lys

```

&lt;210&gt; 136

&lt;211&gt; 5519

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 136

```

aagtactgac tgttcaaagc tcaggcaaac catgcagatc cacgtgttgt tggaggaggc 60
gctcccttca ggagaccaca gagggggagt gactgtggct gaccatgtgg gcagaggggc 120
tggggggctg gccctgcga gaggcggact cagggctgct ggatgctccg tccttgccg 180
ctttgatctg gagccacgtg tcaccagag ctttgcaaa gtggtcgtcc acggagccc 240

```



tgatggacac	ggagttgggt	gccggctcgg	gctccttgta	attcttgccc	aggctcctgc	300
ggaaatgctc	ctccaccacg	gggtcacagg	tggtggcagc	gctcgggtggc	ctccggtagc	360
tggcaggccc	ggcgcgcgcc	tcgtgccgaa	ttcggcacga	gggggtttcg	gcggccggga	420
gggagttgtc	ggcgcccgcg	ccgctgcgga	cgacgcctcg	cctgccggct	gaggaaaaag	480
aagcaactaa	caaaacactg	tgataataag	gattattcag	tatgcagttt	gcaggatata	540
catgacgaca	ttgaaaatga	atTTTTTgtA	ttcaccagat	attcttatata	gagaagatct	600
atTTTaaaca	gtctaaatat	TTTTTcttct	gttggaccag	catggcagga	TTTaaagcag	660
ggtatgatgg	aaagattgct	ggattatatg	atctggataa	aaccttgggt	cgaggccatt	720
ttgccgtggt	taaacttgcc	aggcatgtct	ttacgggtga	aaaggtggca	gtaaaagtta	780
ttgacaagac	aaaactggac	actctagcta	ctggtcatct	ttccaggaa	gtgagatgca	840
tgaaactagt	gcagcatcct	aacatcgctc	gcTTTTatga	agttattgac	accagacca	900
aactatatct	tattctagaa	cttggggatg	aaggagatat	gtttgattat	ataatgaaac	960
atgaggaggg	tcttaatgaa	gacttgccca	agaagtattt	tgctcagata	gttcatgcta	1020
tatcttattg	ccataaactc	catgtggttc	acagagactt	aaaaccagag	aatgtagtct	1080
tctttgaaaa	acaaggtctt	gtaaagttga	cagactttgg	gttcagcaac	aaatttcaac	1140
cagggaagaa	gctcactaca	agctgtggat	ctcttgcata	ttccgctcca	gaaattctgc	1200
ttggtgatga	gtatgatgca	cctgcagtag	atatttggag	tctgggagtg	atccttttca	1260
tggttggtgtg	tgggcagccg	ccctttcaag	aagccaatga	cagtgaagaa	ctgacaatga	1320
tcatggtattg	caaataatac	gtaccatccc	atgtgtctaa	agagtgtaaa	gacctaatca	1380
cacggatgct	acagagagat	cccaagagaa	gggcttcttt	agaagagatt	gaaaatcctc	1440
cttggcttca	gggaagtggac	ccttcaccag	ctacaaaagta	taacattccc	cttgtgtcat	1500
acaaaaatct	ctcggaagag	gagcacaaca	gcattcattca	gcgcattggtg	cttggggaca	1560
tagcggatcg	agacgccatt	gtagaagccc	tggaaccaa	caggtataac	catatcacag	1620
ccacatactt	cctgctggct	gaaaggatcc	tgagagaaaa	gcaagagaaa	gaaatacaga	1680
ccagatctgc	aagcccagag	aatatcaagg	cccagtttag	gcagtcattgg	ccaacccaaa	1740
ttgatgtacc	ccaggacctt	gaggatgacc	tcacggccac	tcctttgtcc	cacgcgactg	1800
tccctcagtc	tcctgctcgg	gctgctgaca	gtgtcctcaa	tggccacagg	agcaaaggcc	1860
tggtgactc	agctaagaaa	gatgacctcc	ctgagttggc	tgaccagca	ctctctacgg	1920
tgccacccgc	aagcttaaaa	cccacagcca	gtggcgga	gtgtctgttc	aggggtggaag	1980
aagatgaaga	ggaagatgag	gaggacaaga	aacctatgtc	cctctcaaca	caagtggttt	2040
tgcccgga	gccatctgta	accaaccgcc	tgacatccag	gaagagtgcg	cccgtcctca	2100
accagatctt	tgagggaagg	gaatctgatg	atgagtttga	catggatgag	aatctgcctc	2160
ccaagttgag	caggttaaag	atgaatatag	cttctccagg	tacagttcac	aaacgctacc	2220
accggaggaa	aagtcagggc	cggggctcca	gctgcagtag	ttcggagacc	agtgatgatg	2280
attctgaaag	ccggcgcgcg	ctcgataaag	atagcgggtt	cacctactcc	tggcaccgac	2340
gggtagcag	cgaggggccc	cctggcagtg	agggggatgg	cgggggccag	agcaagccga	2400
gcaatgcag	tggaggggtg	gacaaggcca	gccccagtga	gaacaatgct	ggtgggggca	2460
gtccctccag	cgctcggggt	ggcaacccta	ccaatacatc	gggtaccaca	cgccgctgtg	2520
ccggccccag	caactccatg	cagctggcct	ctcgcagtcg	tggggagctc	gttgagagcc	2580
tcaaactcat	gagcctctgc	ctcggtccc	agcttcatgg	gagcaccaag	tacattattg	2640
atccacagaa	tggcttgtca	ttttccagtg	tgaaagtcct	agagaaatct	acgtggaaaa	2700
tgtgcattag	ctccacaggg	aatgcagggc	aggtccctgc	agtggcgggc	ataaagtttt	2760
tctctgacca	catggcagat	accaccactg	aattggaacg	gataaagagc	aagaacctga	2820
aaaataacgt	gctgcagcta	cctctgtgcg	aaaagaccat	ctctgtgaac	atccagcgga	2880
accctaagga	gggctgctg	tgcgcatcca	gcccagccag	ctgttgccat	gtcatctgac	2940
tgtggcccca	tctggcgctg	agcacgcttc	ctgctcagag	cagtgaagac	cggctcactt	3000
cactgttcca	tttggtttta	ctattttaaa	gtggcggtta	ggagcaatta	tttattacct	3060
ttccatttgt	tcgcctgatg	atgtgacaat	gcattggtctt	tgtgcattgct	gctagacact	3120
tttctttccc	agccgaaaag	cctattatgt	aattttttaca	ttcataattt	taatgtggat	3180
gatcaggatt	aaatcaagat	atatatctgg	aacctcttat	aaatggagca	cttagaaatt	3240
tgttgttctg	cacttaacct	agagagagaa	aaaatgcttt	tctttgtgaa	aaatctgaat	3300
tcctgtcctg	accttctgtg	atgtggaac	cctaggctct	gagacacact	ctctggtgtc	3360
tgagacagaa	ccaaagcaat	aacgttgtga	tgcccacagg	cctggagcca	gctagcgacc	3420
ttgtgccgcc	cagctgtcca	tgcccctgac	agagcagagg	acagtgagtg	tctgactga	3480
gaaccttaaa	ccacagttga	acataccac	acctgtttgt	cttaagctat	agtgtaaaaa	3540
caaagtgttg	gctctgaaaa	tttaactgaa	aaagatttcc	ttgtttttgt	aatagtgag	3600
ataaagtact	tagatttata	aggcagcttc	ccctgtagt	ataaattaca	agcagacaat	3660
cttattttgt	aatgtgatga	agtgatgatg	tcttaactct	acttagagag	tgtatgtctg	3720

```

tctaacagaa caaaaagatg ctctgtgtaa attccttccct gtagggcaca ctgcaggatt 3780
tccatgtaga tagaagaact atagggccta gtacagaagg tgcacacaaa tggtggcaaa 3840
gtcaaacccc atgaattaaa acctactgga atttggtttt taggagtttg gtaattagat 3900
tatctctttt gttattttca ttcagttata tcctttggct cagctagctt tgaaattggc 3960
tgatgaaaaa atatacataa aagggtaaaa ttcacacata cagcaaaaaa aaatgcacaa 4020
agcctgcttc gtaacttttt tttctggaat tgtttttcac tttgcctttt tctgccaaaa 4080
caataatcaa agaactcttg ctttaaccta ttctgtgaca aagactgttt ttgaccagat 4140
aatcatctgt tgtggcattc tatctttag gacactgtat attgcaaatt gctgattatg 4200
gaaggggcca gttgctgttt tttcatgcag tgccctggga gtcttaaaag cagtgccttag 4260
caacattggt gatagcatgt ggctgggacc caggggccctt cccactctt cagccccgag 4320
tcatgtgtct gaggtgacgg actgagacgc atctggtcct gtaattcaga gagtgggcac 4380
atcaccaaag aactgcattg ctgtggtcac tgtttcttca agtacacact gactctgcta 4440
ctttaggata aatatatttt actcagaact ctgaatttca cagtatactt actaaactaa 4500
gtaaaaatga tacttaaaat acttatttta ctttctagac ctaggctaga tgttttaagc 4560
tacagctcta gttcattgtg atatttataa tttgaaagct atgagaatag atgtgtgggt 4620
gaagccatag aacatatttg cttgaaattc ttgagcaggg atcttataaa gggccagaaa 4680
taagatgtgt ggttcacata gatagtgagc gtaacatctg tattaacat aggagagaag 4740
tttataaagg gcattggcaa taaactcttt gttgcagctg tttccaagc agtgtaaata 4800
ctttttcctg tgattatgta tagccttgga atggcacctt ttaactaacc catatgtgtt 4860
tggtttcaat ggttttttat attcagatgt atatatgtg ctcactttag gatcagcagt 4920
gttgaccatt tatgctgcat agctgtatta tagccttatt agttgtgtgg ttgacccttg 4980
gggtatacaa atgtcagctc gagtgggtgc ttactcctt gtttataagt gaatgattgt 5040
gcatgttttg tatgtcatag tatgtcgtca cataaaaggg agggagcgaa aaaccattac 5100
attaagataa tattggacca aactacttac ttgctctaaa cagtacttg tacccttaa 5160
cctgtcttca aaagtgtcat atagttacag tagtgtataa attaaatatt gtggaaaaac 5220
agtcttgtat tttctgtat gtgtgtatat atatataatt atgtacttct ggcaattcta 5280
tctgtattta aagatgtgac aatcttgaca ccaattttta gaatagctgt gagaccgaat 5340
taaagataat ccctaccaag tgaaaattga tgtgtgttaa gaggttacag aattatcaac 5400
tgatttggtc agttgcttcc aatgctggtt gatttcctc atttgttaaa cattgacagg 5460
tatgtgacaa atgggaaaaa aaatccaaat aataaagtga catattggtg ttcagcaat 5519

```

&lt;210&gt; 137

&lt;211&gt; 765

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

```

Met Ala Gly Phe Lys Arg Gly Tyr Asp Gly Lys Ile Ala Gly Leu Tyr
 1          5          10          15
Asp Leu Asp Lys Thr Leu Gly Arg Gly His Phe Ala Val Val Lys Leu
 20          25          30
Ala Arg His Val Phe Thr Gly Glu Lys Val Ala Val Lys Val Ile Asp
 35          40          45
Lys Thr Lys Leu Asp Thr Leu Ala Thr Gly His Leu Phe Gln Glu Val
 50          55          60
Arg Cys Met Lys Leu Val Gln His Pro Asn Ile Val Arg Leu Tyr Glu
 65          70          75          80
Val Ile Asp Thr Gln Thr Lys Leu Tyr Leu Ile Leu Glu Leu Gly Asp
 85          90          95
Glu Gly Asp Met Phe Asp Tyr Ile Met Lys His Glu Glu Gly Leu Asn
100          105          110
Glu Asp Leu Pro Lys Lys Tyr Phe Ala Gln Ile Val His Ala Ile Ser
115          120          125
Tyr Cys His Lys Leu His Val His Arg Asp Leu Lys Pro Glu Asn
130          135          140
Val Val Phe Phe Glu Lys Gln Gly Leu Val Lys Leu Thr Asp Phe Gly
145          150          155          160
Phe Ser Asn Lys Phe Gln Pro Gly Lys Lys Leu Thr Thr Ser Cys Gly

```

145

				165					170					175	
Ser	Leu	Ala	Tyr	Ser	Ala	Pro	Glu	Ile	Leu	Leu	Gly	Asp	Glu	Tyr	Asp
			180						185					190	
Ala	Pro	Ala	Val	Asp	Ile	Trp	Ser	Leu	Gly	Val	Ile	Leu	Phe	Met	Leu
		195					200					205			
Val	Cys	Gly	Gln	Pro	Pro	Phe	Gln	Glu	Ala	Asn	Asp	Ser	Glu	Thr	Leu
	210					215					220				
Thr	Met	Ile	Met	Asp	Cys	Lys	Tyr	Thr	Val	Pro	Ser	His	Val	Ser	Lys
225				230						235					240
Glu	Cys	Lys	Asp	Leu	Ile	Thr	Arg	Met	Leu	Gln	Arg	Asp	Pro	Lys	Arg
			245						250					255	
Arg	Ala	Ser	Leu	Glu	Glu	Ile	Glu	Asn	His	Pro	Trp	Leu	Gln	Gly	Val
	260							265					270		
Asp	Pro	Ser	Pro	Ala	Thr	Lys	Tyr	Asn	Ile	Pro	Leu	Val	Ser	Tyr	Lys
	275						280					285			
Asn	Leu	Ser	Glu	Glu	Glu	His	Asn	Ser	Ile	Ile	Gln	Arg	Met	Val	Leu
	290					295					300				
Gly	Asp	Ile	Ala	Asp	Arg	Asp	Ala	Ile	Val	Glu	Ala	Leu	Glu	Thr	Asn
305				310						315					320
Arg	Tyr	Asn	His	Ile	Thr	Ala	Thr	Tyr	Phe	Leu	Leu	Ala	Glu	Arg	Ile
			325						330					335	
Leu	Arg	Glu	Lys	Gln	Glu	Lys	Glu	Ile	Gln	Thr	Arg	Ser	Ala	Ser	Pro
	340						345						350		
Ser	Asn	Ile	Lys	Ala	Gln	Phe	Arg	Gln	Ser	Trp	Pro	Thr	Lys	Ile	Asp
	355					360						365			
Val	Pro	Gln	Asp	Leu	Glu	Asp	Leu	Thr	Ala	Thr	Pro	Leu	Ser	His	
	370					375					380				
Ala	Thr	Val	Pro	Gln	Ser	Pro	Ala	Arg	Ala	Ala	Asp	Ser	Val	Leu	Asn
385				390						395					400
Gly	His	Arg	Ser	Lys	Gly	Leu	Cys	Asp	Ser	Ala	Lys	Lys	Asp	Asp	Leu
			405						410					415	
Pro	Glu	Leu	Ala	Gly	Pro	Ala	Leu	Ser	Thr	Val	Pro	Pro	Ala	Ser	Leu
	420							425					430		
Lys	Pro	Thr	Ala	Ser	Gly	Arg	Lys	Cys	Leu	Phe	Arg	Val	Glu	Glu	Asp
	435					440						445			
Glu	Glu	Glu	Asp	Glu	Glu	Asp	Lys	Lys	Pro	Met	Ser	Leu	Ser	Thr	Gln
	450					455					460				
Val	Val	Leu	Arg	Arg	Lys	Pro	Ser	Val	Thr	Asn	Arg	Leu	Thr	Ser	Arg
465				470						475					480
Lys	Ser	Ala	Pro	Val	Leu	Asn	Gln	Ile	Phe	Glu	Glu	Gly	Glu	Ser	Asp
			485						490					495	
Asp	Glu	Phe	Asp	Met	Asp	Glu	Asn	Leu	Pro	Pro	Lys	Leu	Ser	Arg	Leu
	500							505					510		
Lys	Met	Asn	Ile	Ala	Ser	Pro	Gly	Thr	Val	His	Lys	Arg	Tyr	His	Arg
	515						520					525			
Arg	Lys	Ser	Gln	Gly	Arg	Gly	Ser	Ser	Cys	Ser	Ser	Ser	Glu	Thr	Ser
	530					535					540				
Asp	Asp	Asp	Ser	Glu	Ser	Arg	Arg	Arg	Leu	Asp	Lys	Asp	Ser	Gly	Phe
545				550						555					560
Thr	Tyr	Ser	Trp	His	Arg	Arg	Asp	Ser	Ser	Glu	Gly	Pro	Pro	Gly	Ser
			565						570					575	
Glu	Gly	Asp	Gly	Gly	Gly	Gln	Ser	Lys	Pro	Ser	Asn	Ala	Ser	Gly	Gly
	580							585					590		
Val	Asp	Lys	Ala	Ser	Pro	Ser	Glu	Asn	Asn	Ala	Gly	Gly	Gly	Ser	Pro
	595						600					605			
Ser	Ser	Gly	Ser	Gly	Gly	Asn	Pro	Thr	Asn	Thr	Ser	Gly	Thr	Thr	Arg
	610					615					620				
Arg	Cys	Ala	Gly	Pro	Ser	Asn	Ser	Met	Gln	Leu	Ala	Ser	Arg	Ser	Ala

146

625		630		635		640									
Gly	Glu	Leu	Val	Glu	Ser	Leu	Lys	Leu	Met	Ser	Leu	Cys	Leu	Gly	Ser
		645		650		655									
Gln	Leu	His	Gly	Ser	Thr	Lys	Tyr	Ile	Ile	Asp	Pro	Gln	Asn	Gly	Leu
		660		665		670									
Ser	Phe	Ser	Ser	Val	Lys	Val	Gln	Glu	Lys	Ser	Thr	Trp	Lys	Met	Cys
		675		680		685									
Ile	Ser	Ser	Thr	Gly	Asn	Ala	Gly	Gln	Val	Pro	Ala	Val	Gly	Gly	Ile
		690		695		700									
Lys	Phe	Phe	Ser	Asp	His	Met	Ala	Asp	Thr	Thr	Thr	Glu	Leu	Glu	Arg
705				710				715							720
Ile	Lys	Ser	Lys	Asn	Leu	Lys	Asn	Asn	Val	Leu	Gln	Leu	Pro	Leu	Cys
			725					730							735
Glu	Lys	Thr	Ile	Ser	Val	Asn	Ile	Gln	Arg	Asn	Pro	Lys	Glu	Gly	Leu
			740					745					750		
Leu	Cys	Ala	Ser	Ser	Pro	Ala	Ser	Cys	Cys	His	Val	Ile			
		755					760					765			

&lt;210&gt; 138

&lt;211&gt; 2029

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 138

gagaagagag	tcgaggacct	ccatgtaggt	gccacggtgg	ccccagcag	cagaagggac	60
tttacctttg	acctctacag	ggccttggt	tccgctgccc	ccagccagaa	catcttcttc	120
tcccctgtga	gcatctccat	gagcctggcc	atgctctccc	tgggggctgg	gtccagcaca	180
aagatgcaga	tcctggaggg	cctgggcctc	aacctccaga	aaagctcaga	gaaggagctg	240
cacagaggct	ttcagcagct	ccttcaggaa	ctcaaccagc	ccagagatgg	cttcagctg	300
agcctcggca	atgccctttt	caccgacctg	gtggtagacc	tgcaggacac	cttcgtaagt	360
gccatgaaga	cgctgtacct	ggcagacact	ttccccacca	actttaggga	ctctgcaggg	420
gccatgaagc	agatcaatga	ttatgtggca	aagcaaacga	agggcaagat	tgtggacttg	480
cttaagaacc	tcgatagcaa	tgcggtcgtg	atcatggtga	attacatctt	ctttaaagct	540
aagtgggaga	caagcttcaa	ccacaaaggc	acccaagagc	aagacttcta	cgtgacctcg	600
gagactgtgg	tgcggttacc	catgatgagc	cgcgaggatc	agtatcacta	cctcctggac	660
cggaacctct	cctgcagggt	ggtgggggtc	ccctaccaag	gcaatgccac	ggctttgttc	720
atttctccca	gtgagggaaa	gatgcagcag	gtggagaatg	gactgagtga	gaaaacgctg	780
aggaagtggc	ttaagatgtt	caaaaagagg	cagctcgagc	tttaccttcc	caaattctcc	840
attgagggct	cctatcagct	ggagaaagtc	ctccccagtc	tggggatcag	taacgtcttc	900
acctcccatg	ctgatctgtc	cggcatcagc	aaccactcaa	atatccaggt	gtctgagatg	960
gtgcacaaag	ctgtggtgga	ggtggacgag	tcgggaacca	gagcagcggc	agccacgggg	1020
acaatcttca	ctttcaggtc	ggcccgcctg	aactctcaga	ggctagtgtt	caacaggccc	1080
tttctgatgt	tcattgtgga	taacaacatc	ctcttccttg	gcaaagtga	ccgcccctga	1140
ggtggggctt	ctcctgaaat	ctacaggcct	cagggtggga	gatgaagggg	gctatgctat	1200
ggcccatctg	tatgctggta	gctagtgatt	tacacagggt	tagttgacta	atgaggcatt	1260
acaaataata	ttactctatg	atgattgctt	ccaccacac	gactgcaaca	tacagggtgcc	1320
ttggggaaat	gtggagaaca	ttcaatcttg	ccgtcactat	tcatcaatga	agattagcac	1380
tgagatccag	agaggctgga	tgacttgctc	aagttcacca	gcatggtagt	ggcaaagaga	1440
ggtccagagt	cctggccctt	gatgccagc	tcagtgccac	aaagctcagt	aggagggatg	1500
ttccagtgga	tgagggccac	cagggaagc	aggtccaagg	ctgggtccac	acttatcagc	1560
agcaacaact	gtcagttcat	cctgcattgg	aaaaatgttg	gaatgggagt	ctgaaatggg	1620
gctactgttt	cagtcctaac	gtgctgtgtg	acattggggc	aacactttcc	ctctctggac	1680
ctcagtttcc	ctctgtatag	aaggatcaga	ttcttgctgt	gaccaagaa	ctcctgaaat	1740
catatagaaa	ggctgggggtg	ggccctgtca	ttcgtgggtg	atttcaatac	actcaagtgc	1800
cattcatcct	ttagaataaa	catctggata	tcaagggtga	aatggcccat	ttaatgattg	1860
attatatcat	tttgtggata	tagttataat	ctgatgggcc	tggctgggag	tggaagaagg	1920
gaagcctttt	gcaaatagta	gagtgtcagt	tgcagggtgcc	aatgactaac	tttttgaatt	1980

ctatgttggc attaacaata aagcattttg caaacactga aaaaaaaaaa

2029

&lt;210&gt; 139

&lt;211&gt; 379

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 139

Glu	Lys	Arg	Val	Glu	Asp	Leu	His	Val	Gly	Ala	Thr	Val	Ala	Pro	Ser
1				5					10					15	
Ser	Arg	Arg	Asp	Phe	Thr	Phe	Asp	Leu	Tyr	Arg	Ala	Leu	Ala	Ser	Ala
			20					25					30		
Ala	Pro	Ser	Gln	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Ile	Ser	Met	Ser
		35					40					45			
Leu	Ala	Met	Leu	Ser	Leu	Gly	Ala	Gly	Ser	Ser	Thr	Lys	Met	Gln	Ile
		50				55					60				
Leu	Glu	Gly	Leu	Gly	Leu	Asn	Leu	Gln	Lys	Ser	Ser	Glu	Lys	Glu	Leu
65					70				75					80	
His	Arg	Gly	Phe	Gln	Gln	Leu	Leu	Gln	Glu	Leu	Asn	Gln	Pro	Arg	Asp
				85					90					95	
Gly	Phe	Gln	Leu	Ser	Leu	Gly	Asn	Ala	Leu	Phe	Thr	Asp	Leu	Val	Val
			100					105					110		
Asp	Leu	Gln	Asp	Thr	Phe	Val	Ser	Ala	Met	Lys	Thr	Leu	Tyr	Leu	Ala
		115						120				125			
Asp	Thr	Phe	Pro	Thr	Asn	Phe	Arg	Asp	Ser	Ala	Gly	Ala	Met	Lys	Gln
		130				135					140				
Ile	Asn	Asp	Tyr	Val	Ala	Lys	Gln	Thr	Lys	Gly	Lys	Ile	Val	Asp	Leu
145					150					155					160
Leu	Lys	Asn	Leu	Asp	Ser	Asn	Ala	Val	Val	Ile	Met	Val	Asn	Tyr	Ile
			165						170					175	
Phe	Phe	Lys	Ala	Lys	Trp	Glu	Thr	Ser	Phe	Asn	His	Lys	Gly	Thr	Gln
			180					185					190		
Glu	Gln	Asp	Phe	Tyr	Val	Thr	Ser	Glu	Thr	Val	Val	Arg	Val	Pro	Met
		195						200				205			
Met	Ser	Arg	Glu	Asp	Gln	Tyr	His	Tyr	Leu	Leu	Asp	Arg	Asn	Leu	Ser
		210				215					220				
Cys	Arg	Val	Val	Gly	Val	Pro	Tyr	Gln	Gly	Asn	Ala	Thr	Ala	Leu	Phe
225					230					235					240
Ile	Leu	Pro	Ser	Glu	Gly	Lys	Met	Gln	Gln	Val	Glu	Asn	Gly	Leu	Ser
			245						250					255	
Glu	Lys	Thr	Leu	Arg	Lys	Trp	Leu	Lys	Met	Phe	Lys	Lys	Arg	Gln	Leu
			260					265					270		
Glu	Leu	Tyr	Leu	Pro	Lys	Phe	Ser	Ile	Glu	Gly	Ser	Tyr	Gln	Leu	Glu
		275					280					285			
Lys	Val	Leu	Pro	Ser	Leu	Gly	Ile	Ser	Asn	Val	Phe	Thr	Ser	His	Ala
		290					295				300				
Asp	Leu	Ser	Gly	Ile	Ser	Asn	His	Ser	Asn	Ile	Gln	Val	Ser	Glu	Met
305					310					315					320
Val	His	Lys	Ala	Val	Val	Glu	Val	Asp	Glu	Ser	Gly	Thr	Arg	Ala	Ala
			325						330					335	
Ala	Ala	Thr	Gly	Thr	Ile	Phe	Thr	Phe	Arg	Ser	Ala	Arg	Leu	Asn	Ser
			340					345					350		
Gln	Arg	Leu	Val	Phe	Asn	Arg	Pro	Phe	Leu	Met	Phe	Ile	Val	Asp	Asn
		355					360					365			
Asn	Ile	Leu	Phe	Leu	Gly	Lys	Val	Asn	Arg	Pro					
							375								

148

<210> 140  
 <211> 2058  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 140

```

gcacgaggaa gccacagatc tcttaagaac tttctgtctc caaacctgtg ctgctcgata 60
aatcagacag aacagttaat cctcaattta agcctgatct aacccttaga aacagatata 120
gaacaatgga agtgacaaca agattgacat ggaatgatga aaatcatctg cgcaactgct 180
tggaatggtt tctttgagtc ttctctataa gtctagtgtt catggaggta gcattgaaga 240
tatgggttgaa agatgcagcc gtcagggatg tactataaca atggcttaca ttgattacaa 300
tatgattgta gcctttatgc ttggaaatta tattaattta cgtgaaagtt ctacagagcc 360
aaatgattcc ctatggtttt cacttcaaaa gaaaaatgac accactgaaa tagaaacttt 420
actcttaaatt acagcaccaa aaattattga tgagcaactg gtgtgtcgtt tatcgaaaac 480
ggatattttt attatatgtc gagataataa aatttatcta gataaaatga taacaagaaa 540
cttgaaacta aggttttatg gccaccgtca gtatttggaa tgtgaagttt ttcgagttga 600
aggaattaag gataacctag acgacataaa gaggataatt aaagccagag agcacagaaa 660
taggcttcta gcagacatca gagactatag gccctatgca gacttgggtt cagaaattcg 720
tattcttttg gtgggtccag ttgggtctgg aaagtccagt tttttcaatt cagtcaagtc 780
tatttttcat ggcctatgtg ctggccaagc cgtagtgggg tctgatacca ccagcataac 840
cgagcgggtat ggcatatatt ctgttaaaaga tggaaaaaat ggaaaatctc tgccatttat 900
gttgtgtgac actatggggc tagatggggc agaaggagca ggactgtgca tggatgacat 960
tccccacatc ttaaaagggt gtatgccaga cagatatcag tttaattccc gtaaaccaat 1020
tacacctgag cattctactt ttatcacctc tccatctctg aaggacagga ttcactgtgt 1080
ggcttatgtc ttagacatca actctattga caatctctac tctaaaatgt tggcaaaagt 1140
gaagcaagtt cacaagaag tattaaactg tggatatgca tatgtggcct tgcttactaa 1200
agtggatgat tgcagtgagg ttcttcaaga caacttttta aacatgagta gatctatgac 1260
ttctcaaagc cgggtcatga atgtccataa aatgctaggc attcctattt ccaatatttt 1320
gatggttgga aattatgctt cagatttggg actggacccc atgaaggata ttctcatcct 1380
ctctgcactg aggcagatgc tgcgggctgc agatgatttt ttagaagatt tgcctcttga 1440
ggaaactggt gcaattgaga ggcgttaca gccctgcatt tgagataagt tgccttgatt 1500
ctgacatttg gccagcctg tactggtgtg ccgcaatgag agtcaatctc tattgacagc 1560
ctgcttcaga ttttgctttt gtctgttttg ccttctgtcc ttggaacagt catatctcaa 1620
gttcaaaggc caaacctga gaagcgggtg gctaagatag gtcctactgc aaaccacccc 1680
tccatatttc cgtaccattt acaattcagt ttctgtgaca tcttttttaa ccactggagg 1740
aaaaatgaga tattctctaa ttattcttc tataacactc tatatagagc tatgtgagta 1800
ctaatacacat tgaataatag ttataaaatt attgtataga catctgcttc ttaaacagat 1860
tgtgagttct ttgagaaaca gcgtggattt tacttatctg tgtattcaca gagcttagca 1920
cagtgcctgg taatgagcaa gcatacttgc cattactttt ccttcccact ctctccaaca 1980
tcacattcac tttaaatttt tctgtatata gaaaggaaaa ctagcctggg caacatgatg 2040
aaaccccatc tccactgc
2058

```

<210> 141  
 <211> 413  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 141

```

Met Val Glu Arg Cys Ser Arg Gln Gly Cys Thr Ile Thr Met Ala Tyr
1           5           10           15
Ile Asp Tyr Asn Met Ile Val Ala Phe Met Leu Gly Asn Tyr Ile Asn
20          25          30
Leu Arg Glu Ser Ser Thr Glu Pro Asn Asp Ser Leu Trp Phe Ser Leu
35          40          45
Gln Lys Lys Asn Asp Thr Thr Glu Ile Glu Thr Leu Leu Leu Asn Thr
50          55          60
Ala Pro Lys Ile Ile Asp Glu Gln Leu Val Cys Arg Leu Ser Lys Thr
65          70          75          80

```

Asp Ile Phe Ile Ile Cys Arg Asp Asn Lys Ile Tyr Leu Asp Lys Met  
                             85                            90                            95  
 Ile Thr Arg Asn Leu Lys Leu Arg Phe Tyr Gly His Arg Gln Tyr Leu  
                             100                            105                            110  
 Glu Cys Glu Val Phe Arg Val Glu Gly Ile Lys Asp Asn Leu Asp Asp  
                             115                            120                            125  
 Ile Lys Arg Ile Ile Lys Ala Arg Glu His Arg Asn Arg Leu Leu Ala  
                             130                            135                            140  
 Asp Ile Arg Asp Tyr Arg Pro Tyr Ala Asp Leu Val Ser Glu Ile Arg  
 145                            150                            155                            160  
 Ile Leu Leu Val Gly Pro Val Gly Ser Gly Lys Ser Ser Phe Phe Asn  
                             165                            170                            175  
 Ser Val Lys Ser Ile Phe His Gly His Val Thr Gly Gln Ala Val Val  
                             180                            185                            190  
 Gly Ser Asp Thr Thr Ser Ile Thr Glu Arg Tyr Arg Ile Tyr Ser Val  
                             195                            200                            205  
 Lys Asp Gly Lys Asn Gly Lys Ser Leu Pro Phe Met Leu Cys Asp Thr  
                             210                            215                            220  
 Met Gly Leu Asp Gly Ala Glu Gly Ala Gly Leu Cys Met Asp Asp Ile  
 225                            230                            235                            240  
 Pro His Ile Leu Lys Gly Cys Met Pro Asp Arg Tyr Gln Phe Asn Ser  
                             245                            250                            255  
 Arg Lys Pro Ile Thr Pro Glu His Ser Thr Phe Ile Thr Ser Pro Ser  
                             260                            265                            270  
 Leu Lys Asp Arg Ile His Cys Val Ala Tyr Val Leu Asp Ile Asn Ser  
                             275                            280                            285  
 Ile Asp Asn Leu Tyr Ser Lys Met Leu Ala Lys Val Lys Gln Val His  
                             290                            295                            300  
 Lys Glu Val Leu Asn Cys Gly Ile Ala Tyr Val Ala Leu Leu Thr Lys  
 305                            310                            315                            320  
 Val Asp Asp Cys Ser Glu Val Leu Gln Asp Asn Phe Leu Asn Met Ser  
                             325                            330                            335  
 Arg Ser Met Thr Ser Gln Ser Arg Val Met Asn Val His Lys Met Leu  
                             340                            345                            350  
 Gly Ile Pro Ile Ser Asn Ile Leu Met Val Gly Asn Tyr Ala Ser Asp  
                             355                            360                            365  
 Leu Glu Leu Asp Pro Met Lys Asp Ile Leu Ile Leu Ser Ala Leu Arg  
                             370                            375                            380  
 Gln Met Leu Arg Ala Ala Asp Asp Phe Leu Glu Asp Leu Pro Leu Glu  
 385                            390                            395                            400  
 Glu Thr Gly Ala Ile Glu Arg Ala Leu Gln Pro Cys Ile  
                             405                            410

&lt;210&gt; 142

&lt;211&gt; 1032

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 142

ggagggtggg cagcaactcgc tttattgtcc agcattccac atggatagtc gccacacctt 60  
 tgcccctgct gcgatgaccc tgtcgccact tctgctgttc ctgccaccgc tgctgctgct 120  
 gctggacgtc cccacggcgg cgggtgcaggc gtcccctctg caagcgtagt acttcttttg 180  
 gaatgggcca ccagttaact acaagacagg caatctatac ctgcgggggc ccctgaagaa 240  
 gtccaatgca ccgcttgtca atgtgaccct ctactatgaa gcactgtgcg gtggctgccg 300  
 agccttctctg atccgggagc tcttcccaac atggctgttg gtcattggaga tcctcaatgt 360  
 cacgtcgggtg ccctacggaa acgcacagga acaaaatgtc agtggcagggt gggagttcaa 420  
 gtgccagctt ggagaagagg agtgcaaatt caacaagggt gaggcctgcg tgttgatga 480

150

```

acttgacatg gagctagcct tcctgaccat gtctggcatg gcatggaaga gtttgaggac 540
atggagagaa gtctgccact atgcctgcag ctctacgcc cagggctgtc gccagaacta 600
tcatggagtg tgcaatgggg gaccgcggca tgcagtcac gacgcgaac gccagcggga 660
cagatgtctt ccagccaccg cagcagtatg tgcctgggt caccgtcaat gggaaaccct 720
tggaagatca gaccagctc cttacccttg tctgccagt gtaccagggc aagaagccgg 780
atgtctgccc ttctcaacc agctccctcc ggagtgttg cttcgagtgt tggccggtgg 840
gctgcggaga gctcatggaa ggcgagtggg aactcggctg cctgcctttt tttctgatcc 900
agaccctcgg cacctgctac ttaccaactg gaaaatttta tgcatcccat gaagcccaga 960
tacacaaaat tccacccta gatcaagaat cctgctccac taagaatggt gctaaagtaa 1020
aactagttta at 1032

```

&lt;210&gt; 143

&lt;211&gt; 303

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 143

```

Met Asp Ser Arg His Thr Phe Ala Pro Ala Ala Met Thr Leu Ser Pro
1      5      10      15
Leu Leu Leu Phe Leu Pro Pro Leu Leu Leu Leu Asp Val Pro Thr
20      25      30
Ala Ala Val Gln Ala Ser Pro Leu Gln Ala Leu Asp Phe Phe Gly Asn
35      40      45
Gly Pro Pro Val Asn Tyr Lys Thr Gly Asn Leu Tyr Leu Arg Gly Pro
50      55      60
Leu Lys Lys Ser Asn Ala Pro Leu Val Asn Val Thr Leu Tyr Tyr Glu
65      70      75      80
Ala Leu Cys Gly Gly Cys Arg Ala Phe Leu Ile Arg Glu Leu Phe Pro
85      90      95
Thr Trp Leu Leu Val Met Glu Ile Leu Asn Val Thr Ser Val Pro Tyr
100     105     110
Gly Asn Ala Gln Glu Gln Asn Val Ser Gly Arg Trp Glu Phe Lys Cys
115     120     125
Gln Leu Gly Glu Glu Glu Cys Lys Phe Asn Lys Val Glu Ala Cys Val
130     135     140
Leu Asp Glu Leu Asp Met Glu Leu Ala Phe Leu Thr Met Ser Gly Met
145     150     155     160
Ala Trp Lys Ser Leu Arg Thr Trp Arg Glu Val Cys His Tyr Ala Cys
165     170     175
Ser Ser Thr Pro Gln Gly Cys Arg Gln Asn Tyr His Gly Val Cys Asn
180     185     190
Gly Gly Pro Arg His Ala Ala His Ala Arg Gln Arg Pro Ala Asp Arg
195     200     205
Cys Ser Pro Ala Thr Ala Arg Val Cys Ala Leu Gly His Arg Gln Trp
210     215     220
Glu Thr Leu Gly Arg Ser Asp Pro Ala Pro Tyr Pro Cys Leu Pro Val
225     230     235     240
Val Pro Gly Gln Glu Ala Gly Cys Leu Pro Phe Leu Asn Gln Leu Pro
245     250     255
Pro Glu Cys Leu Leu Arg Val Leu Ala Gly Gly Leu Arg Arg Ala His
260     265     270
Gly Arg Arg Val Gly Thr Arg Leu Pro Ala Phe Phe Ser Asp Pro Asp
275     280     285
Pro Arg His Leu Leu Leu Thr Asn Trp Lys Ile Leu Cys Ile Pro
290     295     300

```

&lt;210&gt; 144



151

&lt;211&gt; 1356

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 144

```

ttctcccgca accttccctt cgctccctcc cgtccccccc agctcctagc ctccgactcc 60
ctccccccct cagcccgcc ctctcgctt cgccgaacca aagtggatta attacacgct 120
ttctgtttct ctccgtgctg ttctctcccg ctgtgcgcct gcccgctct cgtgtctctc 180
tctccccctc gccctctctt cggccccccc ctttcacgtt cactctgtct ctcccactat 240
ctctgcccc ctctatcctt gatacaacag ctgacctcat ttcccgatac cttttcccc 300
ccgaaaagta caacatctgg cccgcccag cccgaagaca gcccgctct cctggacaat 360
cagacgaatt ctccccccc ccccaaaaaa aaaagccatc cccccgctct gcccgctcgc 420
acattcggcc cccgcgactc ggccagagcg gcgctggcag aggagtgtcc ggcaggagg 480
ccaacgccc ctgttcggtt tgcgacacgc agcagggagg tggcggcag cgtcgccggc 540
ttccagacac caatgggaat cccaatgggg aagtcgatgc tgggtcttct caccttcttg 600
gccttcgcct cgtgctgcat tgctgcttac cgccccagt agaccctgtg cggcggggag 660
ctggtggaca cctccagtt cgtctgtggg gaccgcggct tctacttcag caggccccga 720
agcgtgtga gccgtcgag ccgtggcatc gttgaggagt gctgtttccg cagctgtgac 780
ctggccctcc tggagacgta ctgtgtacc cccgccaagt ccgagaggga cgtgtcgacc 840
cctccgacc tgcttcgga caactcccc agatacccc tgggcaagtt cttccaatat 900
gacacctgga agcagtcac ccagcgctg cgcaggggcc tgcctgccct cctgcgtgcc 960
cgccggggtc acgtgctgc caaggagctc gaggcgttca gggaggccaa acgtcaccgt 1020
cccctgatt ctctaccac ccaagacccc gccacgggg gcgcccccc agagatggcc 1080
agcaatcgga agtgagcaaa actgccgaa gtctgcagcc cggcgccacc atcctgcagc 1140
ctcctcctga ccacggacgt ttccatcagg ttccatccc aaaaatctctc gggtccacgt 1200
ccccctggg cttctcctga cccagtcccc gtgccccgc tccccgaaac aggctactct 1260
cctcgccccc ctccatcggg ctgaggaagc acagcagcat cttcaaacat gtacaaaatc 1320
gattggcttt aaacaccctt cacataccct ccccc 1356

```

&lt;210&gt; 145

&lt;211&gt; 180

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 145

```

Met Gly Ile Pro Met Gly Lys Ser Met Leu Val Leu Leu Thr Phe Leu
1 5 10 15
Ala Phe Ala Ser Cys Cys Ile Ala Ala Tyr Arg Pro Ser Glu Thr Leu
20 25 30
Cys Gly Gly Glu Leu Val Asp Thr Leu Gln Phe Val Cys Gly Asp Arg
35 40 45
Gly Phe Tyr Phe Ser Arg Pro Ala Ser Arg Val Ser Arg Arg Ser Arg
50 55 60
Gly Ile Val Glu Glu Cys Cys Phe Arg Ser Cys Asp Leu Ala Leu Leu
65 70 75 80
Glu Thr Tyr Cys Ala Thr Pro Ala Lys Ser Glu Arg Asp Val Ser Thr
85 90 95
Pro Pro Thr Val Leu Pro Asp Asn Phe Pro Arg Tyr Pro Val Gly Lys
100 105 110
Phe Phe Gln Tyr Asp Thr Trp Lys Gln Ser Thr Gln Arg Leu Arg Arg
115 120 125
Gly Leu Pro Ala Leu Leu Arg Ala Arg Arg Gly His Val Leu Ala Lys
130 135 140
Glu Leu Glu Ala Phe Arg Glu Ala Lys Arg His Arg Pro Leu Ile Ala
145 150 155 160
Leu Pro Thr Gln Asp Pro Ala His Gly Gly Ala Pro Pro Glu Met Ala
165 170 175
Ser Asn Arg Lys

```

180

<210> 146  
 <211> 3667  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 146

```

tatatcatgt aagctagtca cacctatattg aattcacttt tctttgtttc ttgatttctt 60
atggctatta ttgcaacaat caaacaattt ttgaatacct tttgtgagct agcactgtgg 120
aaatatgagg gaagtttatt gtgttcttac tttaaatagt ttgcagtttt attgtgtata 180
caaatgtatg catgtgaaat atacagattt taaaaaagca gatcattaaa gattaggtca 240
taagggtgtag tctgtacatg gaggaagagc taagttgatt cagaataaca tggtttagatt 300
tcgaagctag cctggatttg aatcttggat ccaccactga ctagctatgt aagcttagtc 360
aagcaactca acggaggagg cgaggagcgc cgggtaccgg gccgggggag ccgcgggctc 420
tcggggaaga gacggatgat gaacaagctt tacatcgggg acctgagccc cgccgtcacc 480
gccgacgacc tccggcagct ctttggggac aggaagctgc ccctggcggg acaggtcctg 540
ctgaagtcct gctacgcctt cgtggactac cccgaccaga actgggcat ccgcgccatc 600
gagaccctct cgggtaaagt ggaattgcat gggaaaatca tggaagtga ttactcagtc 660
tctaaaaagc taaggagcag gaaaattcag attcgaaaca tccctcctca cctgcagtgg 720
gagggtgttg atggactttt ggctcaatat gggacagtgg agaattgtga acaagtcaac 780
acagacacag aaaccgccgt tgtcaacgtc acatatgcaa caagagaaga agcaaaaata 840
gcatatggaga agctaagcgg gcatcagttt gagaactact ccttcaagat ttcctacatc 900
ccgatgaag aggtgagctc cccttcgccc cctcagcgag ccagcgtgg ggaccactct 960
tcccgggagc aaggccacgc ccctgggggc acttctcagg ccagacagat tgatttcccg 1020
ctgcgatcc tggccccac ccagtttgtt ggtgccatca tcggaaagga gggcttgacc 1080
ataaagaaca tcactaagca gaccagtcgc cgggtagata tccatagaaa agagaactct 1140
ggagctgcag agaagcctgt caccatccat gccacccag aggggacttc tgaagcatgc 1200
cgcattgattc ttgaaatcat gcagaaagag gcagatgaga ccaaactagc cgaagagatt 1260
cctctgaaaa tcttggcaca caatggcttg gttggaagac tgattggaaa agaaggcaga 1320
aatttgaaga aaattgaaca tgaaacaggg accaagataa caatctcatc tttgcaggat 1380
ttgagcatat acaaccggga aagaaccatc actgtgaagg gcacagtga ggccctgtgc 1440
agtgtgaga tagagattat gaagaagctg cgtgaggcct ttgaaaatga tatgtctggc 1500
gttaacaccc actccggata cttctccagc ctgtaccccc atcaccagtt tggcccgttc 1560
ccgcatcatc actcttatcc agagcaggag attgtgaatc tcttcatccc aaccagggt 1620
gtgggcgcca tcacgggaa gaagggggca ccatcaaac agctggcgag attcgccga 1680
gcctctatca agattgcccc tgcggaaggc ccagacgtca gcgaaaggat ggtcatcatc 1740
accgggccac cggaagccca gttcaaggcc caggagcgga tctttgggaa actgaaagag 1800
gaaaacttct ttaaccccaa agaagaagtg aagctggaag cgcatatcag agtgccctct 1860
tccacagctg gccgggtgat tggcaaaggt ggcaagaccg tgaacgaact gcagaactta 1920
accagtgcag aagtcacgtg gcctcgtgac caaacgccag atgaaaatga ggaagtgatc 1980
gtcagaatta tcgggcactt ctttgttagc cagactgcac agcgcaagat cagggaaatt 2040
gtacaacagg tgaagcagca ggagcagaaa taccctcagg gactcgccct acagcgagc 2100
aagtgaggct cccacaggca ccagcaaaac aacggatgaa tgtagccctt ccaacacctg 2160
acagaatgag accaaacgca gccagccaga tcgggagcaa accaaagacc atctgaggaa 2220
tgagaagtct gcggaggcgg ccagggactc tgccgaggcc ctgagaaccc caggggccga 2280
ggagggggcg ggaaggtcag ccaggtttgc cagaaccacc gagccccgcc tccgcccccc 2340
cagggttctt gcaggcttca gccatccact tcaccatcca ctcgatctc tcctgaactc 2400
ccacgacgct atccctttta gttgaactaa cataggtgaa cgtgttcaaa gccaaagcaa 2460
atgcacaccc tttttctgtg gcaaatcgtc tctgtacatg tgtgtacata ttagaaaggg 2520
aagatgttaa gatatgtggc ctgtgggtta cacagggtgc ctgcagcggg aatatatttt 2580
agaaataata tatcaaataa ctcaactaac tccaattttt aatcaattat taattttttt 2640
ttctttttta agagaaagca ggcttttcta gactttaaag aataaagtct ttgggaggtc 2700
tcacgggtga gagaggagct ttgaggccac ccgcacaaaa ttcaaccaga gggaaatctc 2760
gtcgggaagga cactcacggc agttctggat cacctgtgta tgtcaacaga agggataccg 2820
tctccttgaa gaggaaactc tgtcactcct catgcctgtc tagctcatac acccatttct 2880
ctttgcttca caggttttaa actggttttt tgcatactgc tatataattc tctgtctctc 2940

```

```

tctgtttatc tctccctcc ctcccctccc cttcttctcc atctccattc ttttgaattt 3000
cctcatccct ccattcfaat cccgtatcta cgcaccccc ccccccaggc aaagcagtg 3060
tctgagtatc acatcacaca aaaggaacaa aagcgaaaca cacaaaccag cctcaactta 3120
cacttggtta ctcaaaagaa caagagtcaa tggtagttgt cctagcgttt tggaagagga 3180
aaacaggaac ccaccaaacc aaccaatcaa ccaaacaag aaaaaattcc acaatgaaag 3240
aatgtatttt gtctttttgc attttggtgt ataagccatc aatattcagc aaaatgattc 3300
ctttctttta aaaaaaaaaa tgtggaggaa agtagaaatt taccaagggt gttggcccag 3360
ggcggttaaat tcacagattt ttttaacgag aaaaacacac agaagaagct acctcaggtg 3420
tttttacctc agcaccttga tcttggtgtt cccttagaga ttttgtaaag ctgatagttg 3480
gagcattttt ttattttttt aataaaaaat agttggaaaa aaaataagat atcaactgcc 3540
agcctggaga aggtgacagt ccaagtgtgc aacagctgtt ctgaattgtc ttccgctagc 3600
caagaaccta tatggccttc ttttgacaaa accttgaaaa tgtttattta aaaaaaaaaa 3660
aaaaaaa 3667

```

&lt;210&gt; 147

&lt;211&gt; 556

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 147

```

Met Met Asn Lys Leu Tyr Ile Gly Asn Leu Ser Pro Ala Val Thr Ala
  1           5           10           15
Asp Asp Leu Arg Gln Leu Phe Gly Asp Arg Lys Leu Pro Leu Ala Gly
      20           25           30
Gln Val Leu Leu Lys Ser Gly Tyr Ala Phe Val Asp Tyr Pro Asp Gln
      35           40           45
Asn Trp Ala Ile Arg Ala Ile Glu Thr Leu Ser Gly Lys Val Glu Leu
      50           55           60
His Gly Lys Ile Met Glu Val Asp Tyr Ser Val Ser Lys Lys Leu Arg
      65           70           75           80
Ser Arg Lys Ile Gln Ile Arg Asn Ile Pro Pro His Leu Gln Trp Glu
      85           90           95
Val Leu Asp Gly Leu Leu Ala Gln Tyr Gly Thr Val Glu Asn Val Glu
      100          105          110
Gln Val Asn Thr Asp Thr Glu Thr Ala Val Val Asn Val Thr Tyr Ala
      115          120          125
Thr Arg Glu Glu Ala Lys Ile Ala Met Glu Lys Leu Ser Gly His Gln
      130          135          140
Phe Glu Asn Tyr Ser Phe Lys Ile Ser Tyr Ile Pro Asp Glu Glu Val
      145          150          155          160
Ser Ser Pro Ser Pro Pro Gln Arg Ala Gln Arg Gly Asp His Ser Ser
      165          170          175
Arg Glu Gln Gly His Ala Pro Gly Gly Thr Ser Gln Ala Arg Gln Ile
      180          185          190
Asp Phe Pro Leu Arg Ile Leu Val Pro Thr Gln Phe Val Gly Ala Ile
      195          200          205
Ile Gly Lys Glu Gly Leu Thr Ile Lys Asn Ile Thr Lys Gln Thr Gln
      210          215          220
Ser Arg Val Asp Ile His Arg Lys Glu Asn Ser Gly Ala Ala Glu Lys
      225          230          235          240
Pro Val Thr Ile His Ala Thr Pro Glu Gly Thr Ser Glu Ala Cys Arg
      245          250          255
Met Ile Leu Glu Ile Met Gln Lys Glu Ala Asp Glu Thr Lys Leu Ala
      260          265          270
Glu Glu Ile Pro Leu Lys Ile Leu Ala His Asn Gly Leu Val Gly Arg
      275          280          285
Leu Ile Gly Lys Glu Gly Arg Asn Leu Lys Lys Ile Glu His Glu Thr
      290          295          300

```

154

Gly Thr Lys Ile Thr Ile Ser Ser Leu Gln Asp Leu Ser Ile Tyr Asn  
 305 310 315 320  
 Pro Glu Arg Thr Ile Thr Val Lys Gly Thr Val Glu Ala Cys Ala Ser  
 325 330 335  
 Ala Glu Ile Glu Ile Met Lys Lys Leu Arg Glu Ala Phe Glu Asn Asp  
 340 345 350  
 Met Leu Ala Val Asn Thr His Ser Gly Tyr Phe Ser Ser Leu Tyr Pro  
 355 360 365  
 His His Gln Phe Gly Pro Phe Pro His His His Ser Tyr Pro Glu Gln  
 370 375 380  
 Glu Ile Val Asn Leu Phe Ile Pro Thr Gln Ala Val Gly Ala Ile Ile  
 385 390 395 400  
 Gly Lys Lys Gly Ala His Ile Lys Gln Leu Ala Arg Phe Ala Gly Ala  
 405 410 415  
 Ser Ile Lys Ile Ala Pro Ala Glu Gly Pro Asp Val Ser Glu Arg Met  
 420 425 430  
 Val Ile Ile Thr Gly Pro Pro Glu Ala Gln Phe Lys Ala Gln Gly Arg  
 435 440 445  
 Ile Phe Gly Lys Leu Lys Glu Glu Asn Phe Phe Asn Pro Lys Glu Glu  
 450 455 460  
 Val Lys Leu Glu Ala His Ile Arg Val Pro Ser Ser Thr Ala Gly Arg  
 465 470 475 480  
 Val Ile Gly Lys Gly Gly Lys Thr Val Asn Glu Leu Gln Asn Leu Thr  
 485 490 495  
 Ser Ala Glu Val Ile Val Pro Arg Asp Gln Thr Pro Asp Glu Asn Glu  
 500 505 510  
 Glu Val Ile Val Arg Ile Ile Gly His Phe Phe Ala Ser Gln Thr Ala  
 515 520 525  
 Gln Arg Lys Ile Arg Glu Ile Val Gln Gln Val Lys Gln Gln Glu Gln  
 530 535 540  
 Lys Tyr Pro Gln Gly Val Ala Ser Gln Arg Ser Lys  
 545 550 555

&lt;210&gt; 148

&lt;211&gt; 1475

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 148

cccagaggag cagactacaa gaatggcaca cgctatggaa aactcctgga caatcagtaa 60  
 agagtacat attgatgaag aagtgggctt tgctctgcc aatccacagg aaaatctacc 120  
 tgatttttat aatgactgga tgttcattgc taaacatctg cctgatctca tagagtctgg 180  
 ccagcttcga gaaagagttg agaagttaaa catgctcagc attgatcatc tcacagacca 240  
 caagtcacag cgccttgacac gtctagttct gggatgcac accatggcat atgtgtgggg 300  
 caaagtcac ggagatgtcc gtaaggtctt gccagaaat attgctgttc cttactgcca 360  
 actctccaag aaactggaac tgcctcctat tttggtttat gcagactgtg tcttggcaaa 420  
 ctggaagaaa aaggatccta ataagcccct gacttatgag aacatggacg ttttgttctc 480  
 atttctgat ggagactgca gtaaaggatt cttcctggtc tctctatttg tggaaatagc 540  
 agctgcttct gcaatcaaag taattcctac tgtattcaag gcaatgcaaa tgcaagaacg 600  
 ggacactttg ctaaaggcgc tgttggaat agcttcttgc ttggagaaag cccttcaagt 660  
 gtttcaccaa atccacgac atgtgaaccc aaaagcattt ttcagtgttc ttcgcatata 720  
 tttgtctggc tggaaaggca acccccagct atcagacggt ctgggtgatg aagggttctg 780  
 ggaagacca aaggagtttg cagggggcag tgcaggccaa agcagcgtct ttcagtgtct 840  
 tgacgtcctg ctgggcatcc agcagactgc tgggtggagga catgctgtct agttcctcca 900  
 ggacatgaga agatatatgc caccagctca caggaaactc ctgtgtcat tagagtcaaa 960  
 tccctcagtc cgtgagtttg tcccttcaaa aggtgatgct ggctgcggg aagcttatga 1020  
 cgctgtgtg aaagctctgg tctcctgag gagctaccat ctgcaaatcg tgactaagta 1080

```

catcctgatt cctgcaagcc agcagccaaa ggagaataag acctctgaag acccttcaaa 1140
actggaagcc aaaggaactg gaggcactga tttaatgaat ttcctgaaga ctgtaagaag 1200
tacaactgag aaatcccttt tgaaggaagg ttaatgtaac ccaacaagag cacattttat 1260
catagcagag acatctgtat gcattcctgt cattacccat tgtaacagag ccacaaacta 1320
atactatgca atgttttacc aataatgcaa tacaaaagac ctcaaaatac ctgtgcattt 1380
cttgtaggaa aacaacaaaa ggtaattatg tgtaattata ctagaagttt tgtaatctgt 1440
atcttatcat tggaataaaa tgacattcaa taaat 1475

```

&lt;210&gt; 149

&lt;211&gt; 403

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 149

```

Met Ala His Ala Met Glu Asn Ser Trp Thr Ile Ser Lys Glu Tyr His
1      5      10      15
Ile Asp Glu Glu Val Gly Phe Ala Leu Pro Asn Pro Gln Glu Asn Leu
20     25     30
Pro Asp Phe Tyr Asn Asp Trp Met Phe Ile Ala Lys His Leu Pro Asp
35     40     45
Leu Ile Glu Ser Gly Gln Leu Arg Glu Arg Val Glu Lys Leu Asn Met
50     55     60
Leu Ser Ile Asp His Leu Thr Asp His Lys Ser Gln Arg Leu Ala Arg
65     70     75     80
Leu Val Leu Gly Cys Ile Thr Met Ala Tyr Val Trp Gly Lys Gly His
85     90     95
Gly Asp Val Arg Lys Val Leu Pro Arg Asn Ile Ala Val Pro Tyr Cys
100    105    110
Gln Leu Ser Lys Lys Leu Glu Leu Pro Pro Ile Leu Val Tyr Ala Asp
115    120    125
Cys Val Leu Ala Asn Trp Lys Lys Lys Asp Pro Asn Lys Pro Leu Thr
130    135    140
Tyr Glu Asn Met Asp Val Leu Phe Ser Phe Arg Asp Gly Asp Cys Ser
145    150    155    160
Lys Gly Phe Phe Leu Val Ser Leu Leu Val Glu Ile Ala Ala Ala Ser
165    170    175
Ala Ile Lys Val Ile Pro Thr Val Phe Lys Ala Met Gln Met Gln Glu
180    185    190
Arg Asp Thr Leu Leu Lys Ala Leu Leu Glu Ile Ala Ser Cys Leu Glu
195    200    205
Lys Ala Leu Gln Val Phe His Gln Ile His Asp His Val Asn Pro Lys
210    215    220
Ala Phe Phe Ser Val Leu Arg Ile Tyr Leu Ser Gly Trp Lys Gly Asn
225    230    235    240
Pro Gln Leu Ser Asp Gly Leu Val Tyr Glu Gly Phe Trp Glu Asp Pro
245    250    255
Lys Glu Phe Ala Gly Gly Ser Ala Gly Gln Ser Ser Val Phe Gln Cys
260    265    270
Phe Asp Val Leu Leu Gly Ile Gln Gln Thr Ala Gly Gly Gly His Ala
275    280    285
Ala Gln Phe Leu Gln Asp Met Arg Arg Tyr Met Pro Pro Ala His Arg
290    295    300
Asn Phe Leu Cys Ser Leu Glu Ser Asn Pro Ser Val Arg Glu Phe Val
305    310    315    320
Leu Ser Lys Gly Asp Ala Gly Leu Arg Glu Ala Tyr Asp Ala Cys Val
325    330    335
Lys Ala Leu Val Ser Leu Arg Ser Tyr His Leu Gln Ile Val Thr Lys
340    345    350

```

156

Tyr Ile Leu Ile Pro Ala Ser Gln Gln Pro Lys Glu Asn Lys Thr Ser  
 355 360 365  
 Glu Asp Pro Ser Lys Leu Glu Ala Lys Gly Thr Gly Gly Thr Asp Leu  
 370 375 380  
 Met Asn Phe Leu Lys Thr Val Arg Ser Thr Thr Glu Lys Ser Leu Leu  
 385 390 395 400  
 Lys Glu Gly

<210> 150  
 <211> 2129  
 <212> DNA  
 <213> Homo sapiens

<400> 150  
 cagactgcca taagatggcg tccgtggcgg ctgcacgagc agttcctgtg ggcagtgggc 60  
 tcaggggcct gcaacggacc ctacctcttg tagtgattct cggggccacg ggcacssgm 120  
 aatccacgct ggcgttgacg ctaggccagc ggctcggcgg tgagatcgtc agcgctgact 180  
 ccatgcaggt ctatgaaggc ctagacatca tcaccaacaa ggtttctgcc caagagcaga 240  
 gaatctgccg gcaccacatg atcagctttg tggatcctct tgtgaccaat tacacagtgg 300  
 tggacttcag aaatagagca actgctctga ttgaagatat atttgccga gacaaaattc 360  
 ctattgttgt gggaggaacc aattattaca ttgaatctct gctctggaaa gttcttgtca 420  
 ataccaagcc ccaggagatg ggcactgaga aagtgattga ccgaaaagtg gagcttgaaa 480  
 aggaggatgg tcttgactt cacaacgcc taagccaggt ggaccagaa atggctgcca 540  
 agctgcatcc acatgacaaa cgcaaagtgg ccaggagctt gcaagtttt gaagaaacag 600  
 gaatctctca tagtgaattt ctccatcgtc aacatacga agaaggtggt ggtccccttg 660  
 gaggtcctct gaagttctct aacccttgca tcctttggct tcatgctgac caggcagttc 720  
 tagatgagcg cttggataag aggggtggatg acatgcttgc tgctgggctc ttggaggaac 780  
 taagagattt tcacagacgc tataatcaga agaattgttc ggaaaatagc caggactatc 840  
 aacatggtat cttccaatca attggcttca aggaatttca cgagtacctg atcactgagg 900  
 gaaaatgcac actggagact agtaaccagc ttctaaagaa aggtattgag gctctgaaac 960  
 aagtaactaa gagatatgcc cggaaacaaa accgatgggt taaaaccgt tttttgagca 1020  
 gacctggctc cattgtcccc cctgtctayg gcttagaggt atctgatgtc tcgaagtggg 1080  
 aagagtctgt tcttgaacct gctcttgaag tcgtgcaaag tttcatccag ggccacaagc 1140  
 ctacagccac tccaataaag atgccataga atgaagctga gaacaagaga agttatcacc 1200  
 tgtgtgacct ctgtgatcga atcatcattg gggatcgcg cacataaaat 1260  
 ccaaattcca cttgaaccaa ctgaagaaaa gaagaagatt ggactcagat gctgtcaaca 1320  
 ccatagaaag tcagagtgtt tccccagacc ataacaaaga acctaaagag aagggatccc 1380  
 cagggcagaa tgatcaagag ctgaaatgca gcgtttaaga gacatgtcca gtggcctttg 1440  
 gaaaggtggt ggggatccag ttcaggaggg aggggtatgt ttgtctccca gtctgggcaa 1500  
 aggagtgcta tgcggaattc tctgcatagc agaaaagctc ccaccatttt cttttgatgt 1560  
 ggttttaaag tctcacgttc tctataatag aaacagcagg tcttgtcagc tccttgtgtg 1620  
 gctgatgtgt ctggaaatga tgtagttcag gaaagcattt ttttttctt tgaaccttaa 1680  
 aggttctatt attaaaagca gcacagattc cacattttta tacatgagga tcttctttgt 1740  
 ggtgaatacc aggattgact gcattccctt aaagaagttt tatgtccctg actctggcta 1800  
 aaattatcta atttccagat gctttttag atgactgaag tatttgtgag ccacatattg 1860  
 ggagttctag atttgagtga atggcaggaa agggccatct ccattgagat gattaagtga 1920  
 accaaactag ttctcggaat tctacagaga aggagggaat cagactgaag aagctgtgac 1980  
 ataggacttg aagaccaaag actttgaaat ttgcgagctg ctcatgtgtg agttattatc 2040  
 actgctgtct ttctattgag ttacaaatct atatttttat tgaagtttaa ataaagaaaa 2100  
 aatttaaaaa aaaaaaaaaa aaaaaaaaaa 2129

<210> 151  
 <211> 465  
 <212> PRT  
 <213> Homo sapiens

157

&lt;400&gt; 151

```

Met Ala Ser Val Ala Ala Ala Arg Ala Val Pro Val Gly Ser Gly Leu
 1          5          10          15
Arg Gly Leu Gln Arg Thr Leu Pro Leu Val Val Ile Leu Gly Ala Thr
 20          25          30
Gly Thr Ser Thr Leu Ala Leu Gln Leu Gly Gln Arg Leu Gly Gly Glu
 35          40          45
Ile Val Ser Ala Asp Ser Met Gln Val Tyr Glu Gly Leu Asp Ile Ile
 50          55          60
Thr Asn Lys Val Ser Ala Gln Glu Gln Arg Ile Cys Arg His His Met
 65          70          75          80
Ile Ser Phe Val Asp Pro Leu Val Thr Asn Tyr Thr Val Val Asp Phe
 85          90          95
Arg Asn Arg Ala Thr Ala Leu Ile Glu Asp Ile Phe Ala Arg Asp Lys
100          105          110
Ile Pro Ile Val Val Gly Gly Thr Asn Tyr Tyr Ile Glu Ser Leu Leu
115          120          125
Trp Lys Val Leu Val Asn Thr Lys Pro Gln Glu Met Gly Thr Glu Lys
130          135          140
Val Ile Asp Arg Lys Val Glu Leu Glu Lys Glu Asp Gly Leu Val Leu
145          150          155          160
His Lys Arg Leu Ser Gln Val Asp Pro Glu Met Ala Ala Lys Leu His
165          170          175
Pro His Asp Lys Arg Lys Val Ala Arg Ser Leu Gln Val Phe Glu Glu
180          185          190
Thr Gly Ile Ser His Ser Glu Phe Leu His Arg Gln His Thr Glu Glu
195          200          205
Gly Gly Gly Pro Leu Gly Gly Pro Leu Lys Phe Ser Asn Pro Cys Ile
210          215          220
Leu Trp Leu His Ala Asp Gln Ala Val Leu Asp Glu Arg Leu Asp Lys
225          230          235          240
Arg Val Asp Asp Met Leu Ala Ala Gly Leu Leu Glu Glu Leu Arg Asp
245          250          255
Phe His Arg Arg Tyr Asn Gln Lys Asn Val Ser Glu Asn Ser Gln Asp
260          265          270
Tyr Gln His Gly Ile Phe Gln Ser Ile Gly Phe Lys Glu Phe His Glu
275          280          285
Tyr Leu Ile Thr Glu Gly Lys Cys Thr Leu Glu Thr Ser Asn Gln Leu
290          295          300
Leu Lys Lys Gly Ile Glu Ala Leu Lys Gln Val Thr Lys Arg Tyr Ala
305          310          315          320
Arg Lys Gln Asn Arg Trp Val Lys Asn Arg Phe Leu Ser Arg Pro Gly
325          330          335
Pro Ile Val Pro Pro Val Tyr Gly Leu Glu Val Ser Asp Val Ser Lys
340          345          350
Trp Glu Glu Ser Val Leu Glu Pro Ala Leu Glu Ile Val Gln Ser Phe
355          360          365
Ile Gln Gly His Lys Pro Thr Ala Thr Pro Ile Lys Met Pro Tyr Asn
370          375          380
Glu Ala Glu Asn Lys Arg Ser Tyr His Leu Cys Asp Leu Cys Asp Arg
385          390          395          400
Ile Ile Ile Gly Asp Arg Glu Trp Ala Ala His Ile Lys Ser Lys Ser
405          410          415
His Leu Asn Gln Leu Lys Lys Arg Arg Arg Leu Asp Ser Asp Ala Val
420          425          430
Asn Thr Ile Glu Ser Gln Ser Val Ser Pro Asp His Asn Lys Glu Pro
435          440          445
Lys Glu Lys Gly Ser Pro Gly Gln Asn Asp Gln Glu Leu Lys Cys Ser

```

158

450  
Val  
465

455

460

<210> 152  
<211> 2129  
<212> DNA  
<213> Homo sapiens

<400> 152  
cagactgcca taagatggcg tccgtggcgg ctgcacgagc agttcctgtg ggcagtgggc 60  
tcaggggcct gcaacggacc ctacctcttg tagtgattct cggggccacg ggcaccggca 120  
aatccacgct ggcgttgacg ctaggccagc ggctcggcgg tgagatcgtc agcgctgact 180  
ccatgcaggc ctatgaaggc ctagacatca tcaccaacaa ggtttctgcc caagagcaga 240  
gaatctgccc gcaccacatg atcagctttg tggatcctct tgtgaccaat tacacagtgg 300  
tggacttcag aaatagagca actgctctga ttgaagatat atttgcccga gacaaaattc 360  
ctattgttgt gggaggaacc aattattaca ttgaatctct gctctggaaa gttcttgtca 420  
ataccaagcc ccaggagatg ggcactgaga aagtgattga ccgaaaagtg gagcttgaaa 480  
aggaggatgg tcttgtactt cacaacgcc taagccaggg ggaccagaa atggctgcca 540  
agctgcatcc acatgacaaa cgcaaagtgg ccaggagctt gcaagttttt gaagaaacag 600  
gaatctctca tagtgaattt ctccatcgtc aacatacgga agaaggtggg ggtccccttg 660  
gaggtcctct gaagttctct aacccttgca tcctttggct tcatgctgac caggcagttc 720  
tagatgagcg cttggataag aggggtggatg acatgcttgc tgctgggctc ttggaggaa 780  
taagagattt tcacagacgc tataatcaga agaattgttc ggaaaatagc caggactatc 840  
aacatggtat cttccaatca attggcttca aggaatttca cgagtacctg atcactgagg 900  
gaaaatgcac actggagact agtaaccagc ttctaaagaa aggtattgag gctctgaaac 960  
aagtaactaa gagatatgcc cggaaacaaa accgatgggt taaaaaccgt tttttgagca 1020  
gacctgggtc cattgtcccc cctgtctayg gcttagaggt atctgatgtc tcgaagtggg 1080  
aagagtctgt tcttgaacct gctcttgaag tcgtgcaaaag tttcatccag ggccacaagc 1140  
ctacagccac tccaataaag atgccataca atgaagctga gaacaagaga agttatcacc 1200  
tgtgtgacct ctgtgatcga atcatcattg gggatcgaga atgggcagcg cacataaaat 1260  
ccaaatccca cttgaaccaa ctgaagaaaa gaagaagatt ggactcagat gctgtcaaca 1320  
ccatagaaaag tcagagtgtt tccccagacc ataacaaaga acctaaagag aagggatccc 1380  
cagggcagaa tgatcaagag ctgaaatgca gcgtttaaga gacatgtcca gtggcctttg 1440  
gaaaggtggg ggggatccag ttcaggaggg aggggtatgt ttgtctccca gtctgggcaa 1500  
aggagtgcta tgcggaattc tctgcatagc agaaaagctc ccaccatttt cttttgatgt 1560  
ggttttaaag tctcacgttc tctataatag aaacagcagg tcttgtcagc tccttgtgtg 1620  
gctgatgtgt ctggaaatga tgtagttcag gaaagcattt tttttttctt tgaaccttaa 1680  
aggttctatt attaaaagca gcacagattc cacattttta tacatgagga tcttctttgt 1740  
ggtgaatacc aggattgact gcaccccttt aaagaagttt tatgtccctg actctggcta 1800  
aaattatcta atttcagat gctttttag atgactgaag tatttgtgag ccacatattg 1860  
ggagtcttag atttgagtga atggcaggaa agggccatct ccattgagat gattaagtga 1920  
accaaactag ttctcggaat tctacagaga aggagggaat cagactgaag aagctgtgac 1980  
ataggacttg aagaccaaag actttgaaat ttgcgagctg ctcatgtgtg agttattatc 2040  
actgctgtct ttctattgag ttacaaatct atatttttat tgaagtttaa ataaagaaaa 2100  
aatttaaaaa aaaaaaaaaa aaaaaaaaaa 2129

<210> 153  
<211> 467  
<212> PRT  
<213> Homo sapiens

<400> 153  
Met Ala Ser Val Ala Ala Ala Arg Ala Val Pro Val Gly Ser Gly Leu  
1 5 10 15  
Arg Gly Leu Gln Arg Thr Leu Pro Leu Val Val Ile Leu Gly Ala Thr  
20 25 30



Gly Thr Gly Lys Ser Thr Leu Ala Leu Gln Leu Gly Gln Arg Leu Gly  
 35 40 45  
 Gly Glu Ile Val Ser Ala Asp Ser Met Gln Val Tyr Glu Gly Leu Asp  
 50 55 60  
 Ile Ile Thr Asn Lys Val Ser Ala Gln Glu Gln Arg Ile Cys Arg His  
 65 70 75 80  
 His Met Ile Ser Phe Val Asp Pro Leu Val Thr Asn Tyr Thr Val Val  
 85 90 95  
 Asp Phe Arg Asn Arg Ala Thr Ala Leu Ile Glu Asp Ile Phe Ala Arg  
 100 105 110  
 Asp Lys Ile Pro Ile Val Val Gly Thr Asn Tyr Tyr Ile Glu Ser  
 115 120 125  
 Leu Leu Trp Lys Val Leu Val Asn Thr Lys Pro Gln Glu Met Gly Thr  
 130 135 140  
 Glu Lys Val Ile Asp Arg Lys Val Glu Leu Glu Lys Glu Asp Gly Leu  
 145 150 155 160  
 Val Leu His Lys Arg Leu Ser Gln Val Asp Pro Glu Met Ala Ala Lys  
 165 170 175  
 Leu His Pro His Asp Lys Arg Lys Val Ala Arg Ser Leu Gln Val Phe  
 180 185 190  
 Glu Glu Thr Gly Ile Ser His Ser Glu Phe Leu His Arg Gln His Thr  
 195 200 205  
 Glu Glu Gly Gly Gly Pro Leu Gly Gly Pro Leu Lys Phe Ser Asn Pro  
 210 215 220  
 Cys Ile Leu Trp Leu His Ala Asp Gln Ala Val Leu Asp Glu Arg Leu  
 225 230 235 240  
 Asp Lys Arg Val Asp Asp Met Leu Ala Ala Gly Leu Leu Glu Glu Leu  
 245 250 255  
 Arg Asp Phe His Arg Arg Tyr Asn Gln Lys Asn Val Ser Glu Asn Ser  
 260 265 270  
 Gln Asp Tyr Gln His Gly Ile Phe Gln Ser Ile Gly Phe Lys Glu Phe  
 275 280 285  
 His Glu Tyr Leu Ile Thr Glu Gly Lys Cys Thr Leu Glu Thr Ser Asn  
 290 295 300  
 Gln Leu Leu Lys Lys Gly Ile Glu Ala Leu Lys Gln Val Thr Lys Arg  
 305 310 315 320  
 Tyr Ala Arg Lys Gln Asn Arg Trp Val Lys Asn Arg Phe Leu Ser Arg  
 325 330 335  
 Pro Gly Pro Ile Val Pro Pro Val Tyr Gly Leu Glu Val Ser Asp Val  
 340 345 350  
 Ser Lys Trp Glu Glu Ser Val Leu Glu Pro Ala Leu Glu Ile Val Gln  
 355 360 365  
 Ser Phe Ile Gln Gly His Lys Pro Thr Ala Thr Pro Ile Lys Met Pro  
 370 375 380  
 Tyr Asn Glu Ala Glu Asn Lys Arg Ser Tyr His Leu Cys Asp Leu Cys  
 385 390 395 400  
 Asp Arg Ile Ile Ile Gly Asp Arg Glu Trp Ala Ala His Ile Lys Ser  
 405 410 415  
 Lys Ser His Leu Asn Gln Leu Lys Lys Arg Arg Arg Leu Asp Ser Asp  
 420 425 430  
 Ala Val Asn Thr Ile Glu Ser Gln Ser Val Ser Pro Asp His Asn Lys  
 435 440 445  
 Glu Pro Lys Glu Lys Gly Ser Pro Gly Gln Asn Asp Gln Glu Leu Lys  
 450 455 460  
 Cys Ser Val  
 465

<210> 154  
 <211> 4495  
 <212> DNA  
 <213> Homo sapiens

<400> 154

```

aggtgaacag gtcctcacgc ccagctccgc cccctcacgc gctctcgccg ggaccccgcct 60
tccgctggca gccatgggcc ccggccccag ccgcgcgcgc cgcgccccac gcctgatgct 120
ctgtgcgctc gccttgatgg tggcgcccg cggtgcgctc gtctccgcct tcaacctgga 180
tacccgattc ctggtagtga aggaggccgg gaacccgggc agcctcttcg gctactcggg 240
cgccctccat cggcagacag agcggcagca gcgctacctg ctctggctg gtgcccccg 300
ggagctcgct gtgccgatg gctacaccaa ccggactggg gctgtgtacc tgtgccact 360
cactgccac aaggatgact gtgagcggat gaacatcaca gtgaaaaatg accctggcca 420
tcacattatt gaggacatgt ggcttgaggt gactgtggcc agccagggcc ctgcaggcag 480
agttctggtc tgtgccacc gctacacca ggtgctgtgg tcagggtcag aagaccagcg 540
gcgcagtgtg ggcaagtgt acgtgcgagg caatgacctg gagctggact ccagtgtgga 600
ctggcagacc taccacaacg agatgtgcaa tagcaacaca gactacctgg agacgggcat 660
gtgccagctg ggcaccagcg gtggcttcac ccagaacact gtgtacttcg gcgcccccg 720
tgctacaac tggaaaggaa acagctacat gattcagcgc aaggagtggg acttatctga 780
gtatagttag aaggaccag aggaccaagg aaacctctat attgggtaca cgatgcagg 840
aggcagcttc atcctgcacc ccaaaaacat caccattgtg acagtgccc cagggcaccg 900
acatatgggc gcggtgttct tgctgagcca ggaggcaggc ggagacctgc ggaggagcca 960
gggtgctggag ggctcgagg tgggcgccta ttttggcagc gcaattgcc tggcagacct 1020
gaacaatgat ggggtggcagg acctcctggt gggcgcccc tactacttcg agaggaaaga 1080
ggaagtggg ggtgccatct atgtcttcat gaaccaggcg ggaacctcct tcctgtctca 1140
cccctcactc cttctcatg gcccagtggt ctctgccttt ggtttatctg tggccagcat 1200
tggtgacatc aaccaggatg gatttcagga tattgctgtg ggagctccgt ttgaaggctt 1260
gggcaaagtg tacatctatc acagtagctc taaggggctc cttagacagc ccagcagggt 1320
aatccatgga gagaagtgg gactgcctgg gttggccacc ttcggctatt ccctcagtgg 1380
gcagatggat tggtatgaga acttctacc agaccttcta gtgggaagcc tgtcagacca 1440
cattgtgctg ctgcgggccc ggccagtcac caacatcgtc cacaagacct tggtgcccag 1500
gccagctgtg ctggacctg cactttgcac ggccacctct tgtgtgcaag tggagctgtg 1560
ctttgcttac aaccagagtg ccgggaaccc caactacagg cgaaacatca ccctggccta 1620
cactctggag gctgacaggg accgccggcc gccccggctc cgctttgccg gcagtgagtc 1680
cgctgtcttc cagggcttct tctccatgcc cgagatgcgc tgccagaagc tggagctgct 1740
cctgatggac aacctccgtg acaaactccg ccccatcact atctccatga actactctt 1800
acctttgcgg atgcccgatc gccccggct ggggctgcgg tccctggacg cctaccgat 1860
cctcaaccag gcacaggctc tggagaacca cactgaggtc cagttccaga aggagtgcgg 1920
gcctgaacaac aagtgtgaga gcaacttgca gatgcgggca gccttcgtgt cagagcagca 1980
gcagaagctg agcaggctcc agtacagcag agacgtccgg aaattgctcc tgagcatcaa 2040
cgtgacgaac acccggaact cggagcgctc cggggaggac gcccacgagg cgtgctcac 2100
cctgggtggg cctcccgccc tgcctgtgtc ctgagtgccc cccccgggg cctgccaagc 2160
taatgagacc atcttttgcg agctggggaa ccccttcaaa cggaaccaga ggatggagct 2220
gctcatcgcc tttgaggtca tcgggggtgac cctgcacaca agggaccttc aggtgcagct 2280
gcagctctcc acgtcgagtc accaggacaa cctgtggccc atgatcctca ctctgctggt 2340
ggactataca ctccagacct cgcttagcat ggtaaatac cggtacaaa gcttctttg 2400
ggggacagtg atgggtgagt ctggcatgaa aactgtggag gatgtaggaa gccccctca 2460
gtatgaattc cagtggggcc caatggggga ggggctggtg ggcctgggga ccctggtcct 2520
aggtctggag tggccctacg aagtcagcaa tgccaagtgg ctgctgtatc ccacggagat 2580
cacgctccat ggcaatgggt cctggccctg ccgaccacct ggagacctta tcaacctct 2640
caacctcact cttctgacc ctggggacag gccatcatcc ccacagcgca ggcgccgaca 2700
gctggatcca gggggaggcc agggcccccc acctgtcact ctggctgctg ccaaaaaagc 2760
caagtctgag actgtgctga cctgtgccac agggcggtgc cactgtgtgt ggctagagt 2820
ccccatccct gatcccccg ttgtcaccaa cgtgactgtg aaggcacgag tgtggaacag 2880
caccttcac accagcatcc ccaccatcaa catggagaac aagaccaggt ggttctctgt 3000
ggacattgac tcggagctgg tggaggagct gccggccgaa atcgagctgt ggctggtgct 3060
ggtggccgtg ggtgcagggc tgctgctgct ggggctgatc atcctcctgc tgtggaagt 3120

```

```

tgactttcttt aagcgggaccc gctattatca gatcatgccc aagtaccacg cagtgcggat 3180
ccgggaggag gagcgctacc cacctccagg gagcaccctg cccaccaaga agcactgggt 3240
gaccagctgg cagactcggg accaatacta ctgacgtcct ccctgatccc accccctcct 3300
ccccagtggt cccctttctt cctatttatc ataagttatg cctctgacag tccacagggg 3360
ccaccacctt tggttgtag cagcaggttc aggcacatac acctcgtcaa gagcatgcac 3420
atgctgtctg gcctgggga tcttccaca ggagggccag cgctgtggac cttacaacgc 3480
cgagtgcact gcattcctgt gccctagatg cacgtggggc cactgctcg tggactgtgc 3540
tggtgcatca cggatggtgc atgggctcgc cgtgtctcag cctctgccag cgccagcgcc 3600
aaaacaagcc aaagagcctc ccaccagagc cgggaggaaa agggccctgc aatgtggtga 3660
cacctccctt ttcacacctg gatccatctt gagagccaca gtcactggat tgactttgct 3720
gtcaaaacta ctgacaggga gcagccccc ggccgctggc tggtgggccc ccaattgaca 3780
cccatgccag agaggtgggg atcctgccta aggttgtcta cgggggcact tggaggacct 3840
ggcgtgctca gacccaacag caaaggaact agaaagaagg acccagaagg cttgctttcc 3900
tgcatctctg tgaagcctct ctcttggtcc acagactgaa ctgcagggga gtgcagcagg 3960
aaggaacaaa gacaggcaaa cggcaacgta gcctgggctc actgtgctgg ggcatggcgg 4020
gatcctccac agagaggagg ggaccaatc tggacagaca gatgttggga ggatacagag 4080
gagatgccac ttctcactca ccactaccag ccagcctcca gaaggcccca gagagaccct 4140
gcaagaccac ggaggagacc gacacttgaa tgtagtaata ggcagggggc cctgccaccc 4200
catccagcca gacccagct gaacctgcg tcaggggcct agaggtggag ttcttagcta 4260
tccttggtt tctgtgccag cctggctctg cccctcccc atgggctgtg tcctaaggcc 4320
catttgagaa gctgaggcta gttccaaaaa cctctcctga cccctgcctg ttggcagccc 4380
actcccagc cccagccct tccatggtac tgtagcagg gaattccctc cccctccttg 4440
tgctttcttt gtatataggc ttctcaccgc gaccaataaa cagctcccag tttgt 4495

```

&lt;210&gt; 155

&lt;211&gt; 1066

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 155

```

Met Gly Pro Gly Pro Ser Arg Ala Pro Arg Ala Pro Arg Leu Met Leu
 1          5          10          15
Cys Ala Leu Ala Leu Met Val Ala Ala Gly Gly Cys Val Val Ser Ala
 20          25          30
Phe Asn Leu Asp Thr Arg Phe Leu Val Val Lys Glu Ala Gly Asn Pro
 35          40          45
Gly Ser Leu Phe Gly Tyr Ser Val Ala Leu His Arg Gln Thr Glu Arg
 50          55          60
Gln Gln Arg Tyr Leu Leu Leu Ala Gly Ala Pro Arg Glu Leu Ala Val
 65          70          75          80
Pro Asp Gly Tyr Thr Asn Arg Thr Gly Ala Val Tyr Leu Cys Pro Leu
 85          90          95
Thr Ala His Lys Asp Asp Cys Glu Arg Met Asn Ile Thr Val Lys Asn
100          105          110
Asp Pro Gly His His Ile Ile Glu Asp Met Trp Leu Gly Val Thr Val
115          120          125
Ala Ser Gln Gly Pro Ala Gly Arg Val Leu Val Cys Ala His Arg Tyr
130          135          140
Thr Gln Val Leu Trp Ser Gly Ser Glu Asp Gln Arg Arg Met Val Gly
145          150          155          160
Lys Cys Tyr Val Arg Gly Asn Asp Leu Glu Leu Asp Ser Ser Asp Asp
165          170          175
Trp Gln Thr Tyr His Asn Glu Met Cys Asn Ser Asn Thr Asp Tyr Leu
180          185          190
Glu Thr Gly Met Cys Gln Leu Gly Thr Ser Gly Gly Phe Thr Gln Asn
195          200          205
Thr Val Tyr Phe Gly Ala Pro Gly Ala Tyr Asn Trp Lys Gly Asn Ser
210          215          220

```

Tyr	Met	Ile	Gln	Arg	Lys	Glu	Trp	Asp	Leu	Ser	Glu	Tyr	Ser	Tyr	Lys
225					230					235					240
Asp	Pro	Glu	Asp	Gln	Gly	Asn	Leu	Tyr	Ile	Gly	Tyr	Thr	Met	Gln	Val
				245					250					255	
Gly	Ser	Phe	Ile	Leu	His	Pro	Lys	Asn	Ile	Thr	Ile	Val	Thr	Gly	Ala
				260				265					270		
Pro	Arg	His	Arg	His	Met	Gly	Ala	Val	Phe	Leu	Leu	Ser	Gln	Glu	Ala
		275					280					285			
Gly	Gly	Asp	Leu	Arg	Arg	Arg	Gln	Val	Leu	Glu	Gly	Ser	Gln	Val	Gly
	290					295					300				
Ala	Tyr	Phe	Gly	Ser	Ala	Ile	Ala	Leu	Ala	Asp	Leu	Asn	Asn	Asp	Gly
305					310					315					320
Trp	Gln	Asp	Leu	Leu	Val	Gly	Ala	Pro	Tyr	Tyr	Phe	Glu	Arg	Lys	Glu
				325					330					335	
Glu	Val	Gly	Gly	Ala	Ile	Tyr	Val	Phe	Met	Asn	Gln	Ala	Gly	Thr	Ser
				340				345					350		
Phe	Pro	Ala	His	Pro	Ser	Leu	Leu	Leu	His	Gly	Pro	Ser	Gly	Ser	Ala
		355					360					365			
Phe	Gly	Leu	Ser	Val	Ala	Ser	Ile	Gly	Asp	Ile	Asn	Gln	Asp	Gly	Phe
	370					375				380					
Gln	Asp	Ile	Ala	Val	Gly	Ala	Pro	Phe	Glu	Gly	Leu	Gly	Lys	Val	Tyr
385					390					395					400
Ile	Tyr	His	Ser	Ser	Ser	Lys	Gly	Leu	Leu	Arg	Gln	Pro	Gln	Gln	Val
				405					410					415	
Ile	His	Gly	Glu	Lys	Leu	Gly	Leu	Pro	Gly	Leu	Ala	Thr	Phe	Gly	Tyr
			420					425					430		
Ser	Leu	Ser	Gly	Gln	Met	Asp	Val	Asp	Glu	Asn	Phe	Tyr	Pro	Asp	Leu
		435					440					445			
Leu	Val	Gly	Ser	Leu	Ser	Asp	His	Ile	Val	Leu	Leu	Arg	Ala	Arg	Pro
	450					455					460				
Val	Ile	Asn	Ile	Val	His	Lys	Thr	Leu	Val	Pro	Arg	Pro	Ala	Val	Leu
465					470					475					480
Asp	Pro	Ala	Leu	Cys	Thr	Ala	Thr	Ser	Cys	Val	Gln	Val	Glu	Leu	Cys
				485					490					495	
Phe	Ala	Tyr	Asn	Gln	Ser	Ala	Gly	Asn	Pro	Asn	Tyr	Arg	Arg	Asn	Ile
			500					505					510		
Thr	Leu	Ala	Tyr	Thr	Leu	Glu	Ala	Asp	Arg	Asp	Arg	Arg	Pro	Pro	Arg
		515					520					525			
Leu	Arg	Phe	Ala	Gly	Ser	Glu	Ser	Ala	Val	Phe	His	Gly	Phe	Phe	Ser
		530				535					540				
Met	Pro	Glu	Met	Arg	Cys	Gln	Lys	Leu	Glu	Leu	Leu	Leu	Met	Asp	Asn
545					550					555					560
Leu	Arg	Asp	Lys	Leu	Arg	Pro	Ile	Ile	Ile	Ser	Met	Asn	Tyr	Ser	Leu
				565					570					575	
Pro	Leu	Arg	Met	Pro	Asp	Arg	Pro	Arg	Leu	Gly	Leu	Arg	Ser	Leu	Asp
			580					585					590		
Ala	Tyr	Pro	Ile	Leu	Asn	Gln	Ala	Gln	Ala	Leu	Glu	Asn	His	Thr	Glu
		595					600					605			
Val	Gln	Phe	Gln	Lys	Glu	Cys	Gly	Pro	Asp	Asn	Lys	Cys	Glu	Ser	Asn
	610					615					620				
Leu	Gln	Met	Arg	Ala	Ala	Phe	Val	Ser	Glu	Gln	Gln	Gln	Lys	Leu	Ser
625					630					635					640
Arg	Leu	Gln	Tyr	Ser	Arg	Asp	Val	Arg	Lys	Leu	Leu	Leu	Ser	Ile	Asn
				645					650					655	
Val	Thr	Asn	Thr	Arg	Thr	Ser	Glu	Arg	Ser	Gly	Glu	Asp	Ala	His	Glu
			660					665					670		
Ala	Leu	Leu	Thr	Leu	Val	Val	Pro	Pro	Ala	Leu	Leu	Leu	Ser	Ser	Val
			675				680						685		

163

Arg Pro Pro Gly Ala Cys Gln Ala Asn Glu Thr Ile Phe Cys Glu Leu  
 690 695 700  
 Gly Asn Pro Phe Lys Arg Asn Gln Arg Met Glu Leu Leu Ile Ala Phe  
 705 710 715 720  
 Glu Val Ile Gly Val Thr Leu His Thr Arg Asp Leu Gln Val Gln Leu  
 725 730 735  
 Gln Leu Ser Thr Ser Ser His Gln Asp Asn Leu Trp Pro Met Ile Leu  
 740 745 750  
 Thr Leu Leu Val Asp Tyr Thr Leu Gln Thr Ser Leu Ser Met Val Asn  
 755 760 765  
 His Arg Leu Gln Ser Phe Phe Gly Gly Thr Val Met Gly Glu Ser Gly  
 770 775 780  
 Met Lys Thr Val Glu Asp Val Gly Ser Pro Leu Lys Tyr Glu Phe Gln  
 785 790 795 800  
 Val Gly Pro Met Gly Glu Gly Leu Val Gly Leu Gly Thr Leu Val Leu  
 805 810 815  
 Gly Leu Glu Trp Pro Tyr Glu Val Ser Asn Gly Lys Trp Leu Leu Tyr  
 820 825 830  
 Pro Thr Glu Ile Thr Val His Gly Asn Gly Ser Trp Pro Cys Arg Pro  
 835 840 845  
 Pro Gly Asp Leu Ile Asn Pro Leu Asn Leu Thr Leu Ser Asp Pro Gly  
 850 855 860  
 Asp Arg Pro Ser Ser Pro Gln Arg Arg Arg Arg Gln Leu Asp Pro Gly  
 865 870 875 880  
 Gly Gly Gln Gly Pro Pro Pro Val Thr Leu Ala Ala Ala Lys Lys Ala  
 885 890 895  
 Lys Ser Glu Thr Val Leu Thr Cys Ala Thr Gly Arg Ala His Cys Val  
 900 905 910  
 Trp Leu Glu Cys Pro Ile Pro Asp Ala Pro Val Val Thr Asn Val Thr  
 915 920 925  
 Val Lys Ala Arg Val Trp Asn Ser Thr Phe Ile Glu Asp Tyr Arg Asp  
 930 935 940  
 Phe Asp Arg Val Arg Val Asn Gly Trp Ala Thr Leu Phe Leu Arg Thr  
 945 950 955 960  
 Ser Ile Pro Thr Ile Asn Met Glu Asn Lys Thr Thr Trp Phe Ser Val  
 965 970 975  
 Asp Ile Asp Ser Glu Leu Val Glu Glu Leu Pro Ala Glu Ile Glu Leu  
 980 985 990  
 Trp Leu Val Leu Val Ala Val Gly Ala Gly Leu Leu Leu Leu Gly Leu  
 995 1000 1005  
 Ile Ile Leu Leu Leu Trp Lys Cys Asp Phe Phe Lys Arg Thr Arg Tyr  
 1010 1015 1020  
 Tyr Gln Ile Met Pro Lys Tyr His Ala Val Arg Ile Arg Glu Glu Glu  
 1025 1030 1035 1040  
 Arg Tyr Pro Pro Pro Gly Ser Thr Leu Pro Thr Lys Lys His Trp Val  
 1045 1050 1055  
 Thr Ser Trp Gln Thr Arg Asp Gln Tyr Tyr  
 1060 1065

&lt;210&gt; 156

&lt;211&gt; 8747

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 156

cccagagccg cctccccctg ttgctggcat cccgagcttc ctccottgcc agccaggacg 60  
 ctgccgactt gtctttgccc gctgctccgc agacggggct gcaaagctgc aactaatggt 120

gttggcctcc	ctgcccacct	gtggaagcaa	ctgcgctgat	tgatgcgcca	cagacttttt	180
tcccctcgac	ctcgccggcg	taccctccca	cagatccagc	atcaccaggt	gaatgtacat	240
taggggtggt	tccccccag	cttcgggctt	tgtttggtt	tgattgtgtt	tggtctctcg	300
ctaagctgat	ttatgcagca	gaagccccac	cggttgagga	gaaacaaaag	ctcttttctt	360
tgtcccgag	caggctgcgg	agcccttgca	gagccctctc	tccagtcgcc	gccggggcct	420
tggccgtcga	aggaggtgct	tctcgcgag	accgcgggac	ccgccgtgcc	gagccgggag	480
ggccgtagg	gccctgagat	gccgagcgg	gcccgggccc	gcttacctgc	accgcttgct	540
ccgagccgcg	gggtccgcct	gctaggcctg	cggaaaacgt	cctagcgaca	ctcgcccgcg	600
ggccccgag	tcgcccggga	ggccgagccc	gcgtccggaa	ggcagccagg	cggcggggcg	660
ggggcgggct	gttttgcat	atgtgcggct	cgcccttgcc	tttttttacc	gctgcatttg	720
tctgcttgca	aaacgaccgg	cgaggtccc	cctcgcttcc	ctgggcagcc	tggtgtttt	780
cacttggtct	tggactgggc	caagtgga	acaatagatg	tgcatcttca	aatgcagcat	840
cctgtgccag	gtgccttgcg	ctgggtccag	aatgtggatg	gtgtgttcaa	gaggatttca	900
tttcaggtgg	atcaagaagt	gaacgttggt	atattgtttc	caatttaata	agcaaaggct	960
gctcagttga	ttcaatagaa	taccatctg	tgcatgttat	aataccact	gaaaatgaaa	1020
ttaatacca	ggtgacacca	ggagaagtgt	ctatccagct	gcgtccagga	gccgaagcta	1080
attttatgct	gaaagtcat	cctctgaaga	aatatcctgt	ggatctttat	tatcttggtg	1140
atgtctcagc	atcaatgcac	aataatatag	aaaaattaaa	ttccgttga	aacgatttat	1200
ctagaaaaat	ggcatttttc	tcccgtagct	ttcgtcttgg	atttggtc	tacgttgata	1260
aaacagtttc	accatccacc	ccgaaaggat	tcataatcaa	tgcatgtact	tgcatgtact	1320
acaatttaga	ctgcatgcct	ccccatggat	acatccatgt	gctgtctttg	acagagaaca	1380
tcactgagtt	tgagaaagca	gttcatagac	agaagatctc	tggaacata	gataaccag	1440
aaggaggttt	tgacgccatg	cttcaggcag	ctgtctgtga	aagtcataatc	ggatggcgaa	1500
aagaggctaa	aagattgctg	ctggtgatga	cagatcagac	gtctcatctc	gctcttgata	1560
gcaaattggc	aggcatagtg	gtgccaatg	acggaaactg	tcatctgaaa	aacaacgtct	1620
acgtcaaatac	gacaaccatg	gaacaccct	cactaggcca	actttcagag	aaattaatag	1680
acaacaacat	taatgtcatc	tttgagttc	aaggaaaaca	atttcatttg	tataaggatc	1740
ttctaccct	cttgccaggc	accattgctg	gtgaaataga	atcaaaggct	gcaaacctca	1800
ataatttggt	agtgaagcc	tatcagaagc	tcatttcaga	agtgaagtt	cagggtgaaa	1860
accaggtaca	aggcatctat	tttaacatta	ccgccatctg	tccagatggg	tccagaaagc	1920
caggcatgga	aggatgcaga	aacgtgacga	gcaatgatga	agttcttttc	aatgtaacag	1980
ttacaatgaa	aaaatgtgat	gtcacaggag	gaaaaaacta	tgcaataatc	aaacctattg	2040
gttttaaatga	aaccgctaaa	attcatatac	acagaaactg	cagctgtcag	tgtgaggaca	2100
acagaggacc	taaaggaaa	tgtgtagatg	aaacttttct	agattccaag	tgtttccagt	2160
gtgatgagaa	taaatgtcat	tttgatgaag	atcagttttc	ttctgagagt	tgcaagtac	2220
acaaggatca	gcctgtttgc	agtggtcgag	gagtttgtgt	ttgtgggaaa	tggtcatgtc	2280
acaaaattaa	gottggaaaa	gtgtatggaa	aatactgtga	aaaggatgac	ttttctgtc	2340
catatcacca	tggaaatctg	tgtgctgggc	atggagagt	tgaagcaggc	agatgccaat	2400
gottcagtg	ctgggaaggt	gatcgatgcc	agtgccttc	agcagcagcc	cagcactgtg	2460
tcaattcaaa	gggccaagt	tgcatggaa	gaggcacgtg	tgtgtgtgga	aggtgtgagt	2520
gcaccgatcc	caggagcatc	ggccgcttct	gtgaacactg	ccccacctgt	tatacagcct	2580
gcaaggaaaa	ctggaattgt	atgcaatgcc	ttcaccctca	caatttgtct	caggctatac	2640
ttgatcagtg	caaaaacctca	tgtgctctca	tggaacaaca	gcattatgtc	gaccaaactt	2700
cagaatgttt	ctccagccca	agctacttga	gaatattttt	catcattttc	atagttacat	2760
tottgattgg	gttgcttaaa	gtcctgatca	ttagacaggt	gatactacaa	tggaatagta	2820
ataaaaattaa	gtcctcatca	gattacagag	tgtagcctc	aaaaaaggat	aagttgattc	2880
tgcaaaagtgt	ttgcacaaga	gcagtcacct	accgacgtga	gaagcctgaa	gaaataaaaa	2940
tggaatcatg	caaattaaat	gctcatgaaa	ctttcaggtg	caacttctaa	aaaaagattt	3000
ttaaacactt	aatgggaaac	tggaattgtt	aataattgct	cctaaagatt	ataattttta	3060
aagtcacagg	aggagacaaa	ttgctcacgg	tcatgccagt	tgctggttgt	acactcgaa	3120
gaagactgac	aagtatcctc	atcatgatgt	gactcacata	gctgctgact	ttttcagaga	3180
aaaatgtgtc	ttactactgt	ttgagactag	tgctggttga	gcactttact	gtaatatata	3240
acttatttag	atcagcatag	aatgtagatc	ctctgaagag	cactgattac	actttacagg	3300
tacctgttat	ccctacgctt	cccagagaga	acaatgctgt	gagagagttt	agcattgtgt	3360
cactacaagg	gtacgataat	ccctgcaatg	gacatgtgag	gaaaaaaata	atctggcaag	3420
tatattctaa	ggttgccaaa	cacttcaaca	gttggtggtt	gaatagacaa	gaacagctag	3480
atgaataaat	gattcgtgtt	tcactctttc	aagaggtgaa	cagatacaac	cttaatctta	3540
aaagattatt	gctttttaaa	gtgtgtagtt	ttatgcatgt	gtgtttatgg	tttgcttatt	3600

tttgcaagat	ggataactaat	tccagcattc	tctcctcttt	gcctttatgt	tttgttttct	3660
tttttacagg	ataagtttat	gtatgtcaca	gatgactgga	ttaattaagt	gctaagttac	3720
tactgccata	aaaaactaat	aatacaatgt	cactttatca	gaatactagt	tttaaaagct	3780
gaatgttaat	aggggacact	gtaaagtatc	atcaaaacct	gaatagcttc	attgtgcaca	3840
agtgtggagt	tttgtatcct	cttacctggt	aaactgaagg	gattgtttgg	ccatttcatt	3900
tatcttatca	ttaattcaca	agatagttag	aaattctgcc	tcaagcaaag	taccacattt	3960
tgaatgtttt	cttagatttt	gattgcaagt	agatatcagc	atTTTTTaaa	tgaaaagcta	4020
tattatcttc	tcccttcaag	gcagcctaag	gatgttcttt	cccagaatca	ctccaaccct	4080
tcttgccaga	attcataaaa	gtacaaaatt	ggagaataga	tgatatctta	gaaataagct	4140
tttttttttt	tttttttttt	ttttgagacg	gagtttctct	cttgtcacc	aggctggagt	4200
gcaatggcgc	aattagggtt	cactgcaacc	tctgcctccc	gggttcaagc	agttctcctg	4260
cctcagcctc	cttagtagct	gggattacag	gcattccacca	ccgtgccag	ctaatttttg	4320
tatttttagt	agagacgggg	ttttgccatg	ttggacaggt	tgatctcaaa	ctcctgacct	4380
caggtgatct	accctcctcg	gcctcccaga	gtgttgaggat	tacaggcatg	agccacatg	4440
ccaggctgct	aattctcctt	tttagtgagt	tagggaactg	agcctcagaa	aacttaaacy	4500
atttctcaga	aaacactcaa	gtgataaagt	ggccacattg	gaaaggagt	tttatcttct	4560
cattgtcagg	ccagtgttca	ttgcacaata	tcatgtctacc	tcttgaatct	ttaaaatatt	4620
caattggcaa	atgtttttca	atgtgattta	ctcatgtctt	aagtgtatga	ggaaagttca	4680
aagcaaaata	gaaaggaata	attcaaactg	aattgtccat	aatcagcttc	cagtctttca	4740
tgctaactcag	cttcttaaga	gactgaagta	tgccatacct	acaggggaat	tccttcacac	4800
catagcctgt	atgaacagt	ttccctggag	ttctccagt	ctcagcttga	gaccttgata	4860
cacgggccat	gagccctgtc	ttccccaatg	gaaatttatt	tacacttacc	ttatccctat	4920
ggacttagtc	tgattttatt	ggctaggagt	ctaacagtcc	tgtgtggata	tacagttttg	4980
cccatgacaa	caaaggaatc	tatccgaaat	atcttttttt	ttataataaa	cttccaagat	5040
ttgctgtctt	ccagcacttg	agttaaagta	ctagatactg	cattttgatg	aagactaacc	5100
ccatctcata	ttctacccta	aagagaactg	aaaaacctat	aataagttgt	tctggagcca	5160
ataaacacag	cagctctgtt	agatgtcttc	tacagccaag	camtttcaat	gctaacttga	5220
actgcatttc	cttcctcaaa	tgagagattg	acataattca	gtactgtgag	tcacttgtat	5280
aagaaacctt	tgatcactaa	aaataatgta	aaaattgggt	ttagtagcct	aatacacata	5340
acgttcttct	tataaaggaa	aatggatgga	tgccctgacaa	ccctccaaaa	gaaaaaagtg	5400
taagatagcc	attaagatga	tgacaatttt	tgaaatgaac	attatgatat	ttatgaacaa	5460
taaacaattt	tccgtatgga	atgaattatc	caaaaagagt	ataacaaaat	gaaatcctta	5520
aaaatccaga	gtttatattt	tttttatacc	ctcacttggt	tgactaact	ttatagtggg	5580
ccaaggctgt	taccatagga	agggacaaac	ttccttgtag	gcaactcagt	gttagacgat	5640
gattgtgggt	atgcttgcaa	agtcttggtc	ttatcttttt	tgtttttact	taaaaagcta	5700
atTTTTTaaag	attgtagggc	ttgtatttta	cttgaataat	tgatatcttc	ctgtgtaatg	5760
atttgtgaga	tgagaattaa	tatttgacta	gttagaatta	attaaatggt	aagggaacac	5820
agggtagctc	taggttaaat	aatgtatgca	attagagtct	atTTTcaact	aatatggcca	5880
caggagcctt	ttgatattca	ttgatattaa	acacaattaa	tgaaatttta	aattgttaac	5940
agaattgaga	acttgaaaca	cacttttagt	actgcagcat	ttttgtgccc	taaagtatgt	6000
aatgatttat	aaatgtgcca	tacatacact	acaacataac	atTTgctttg	ttatgcattt	6060
tatttctctg	gggacaccat	tgactgcag	tgacacgta	tttataaaca	tttgttatat	6120
ttttggaaac	ttgctaatat	ttattaagtc	atagactttt	ctggaggact	taaaaattca	6180
ctaaaaatct	gattatgtct	taaatgttca	gtttatcttt	ggtttattaa	aataaaaaaa	6240
aaatctaaga	ttaaacacag	tagatatctc	tgagggcaat	tttccaaaac	tcaacattaa	6300
aatttgtgga	tgcatgagat	gcaatccttc	aaagaatgaa	tctgaaatat	atTTTTaata	6360
tttacttaat	atccactgaa	gatattctta	tgcaagacaa	gagtcagcca	tcagacactg	6420
aaatatatta	tgatagatta	tgaagaattt	tctctgtaga	attatattct	tcctggaacc	6480
tggtagagta	gattagactc	aaaggctttt	tcttctcttt	cttactcctg	ttttttccac	6540
tcactcttcc	caagagattt	cctaaagctt	caagcttaat	aagcctaata	gtgaaaaata	6600
actgaattta	atggtataat	gaagttcttc	atTTccagac	atctttaatt	gatcttaaag	6660
ctcatttgag	tctttgcccc	tgaacaaaga	cagacccatt	aaaatctaag	aattctaaat	6720
tttcacaact	gtttgagctt	cttttcattt	tgaaggattt	ggaatatata	tgTTTTcata	6780
aaagtatcaa	gtgaaatata	gttacatggg	agctcaatca	tgtgcagatt	gcattctgtt	6840
atggtgactc	aatattttaat	ttacaactat	ccttattttt	attgacctca	agaactccat	6900
tttatgcaat	gcagaccact	gagatatagc	taacattctt	tcaataaatt	ttccttttct	6960
tttataaatt	ctctatagca	aatttttatg	tataactgat	tatacatatc	catattttata	7020
tttcattgat	tccaagacat	cacttttttca	atttaacatc	tctgaaattg	tgacattttct	7080

```

tgcaactgtt ggcacttcag atgcagtgtt taaaattatg cttgaataaa tattacacta 7140
atccaacttt acctaaacgt ttatgcatct aggcaaattt tgttttctta taaagatttg 7200
agagcccatg tatgacaaaa tatgaaggcg aaattttaagg acaattgagt cacgcacaac 7260
tcaacatgga gcctaactga ttatcagctc agatcccgca tatcttgagt ttacaaaagc 7320
tctttcaggt ccccatthtt actttacgtg agtgcgaatg atttcagcaa accctaactt 7380
aactaacaag aatgggtagg tatgtctacg tticattaac aaatttttat tatttttatt 7440
ctattatatg agatcctttt atattatcat ctcactttta aacaaaatta actggaaaaa 7500
tattacatgg aactgtcata gttagggttt gcagcatctt acatgtcttg tatcaatggc 7560
aggagaaaaa tatgataaaa acaatcagtg ctgtgaaaaa caactttctt ctagagtccct 7620
cttacttttt attcttcttt atcatttgtg ggtttttccc ccttggtctt gatcacttta 7680
acttcaagct tatgtaacga ctgttataaa actgcatatt taaattattt gaattatatg 7740
aaataattgt tcagctatct gggcagctgt taatgtaaac ctgagagtaa taacactact 7800
cttttatcta cctggaatac ttttctgcat aaaatttatc tttgtaagct aactctatta 7860
atcagggttc ttctagcctc tgcaacctac ttcagttaga attgtctaata actgctctat 7920
taatcaggtt tctagcctct acaacctact tcagttaaaa ttgtctaata cagcaatatt 7980
taaaaaaaaa acactgcaat tgtcaaggat ggaaaatgtg tgatttgtgt aaacaatttt 8040
taccaacttt acattttcct acagataaat gtgaaatttt gataagaagt ctacgcaatg 8100
acaagtatgg tacataaatt ttattaagaa tattgagtat aaagtacttt aattctaaat 8160
tataagaaaa tatacattht cacatattaa tatagaaatt catttttgtt atatttaaca 8220
tagctttttaa actatthttac attagctact tcattatggt ttcttgaact tctgaaaaaa 8280
attagaaatg tattaacttt atcagtaaca taaaaactta ttttgthtca cctaacgaat 8340
actgcgtttg taaaaataaa tttaatatag aatatathtt taaattaaat atttgaatat 8400
aaaatagctc taagaaagaa gcaaattatc actgaacata tttcttatta tttctggctt 8460
tgaattatac gtaacttaaa ttgtcttaaa tgatacagaa tattggagaa tatgatactt 8520
tcacataata tactatgaac ctgttcataa aactctgatt gactactaac ttctgtttta 8580
tgtattttatt aaagagctga cactgtagtt tgtggtgaga tgthttattt tctaacagag 8640
cttataacag ttaggacaag gcatttaatt aatgcatcat tctgtttagt agtaggtgtt 8700
aatcaatatg aaattctctg ttttaaaaaa aaaatgtaaa aatctaa 8747

```

&lt;210&gt; 157

&lt;211&gt; 769

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 157

```

Met Cys Gly Ser Ala Leu Ala Phe Phe Thr Ala Ala Phe Val Cys Leu
1          5          10          15
Gln Asn Asp Arg Arg Gly Pro Ala Ser Phe Leu Trp Ala Ala Trp Val
20          25          30
Phe Ser Leu Val Leu Gly Leu Gly Gln Gly Glu Asp Asn Arg Cys Ala
35          40          45
Ser Ser Asn Ala Ala Ser Cys Ala Arg Cys Leu Ala Leu Gly Pro Glu
50          55          60
Cys Gly Trp Cys Val Gln Glu Asp Phe Ile Ser Gly Gly Ser Arg Ser
65          70          75          80
Glu Arg Cys Asp Ile Val Ser Asn Leu Ile Ser Lys Gly Cys Ser Val
85          90          95
Asp Ser Ile Glu Tyr Pro Ser Val His Val Ile Ile Pro Thr Glu Asn
100         105         110
Glu Ile Asn Thr Gln Val Thr Pro Gly Glu Val Ser Ile Gln Leu Arg
115         120         125
Pro Gly Ala Glu Ala Asn Phe Met Leu Lys Val His Pro Leu Lys Lys
130         135         140
Tyr Pro Val Asp Leu Tyr Tyr Leu Val Asp Val Ser Ala Ser Met His
145         150         155         160
Asn Asn Ile Glu Lys Leu Asn Ser Val Gly Asn Asp Leu Ser Arg Lys
165         170         175
Met Ala Phe Phe Ser Arg Asp Phe Arg Leu Gly Phe Gly Ser Tyr Val

```



										180					185					190					
Asp	Lys	Thr	Val	Ser	Pro	Tyr	Ile	Ser	Ile	His	Pro	Glu	Arg	Ile	His										
										195					200					205					
Asn	Gln	Cys	Ser	Asp	Tyr	Asn	Leu	Asp	Cys	Met	Pro	Pro	His	Gly	Tyr										
										210					215					220					
Ile	His	Val	Leu	Ser	Leu	Thr	Glu	Asn	Ile	Thr	Glu	Phe	Glu	Lys	Ala										
										225					230					235					
Val	His	Arg	Gln	Lys	Ile	Ser	Gly	Asn	Ile	Asp	Thr	Pro	Glu	Gly	Gly										
										245					250					255					
Phe	Asp	Ala	Met	Leu	Gln	Ala	Ala	Val	Cys	Glu	Ser	His	Ile	Gly	Trp										
										260					265					270					
Arg	Lys	Glu	Ala	Lys	Arg	Leu	Leu	Leu	Val	Met	Thr	Asp	Gln	Thr	Ser										
										275					280					285					
His	Leu	Ala	Leu	Asp	Ser	Lys	Leu	Ala	Gly	Ile	Val	Val	Pro	Asn	Asp										
										290					295					300					
Gly	Asn	Cys	His	Leu	Lys	Asn	Asn	Val	Tyr	Val	Lys	Ser	Thr	Thr	Met										
										305					310					315					
Glu	His	Pro	Ser	Leu	Gly	Gln	Leu	Ser	Glu	Lys	Leu	Ile	Asp	Asn	Asn										
										325					330					335					
Ile	Asn	Val	Ile	Phe	Ala	Val	Gln	Gly	Lys	Gln	Phe	His	Trp	Tyr	Lys										
										340					345					350					
Asp	Leu	Leu	Pro	Leu	Leu	Pro	Gly	Thr	Ile	Ala	Gly	Glu	Ile	Glu	Ser										
										355					360					365					
Lys	Ala	Ala	Asn	Leu	Asn	Asn	Leu	Val	Val	Glu	Ala	Tyr	Gln	Lys	Leu										
										370					375					380					
Ile	Ser	Glu	Val	Lys	Val	Gln	Val	Glu	Asn	Gln	Val	Gln	Gly	Ile	Tyr										
										385					390					395					
Phe	Asn	Ile	Thr	Ala	Ile	Cys	Pro	Asp	Gly	Ser	Arg	Lys	Pro	Gly	Met										
										405					410					415					
Glu	Gly	Cys	Arg	Asn	Val	Thr	Ser	Asn	Asp	Glu	Val	Leu	Phe	Asn	Val										
										420					425					430					
Thr	Val	Thr	Met	Lys	Lys	Cys	Asp	Val	Thr	Gly	Gly	Lys	Asn	Tyr	Ala										
										435					440					445					
Ile	Ile	Lys	Pro	Ile	Gly	Phe	Asn	Glu	Thr	Ala	Lys	Ile	His	Ile	His										
										450					455					460					
Arg	Asn	Cys	Ser	Cys	Gln	Cys	Glu	Asp	Asn	Arg	Gly	Pro	Lys	Gly	Lys										
										465					470					475					
Cys	Val	Asp	Glu	Thr	Phe	Leu	Asp	Ser	Lys	Cys	Phe	Gln	Cys	Asp	Glu										
										485					490					495					
Asn	Lys	Cys	His	Phe	Asp	Glu	Asp	Gln	Phe	Ser	Ser	Glu	Ser	Cys	Lys										
										500					505					510					
Ser	His	Lys	Asp	Gln	Pro	Val	Cys	Ser	Gly	Arg	Gly	Val	Cys	Val	Cys										
										515					520					525					
Gly	Lys	Cys	Ser	Cys	His	Lys	Ile	Lys	Leu	Gly	Lys	Val	Tyr	Gly	Lys										
										530					535					540					
Tyr	Cys	Glu	Lys	Asp	Asp	Phe	Ser	Cys	Pro	Tyr	His	His	Gly	Asn	Leu										
										545					550					555					
Cys	Ala	Gly	His	Gly	Glu	Cys	Glu	Ala	Gly	Arg	Cys	Gln	Cys	Phe	Ser										
										565					570					575					
Gly	Trp	Glu	Gly	Asp	Arg	Cys	Gln	Cys	Pro	Ser	Ala	Ala	Ala	Gln	His										
										580					585					590					
Cys	Val	Asn	Ser	Lys	Gly	Gln	Val	Cys	Ser	Gly	Arg	Gly	Thr	Cys	Val										
										595					600					605					
Cys	Gly	Arg	Cys	Glu	Cys	Thr	Asp	Pro	Arg	Ser	Ile	Gly	Arg	Phe	Cys										
										610					615					620					
Glu	His	Cys	Pro	Thr	Cys	Tyr	Thr	Ala	Cys	Lys	Glu	Asn	Trp	Asn	Cys										
										625					630					635					
Met	Gln	Cys	Leu	His	Pro	His	Asn	Leu	Ser	Gln	Ala	Ile	Leu	Asp	Gln										

				645				650				655			
Cys	Lys	Thr	Ser	Cys	Ala	Leu	Met	Glu	Gln	Gln	His	Tyr	Val	Asp	Gln
660				665				670							
Thr	Ser	Glu	Cys	Phe	Ser	Ser	Pro	Ser	Tyr	Leu	Arg	Ile	Phe	Phe	Ile
675				680				685							
Ile	Phe	Ile	Val	Thr	Phe	Leu	Ile	Gly	Leu	Leu	Lys	Val	Leu	Ile	Ile
690				695				700							
Arg	Gln	Val	Ile	Leu	Gln	Trp	Asn	Ser	Asn	Lys	Ile	Lys	Ser	Ser	Ser
705				710				715				720			
Asp	Tyr	Arg	Val	Ser	Ala	Ser	Lys	Lys	Asp	Lys	Leu	Ile	Leu	Gln	Ser
725				730				735							
Val	Cys	Thr	Arg	Ala	Val	Thr	Tyr	Arg	Arg	Glu	Lys	Pro	Glu	Glu	Ile
740				745				750							
Lys	Met	Asp	Ile	Ser	Lys	Leu	Asn	Ala	His	Glu	Thr	Phe	Arg	Cys	Asn
755				760				765							
Phe															

```
<210> 158
<211> 3999
<212> DNA
<213> Homo sapiens
```

<b>&lt;400&gt;</b>	<b>158</b>					
caagattcca	catttgatgg	ggtgactgac	aaacccatct	tagactgctg	tgcctgcgga	60
actgccaaagt	acagactcac	attttatggg	aattgggtccg	agaagacaca	cccaaaggat	120
taccctcgtc	gggccaacca	ctgggtctgcg	atcatcgagg	gatccactc	caagaattat	180
gtactgtggg	aatatggagg	atgtgccagc	gaaggcgtca	aacaagttgc	agaattgggc	240
tcaccctgga	aaatggagga	agaaattcga	caacagagtg	atgaggtcct	caccgtcac	300
aaagccaaag	cccaatggcc	agcctggcag	cctctcaacg	tgagagcagc	accttcagct	360
gaattttccg	tggacagaac	gcgccattta	atgtccttcc	tgaccatgat	gggcctagt	420
cccgaactgga	acgtaggctt	atctgcagaa	gatctgtgca	ccaaggaatg	tggctgggtc	480
cagaaggtgg	tgcaagacct	gattccctgg	gacgttgga	ccgacagcgg	ggtgacctat	540
gagtcaccca	acaaacccac	cattccccag	gagaaaatcc	ggcccctgac	cagcctggac	600
catcctcaga	gtcctttcta	tgaccagag	ggtgggtcca	tcactcaagt	agccagagtt	660
gtcatcgaga	gaatcgcacg	gaagggtgaa	caatgcaata	ttgtacctga	caatgtcgat	720
gatattgtag	ctgacctggc	tccagaagag	aaagatgaag	atgacacccc	tgaaacctgc	780
atctactcca	actggtcccc	atgggtcgcc	tgcagctcct	ccactgtga	caaaggcaag	840
aggatgcgac	agcgcatgct	agaagcacag	ctggacctca	gcgtcccctg	ccctgacacc	900
caggacttcc	agccctgcat	gggccctggc	tgcagtgacg	aagacggctc	cacctgcacc	960
atgtccgagt	ggatcacctg	gtcgccctgc	agcatctcct	gcggcatggg	catgaggtcc	1020
cgggagaggt	atgtgaagca	gttcccgag	gacggctccg	tgtgcacgct	gcccactgag	1080
gaaacggaga	agtgcacggt	caacgaggag	tgtctcccca	gcagctgcct	gatgaccgag	1140
tggggcgagt	gggacgagtg	cagcgccacc	tgcggcatgg	gcattgaagaa	gcggcaccgc	1200
atgatcaaga	tgaaccccg	agatggctcc	atgtgcaaag	ccgagacatc	acaggcagag	1260
aagtgcattga	tgcagagatg	ccacaccatc	ccatgcttgc	tgtccccatg	gtccgagttg	1320
agtgaactgca	gcgtgacctg	cgggaagggc	atgcgaaccc	gcagcgggat	gctcaagtct	1380
ctggcagaac	ttggagactg	caatgaggat	ctggagcagg	tggagaagtg	catgtctcct	1440
gaatgcccc	ttgactgtga	gtccaccgag	tggtcccagt	ggtcggaatg	taacaagtca	1500
tgtgggaaag	gccacgtgat	tccaacccgg	atgatccaaa	tggagcctca	gtttggaggt	1560
gcaccctgcc	cagagactgt	gcagcgaaaa	aagtgccgca	tccgaaaatg	ccttcgaaat	1620
ccatccatcc	aaaagctacg	ctggagggag	gcccgagaga	gccggcggag	tgagcagctg	1680
aaggaagagt	ctgaagggga	gcagttccca	ggttgtagga	tgcgcccattg	gacggcctgg	1740
tcagaatgca	ccaaactgtg	cggaggtgga	atccaggaac	gttacatgac	tgtaaagaag	1800
agattcaaaa	gtctccagtt	taccagctgc	aaagacaaga	aggagatcag	agcatgcaat	1860
gttcatcctt	gttagcaagg	gtacgagttc	ccaggcgctg	cactctagat	tccagagtca	1920
ccaatggctg	gattatttgc	ttgtttaaga	caattttaaat	tgtgtacqct	agttttcatt	1980

```

tttgcagtgt ggttcgcccc gtagtcttgt ggatgccaga gacatccttt ctgaatactt 2040
cttgatgggt acaggctgag tggggcgccc tcacctccag ccagcctctt cctgcagagg 2100
agtagtgtca gccaccttgt actaagctga aacatgtccc tctggagctt ccacctggcc 2160
agggaggacg gagactttga cctactccac atggagaggc aacctgtctt ggaagtgaact 2220
atgcctgagt cccagggtgc ggcaggtagg aaacattcac agatgaagac agcagattcc 2280
ccacattctc atctttggcc tgttcaatga aaccattgtt tgcccactct ttcttagtgg 2340
aacttttaggt ctcttttcaa gtctcctcag tcatcaatag ttcttgggga aaaacagagc 2400
tggtagactt gaagaggagc attgatgttg ggtggctttt gttctttcac tgagaaattc 2460
ggaatacatt tgtctcacc .ctgataattg ttcttgatgc ccccccaaca aaaataaata 2520
aataaattat ggctgcttta tttaaatata aggtagctag tttttacacc tgagataaat 2580
aataagctta gagtgatttt ttcccttgct tttgggggtt cagaggagta tgtacaattc 2640
ttctgggaag ccagccttct gaactttttg gtactaaatc cttattggaa ccaagacaaa 2700
ggaagcaaaa ttggtctctt tagagaccaa tttgcctaaa ttttaaaatc ttcttacaca 2760
catctagacg ttcaagtttg caaatcagtt tttagcaaga aaacattttt gctatacaaa 2820
catttttgta agtctgcccc aagccccccc aatgcattcc ttcaacaaaa tacaatctct 2880
gtacttttaa gttatttttag tcatgaaatt ttatatgcag agagaaaaag ttaccgagac 2940
agaaaaacaaa tctaagggaag aggaatatta tgggattaag ctgagcaagc aattctggtg 3000
gaaagtcaaaa cctgtcagtg ctccacacca gggctgtggt cctcccagac atgcatagga 3060
atggccacag gtttacctg ccttcccagc aattataagc acaccagatt caggagact 3120
gaccaccaag gcatagtgtg aaaggacatt ttctcagttg ggtccatcag cagtttttct 3180
tcctgcattt attgttgaaa actattgttt catttcttct tttataggcc ttattactgc 3240
ttaatccaaa tgtgtacat tggtagaca catacaatgc tctgaataca ctacgaattt 3300
gtattaaaca catcagaata tttccaaata caacatagta tagtcctgaa tatgtacttt 3360
taacacaaga gagactattc aataaaaact cactgggtct ttcatgtctt taagctaagt 3420
aagtgttcag aaggttcttt tttatattgt cctccacctc catcattttc aataaaaagat 3480
agggcttttg ctcccttggt cttggaggga ccattattac atctctgaac tacctttgta 3540
tccaacatgt tttaaatcct taaatgaatt gctttctccc aaaaaaagca caataaaaag 3600
aaacacaaga ttttaattatt ttttactttg gggggaaaaa agtcctcatg tagaagcacc 3660
cacttttgca atgttgttct aagctatcta tctaactctc agcccatgat aaagttcctt 3720
aagctggtga ttctaataca aggacaagcc accctagtgt ctcatgtttg tatttgggtc 3780
cagttgggta cattttaaaa tcttgatttt ggagacttaa aaccagggtta atggctaaga 3840
atgggtaaca tgactcttgt tggattgtta ttttttgttt gcaatgggga atttataaga 3900
agcatcaagt ctctttctta ccaaagtctt gttaggtggt ttatagttct tttggctaac 3960
aatcattttt ggaaataaag attttttact acaaaaatg 3999

```

&lt;210&gt; 159

&lt;211&gt; 624

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 159

```

Gln Asp Ser Thr Phe Asp Gly Val Thr Asp Lys Pro Ile Leu Asp Cys
 1           5           10           15
Cys Ala Cys Gly Thr Ala Lys Tyr Arg Leu Thr Phe Tyr Gly Asn Trp
 20           25           30
Ser Glu Lys Thr His Pro Lys Asp Tyr Pro Arg Arg Ala Asn His Trp
 35           40           45
Ser Ala Ile Ile Gly Gly Ser His Ser Lys Asn Tyr Val Leu Trp Glu
 50           55           60
Tyr Gly Gly Tyr Ala Ser Glu Gly Val Lys Gln Val Ala Glu Leu Gly
 65           70           75           80
Ser Pro Val Lys Met Glu Glu Glu Ile Arg Gln Gln Ser Asp Glu Val
 85           90           95
Leu Thr Val Ile Lys Ala Lys Ala Gln Trp Pro Ala Trp Gln Pro Leu
100          105          110
Asn Val Arg Ala Ala Pro Ser Ala Glu Phe Ser Val Asp Arg Thr Arg
115          120          125
His Leu Met Ser Phe Leu Thr Met Met Gly Pro Ser Pro Asp Trp Asn

```

170

130		135		140
Val Gly Leu Ser Ala	Glu Asp Leu Cys Thr Lys	Glu Cys Gly Trp Val		
145	150	155	160	
Gln Lys Val Val Gln	Asp Leu Ile Pro Trp Asp	Ala Gly Thr Asp Ser		
	165	170	175	
Gly Val Thr Tyr Glu	Ser Pro Asn Lys Pro Thr	Ile Pro Gln Glu Lys		
	180	185	190	
Ile Arg Pro Leu Thr	Ser Leu Asp His Pro Gln	Ser Pro Phe Tyr Asp		
	195	200	205	
Pro Glu Gly Gly Ser	Ile Thr Gln Val Ala Arg	Val Val Ile Glu Arg		
	210	215	220	
Ile Ala Arg Lys Gly	Glu Gln Cys Asn Ile Val	Pro Asp Asn Val Asp		
225	230	235	240	
Asp Ile Val Ala Asp	Leu Ala Pro Glu Glu Lys	Asp Glu Asp Asp Thr		
	245	250	255	
Pro Glu Thr Cys Ile	Tyr Ser Asn Trp Ser Pro	Trp Ser Ala Cys Ser		
	260	265	270	
Ser Ser Thr Cys Asp	Lys Gly Lys Arg Met Arg	Gln Arg Met Leu Lys		
	275	280	285	
Ala Gln Leu Asp Leu	Ser Val Pro Cys Pro Asp	Thr Gln Asp Phe Gln		
	290	295	300	
Pro Cys Met Gly Pro	Gly Cys Ser Asp Glu Asp	Gly Ser Thr Cys Thr		
305	310	315	320	
Met Ser Glu Trp Ile	Thr Trp Ser Pro Cys Ser	Ile Ser Cys Gly Met		
	325	330	335	
Gly Met Arg Ser Arg	Glu Arg Tyr Val Lys Gln	Phe Pro Glu Asp Gly		
	340	345	350	
Ser Val Cys Thr Leu	Pro Thr Glu Glu Thr Glu	Lys Cys Thr Val Asn		
	355	360	365	
Glu Glu Cys Ser Pro	Ser Ser Cys Leu Met Thr	Glu Trp Gly Glu Trp		
	370	375	380	
Asp Glu Cys Ser Ala	Thr Cys Gly Met Gly Met	Lys Lys Arg His Arg		
385	390	395	400	
Met Ile Lys Met Asn	Pro Ala Asp Gly Ser Met	Cys Lys Ala Glu Thr		
	405	410	415	
Ser Gln Ala Glu Lys	Cys Met Met Pro Glu Cys	His Thr Ile Pro Cys		
	420	425	430	
Leu Leu Ser Pro Trp	Ser Glu Trp Ser Asp Cys	Ser Val Thr Cys Gly		
	435	440	445	
Lys Gly Met Arg Thr	Arg Gln Arg Met Leu Lys	Ser Leu Ala Glu Leu		
	450	455	460	
Gly Asp Cys Asn Glu	Asp Leu Glu Gln Val Glu	Lys Cys Met Leu Pro		
465	470	475	480	
Glu Cys Pro Ile Asp	Cys Glu Leu Thr Glu Trp	Ser Gln Trp Ser Glu		
	485	490	495	
Cys Asn Lys Ser Cys	Gly Lys Gly His Val Ile	Arg Thr Arg Met Ile		
	500	505	510	
Gln Met Glu Pro Gln	Phe Gly Gly Ala Pro Cys	Pro Glu Thr Val Gln		
	515	520	525	
Arg Lys Lys Cys Arg	Ile Arg Lys Cys Leu Arg	Asn Pro Ser Ile Gln		
	530	535	540	
Lys Leu Arg Trp Arg	Glu Ala Arg Glu Ser Arg	Arg Ser Glu Gln Leu		
545	550	555	560	
Lys Glu Glu Ser Glu	Gly Glu Gln Phe Pro Gly	Cys Arg Met Arg Pro		
	565	570	575	
Trp Thr Ala Trp Ser	Glu Cys Thr Lys Leu Cys	Gly Gly Gly Ile Gln		
	580	585	590	
Glu Arg Tyr Met Thr	Val Lys Lys Arg Phe Lys	Ser Ser Gln Phe Thr		

	595		600		605
Ser	Cys Lys Asp Lys Lys Glu Ile Arg Ala Cys	Asn Val His Pro Cys			
610		615		620	

<210> 160  
 <211> 3408  
 <212> DNA  
 <213> Homo sapiens

<400> 160  
 caaaaaggct attacctgtg gggaaaagga aaagcaagat ctcatthaaga gccttgccat 60  
 gttgaaggac ggcttccgca ctgacagggg gtctcactca gacctgtggg ccagcagcag 120  
 ctctctggag agttcgagtt tcccgctacc gaaacagtac ctggatgtga gctcccagac 180  
 agacatctcg ggaagcttcg gcatcaacag caacaatcag ttggcagaga aggtcagatt 240  
 gcgccttcga tatgaagagg ctaagagaag gatcgccaac ctgaagatcc agctggccaa 300  
 gcttgacagt gaggcctggc ctgggggtgct ggactcagag agggaccggc tgatccttat 360  
 caacgagaag gaggagctgc tgaaggagat gcgcttcac agcccccgca agtggacca 420  
 gggggaggtg gacagctgg agatggcccg gaagcggctg gaaaaggacc tgcaggcagc 480  
 ccgggacacc cagagcaagg cgctgacgga gaggttaaag ttaaacagta agaggaacca 540  
 gcttgtgaga gaactggagg aagccaccgg gcaggtggca actctgcact ccagctgaa 600  
 aagtctctca agcagcatgc agtccctgtc ctccagcagc agccccggat ccctcacgtc 660  
 cagccggggc tccctgggtg catccagcct ggactcctcc acttcagcca gcttcactga 720  
 cctctactat gaccctttt agcagctgga ctccagagctg cagagcaagg tggagttcct 780  
 gctcctggag ggggccaccg gcttccggcc ctccaggtgc atcaccacca tccacgagga 840  
 tgaggtggcc aagaccaga aggcagaggg aggtggccgc ctgcaggctc tgcgttccct 900  
 gtctggcacc ccaaagtcca tgacctccct atccccacgt tctctctct cctccccctc 960  
 cccacctgtt tccctctca tggctgacct cctcctggct ggtgatgct tctcaactc 1020  
 cttggagttt gaagaccgg agctgagtc cactctttgt gaactgagcc ttggtaacag 1080  
 cgccaggaa agataccggc tggaggaaac aggaacggag ggcaagcagc tgggccaagc 1140  
 tgtgaatacg gccagggggt gtggcctgaa agtggcctgt gtctcagccg ccgtatcgga 1200  
 cgagtcagtg gctggagaca gtggtgtgta cgaggcttcc gtgcagagac tgggtgcttc 1260  
 agaagctgct gcatttgaca gtgacgaatc ggaagcagtg ggtgcgacc gaattcagat 1320  
 tgccctgaag tatgatgaga agaataagca atttgcaata ttaatcatcc agctgagtaa 1380  
 cctttctgct ctgttgagc aacaagacca gaaagtgaat atccgcgtgg ctgtccttcc 1440  
 ttgctctgaa agcacaacct gcctgttccg gaccggcct ctggacgcct cagacactct 1500  
 agtgttcaat gaggtgttct gggatccat gtccatcca gcccttcacc agaagacctt 1560  
 aagagtcgat gtctgtacca ccgacagggag ccatctggaa gagtgcctgg gagcgccca 1620  
 gatcagcctg gcggaggtct gccggtctgg ggagaggtcg actcgtggtt acaaccttct 1680  
 cagctacaaa tacttgaaga agcagagcag ggagctcaag ccagtgggag ttatggcccc 1740  
 tgccctcagg cctgccagca cggacgctgt gtctgctctg ttggaacaga cagcagtgga 1800  
 gctggagaag aggcaggagg gcaggagcag cacacagaca ctggaagaca gctggaggta 1860  
 tgaggagacc agtgagaatg aggcagtagc cgaggaagag gaggaggagg tggaggagga 1920  
 ggaggagaa gaggatgttt tcaccgagaa agcctcacct gatatggatg ggtaccagc 1980  
 attaaaggtg gacaaagaga ccaacacgga gacccggcc ccatcccca cagtgggtgcg 2040  
 acctaaggac cggagagtg gcacccgctc ccaggggcca tttcttcgag ggagcaccat 2100  
 catccgctct aagaccttct cccagggacc ccagagccag tacgtgtgcc ggctgaatcg 2160  
 gagtgatagt gacagctcca ctctgtccaa aaagccacct tttgttcgaa actccctgga 2220  
 gcgacgcagc gtccggatga agcggccttc ctgggtcaag tcgctgcgct ccgagcgtct 2280  
 gatccgtacc tcgctggacc tggagttaga cctgcaggcg acaagaacct ggcacagcca 2340  
 actgaccag gagatctcgg tgctgaagga gctcaaggag cagctggaac aagccaagag 2400  
 ccacggggag aaggagctgc cacagtgggt gcgtgaggac gagcgtttcc gcctgctgct 2460  
 gaggatgctg gagaagcgga tggaccgagc ggagcacaag ggtgagcttc agacagaaa 2520  
 gatgatgagg gcagctgcca aggatgtgca caggctccga ggccagagct gtaaggaacc 2580  
 cccagaagtt cagtctttca gggagaagat ggcatcttcc acccgccctc ggatgaatat 2640  
 cccagctctc tctgcagatg acgtctaata gccagaaaag tatttccttt gttccactga 2700  
 ccaggctgtg aacattgact gtggctaaag ttatttatgt ggtgttatat gaaggtactg 2760  
 agtcacaagt cctctagtgc tctgttgggt ttgaagatga accgactttt tagtttgggt 2820

172

```

cctactgttg ttattaaaaa cagaacaaaa acaaaacaca cacacacaca aaaacagaaa 2880
caaaaaaaaa cagcattaaa ataataagat tgtatagttt gtatatattag gagtgtattt 2940
ttgggaaaga aaattttaa gaactaaagc agtattgagt tgctgtctctt cttaaaatcg 3000
tttagatttt ttttggtttg tacagctcca ctttttagag gtcttactgc aataagaagt 3060
aatgcctggg ggacggtaat cctaataagga cgtcccgac ttgtcacagt acagctaatt 3120
tttcctagtt aacatatttt gtacaatatt aaaaaaatgc acagaaacca ttggggggga 3180
ttcagagggtg catccacgga tcttcttgag ctgtgacgtg tttttatgtg gctgccaac 3240
gtggagcggg cagtgtgata ggctgggtgg gctaagcagc ctagtctatg tgggtgacag 3300
gccacgtggg tctcagatgc ccagtgaagc cactaacatg agtgagggga gggctgtggg 3360
gaactccatt cagttttatc tccatcaata aagtggcctt tcaaaaag 3408

```

&lt;210&gt; 161

&lt;211&gt; 888

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 161

```

Lys Lys Ala Ile Thr Cys Gly Glu Lys Glu Lys Gln Asp Leu Ile Lys
1      5      10      15
Ser Leu Ala Met Leu Lys Asp Gly Phe Arg Thr Asp Arg Gly Ser His
20     25     30
Ser Asp Leu Trp Ser Ser Ser Ser Ser Leu Glu Ser Ser Ser Phe Pro
35     40     45
Leu Pro Lys Gln Tyr Leu Asp Val Ser Ser Gln Thr Asp Ile Ser Gly
50     55     60
Ser Phe Gly Ile Asn Ser Asn Asn Gln Leu Ala Glu Lys Val Arg Leu
65     70     75     80
Arg Leu Arg Tyr Glu Glu Ala Lys Arg Arg Ile Ala Asn Leu Lys Ile
85     90     95
Gln Leu Ala Lys Leu Asp Ser Glu Ala Trp Pro Gly Val Leu Asp Ser
100    105    110
Glu Arg Asp Arg Leu Ile Leu Ile Asn Glu Lys Glu Glu Leu Leu Lys
115    120    125
Glu Met Arg Phe Ile Ser Pro Arg Lys Trp Thr Gln Gly Glu Val Glu
130    135    140
Gln Leu Glu Met Ala Arg Lys Arg Leu Glu Lys Asp Leu Gln Ala Ala
145    150    155    160
Arg Asp Thr Gln Ser Lys Ala Leu Thr Glu Arg Leu Lys Leu Asn Ser
165    170    175
Lys Arg Asn Gln Leu Val Arg Glu Leu Glu Glu Ala Thr Arg Gln Val
180    185    190
Ala Thr Leu His Ser Gln Leu Lys Ser Leu Ser Ser Ser Met Gln Ser
195    200    205
Leu Ser Ser Gly Ser Ser Pro Gly Ser Leu Thr Ser Ser Arg Gly Ser
210    215    220
Leu Val Ala Ser Ser Leu Asp Ser Ser Thr Ser Ala Ser Phe Thr Asp
225    230    235    240
Leu Tyr Tyr Asp Pro Phe Glu Gln Leu Asp Ser Glu Leu Gln Ser Lys
245    250    255
Val Glu Phe Leu Leu Leu Glu Gly Ala Thr Gly Phe Arg Pro Ser Gly
260    265    270
Cys Ile Thr Thr Ile His Glu Asp Glu Val Ala Lys Thr Gln Lys Ala
275    280    285
Glu Gly Gly Gly Arg Leu Gln Ala Leu Arg Ser Leu Ser Gly Thr Pro
290    295    300
Lys Ser Met Thr Ser Leu Ser Pro Arg Ser Ser Leu Ser Ser Pro Ser
305    310    315    320
Pro Pro Cys Ser Pro Leu Met Ala Asp Pro Leu Leu Ala Gly Asp Ala

```

				325					330					335				
Phe	Leu	Asn	Ser	Leu	Glu	Phe	Glu	Asp	Pro	Glu	Leu	Ser	Ala	Thr	Leu			
			340					345					350					
Cys	Glu	Leu	Ser	Leu	Gly	Asn	Ser	Ala	Gln	Glu	Arg	Tyr	Arg	Leu	Glu			
			355				360					365						
Glu	Pro	Gly	Thr	Glu	Gly	Lys	Gln	Leu	Gly	Gln	Ala	Val	Asn	Thr	Ala			
			370			375					380							
Gln	Gly	Cys	Gly	Leu	Lys	Val	Ala	Cys	Val	Ser	Ala	Ala	Val	Ser	Asp			
385					390					395					400			
Glu	Ser	Val	Ala	Gly	Asp	Ser	Gly	Val	Tyr	Glu	Ala	Ser	Val	Gln	Arg			
				405					410					415				
Leu	Gly	Ala	Ser	Glu	Ala	Ala	Ala	Phe	Asp	Ser	Asp	Glu	Ser	Glu	Ala			
			420					425					430					
Val	Gly	Ala	Thr	Arg	Ile	Gln	Ile	Ala	Leu	Lys	Tyr	Asp	Glu	Lys	Asn			
			435				440					445						
Lys	Gln	Phe	Ala	Ile	Leu	Ile	Ile	Gln	Leu	Ser	Asn	Leu	Ser	Ala	Leu			
			450			455					460							
Leu	Gln	Gln	Gln	Asp	Gln	Lys	Val	Asn	Ile	Arg	Val	Ala	Val	Leu	Pro			
465					470					475					480			
Cys	Ser	Glu	Ser	Thr	Thr	Cys	Leu	Phe	Arg	Thr	Arg	Pro	Leu	Asp	Ala			
				485					490					495				
Ser	Asp	Thr	Leu	Val	Phe	Asn	Glu	Val	Phe	Trp	Val	Ser	Met	Ser	Tyr			
			500					505					510					
Pro	Ala	Leu	His	Gln	Lys	Thr	Leu	Arg	Val	Asp	Val	Cys	Thr	Thr	Asp			
			515				520					525						
Arg	Ser	His	Leu	Glu	Glu	Cys	Leu	Gly	Gly	Ala	Gln	Ile	Ser	Leu	Ala			
			530			535					540							
Glu	Val	Cys	Arg	Ser	Gly	Glu	Arg	Ser	Thr	Arg	Trp	Tyr	Asn	Leu	Leu			
545					550					555					560			
Ser	Tyr	Lys	Tyr	Leu	Lys	Lys	Gln	Ser	Arg	Glu	Leu	Lys	Pro	Val	Gly			
				565					570					575				
Val	Met	Ala	Pro	Ala	Ser	Gly	Pro	Ala	Ser	Thr	Asp	Ala	Val	Ser	Ala			
			580					585					590					
Leu	Leu	Glu	Gln	Thr	Ala	Val	Glu	Leu	Glu	Lys	Arg	Gln	Glu	Gly	Arg			
			595				600					605						
Ser	Ser	Thr	Gln	Thr	Leu	Glu	Asp	Ser	Trp	Arg	Tyr	Glu	Glu	Thr	Ser			
			610			615					620							
Glu	Asn	Glu	Ala	Val	Ala	Glu	Glu	Glu	Glu	Glu	Val	Glu	Glu	Glu	Glu			
625					630					635					640			
Glu	Gly	Glu	Glu	Asp	Val	Phe	Thr	Glu	Lys	Ala	Ser	Pro	Asp	Met	Asp			
				645					650					655				
Gly																		

174

785		790		795		800
His Gly Glu Lys	Glu Leu Pro Gln Trp	Leu Arg	Glu Asp Glu Arg Phe			
	805		810			815
Arg Leu Leu Leu	Arg Met Leu Glu	Lys Arg Met	Asp Arg Ala Glu His			
	820		825			830
Lys Gly Glu Leu	Gln Thr Asp Lys	Met Met Arg	Ala Ala Ala Lys Asp			
	835		840			845
Val His Arg Leu	Arg Gly Gln Ser Cys	Lys Glu	Pro Pro Glu Val Gln			
	850		855			860
Ser Phe Arg Glu	Lys Met Ala Phe	Phe Thr Arg	Pro Arg Met Asn Ile			
865		870		875		880
Pro Ala Leu Ser	Ala Asp Asp Val					
	885					

&lt;210&gt; 162

&lt;211&gt; 5794

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 162

```

ggagtggaaa tgatcgccac tctaagtcaa cagttggatc cagtgcacaac tcattctctc 60
agcccttgaa gaggaaggagg aaaaaagaag acgtgaattc agaaaaactg acgaaattga 120
aacaaaatgt aaaattaaag aattcacaag aaaccattcc aaatagtgat gaaggcattt 180
tcaaagctgg agcagagagg tctgaaacac ggggggcagc agaagtccaa gaagatgaag 240
atactcaggt tgaggttcca gtcgatcaga ggccagcaga aatagtagac gaggaagaag 300
atggagagaa ggcaacaacag gatgcagaac agaaagaaga cttttcagga atgaatggtg 360
accttgaaga ggaaggagggt agggaggcta cagatgcccc tgagcaagtc gaggagattc 420
tggatcacag tgagcagcag gcacgcccctg ctctgtgtaa tggaggcacc gatgaggaga 480
atggtgagga gctgcagcag gttaataatg agcttcaact ggtcctagac aaggaaagaa 540
agtctcaagg agctggcagt ggacaagatg aggctgatgt agaccctcaa agaccaccaa 600
ggccagaagt aaaaattacc agtccagaag aaaatgaaaa caaccaacaa aacaaggact 660
atgctgccgt ggcttagaac atttttaaaa agagagtata tggatcgcaa gaaaaatgaa 720
gggttatcat acttgaaga taagcacata gttattgctg aatataatgt gacactatgg 780
tcgaatacta cctacgaatt ataacattag aagcctagtg gaaagaccag ataacttta 840
atggctacta aaggataatt acttactttt attgcatgtg ttttaaaagt catatagaaa 900
tattaaataa gacggacaga ggagaatttg cactggaaga caattgccac ttgtaaagga 960
tgaaaaatag gatcactctt attgtacgct ttattataag tttagaaggc agtttattct 1020
aaataatatt tctctaggaa ggcgtagaat tttaaagaac tggtaatagg aaagcatgta 1080
ctattttctt aaagcaataa actcttgaat gaacagattg cgattttact tcagacataa 1140
tttgagatg gcagtagatc aaaatgtgtc catgacttgt taacatgcct ttctttcttc 1200
ctccttagcc aaaatccacc tttgaactac aaagacagag caaggcgttc attttggtg 1260
gaggaagcat tggttcagag tgtttagtgac tagtatcgcc atgccgtcac ttaaatgctt 1320
tcaggcttgc atgcttgtgg ctccaatggc gcacactcag gaaggaattg taaaggagca 1380
cccagttata ttataaagcc tggatgtatg gtttgcagat aatggaaatc ctgtggattt 1440
tcaactgatcc agtctatctt taccaatagt atctctctct tctcccttat gttattagag 1500
aacctgatat tggctattcc aaagattaaa ttattttcaa atagttttca acaaaaaataa 1560
aagtgtatta ggaagaaaaa agtagactat atgaagagtt tgtgactgot caatttaact 1620
tgtttttttg cttattttct attagactg ttttactatg tttttgccct agggatatca 1680
gcaaataatt atttttccta gcatgatata gttagaattt caagcagatt tctttgtaat 1740
tagaaggcat ctgatagaaa ttgtaaaact ttagaagtta ttataatgaa accaattcct 1800
gaatcacaaac ttcatggact gactaaattg atttatagtt gccttgtgag gtatgtatgg 1860
ggaaaacata aaaacataat taaaacataa tttcgtcctt tttatgaatt cttaaagat 1920
gttcttccat aaatatagaa ataatatatt tttcttaaag gatataattt taattatgtg 1980
gaagttgtaa gcttgaaatt ttaacttcta gtgcttttct aaaattcaca attacaagtt 2040
taaaacattt tttctcttcc aggtttcatt ttggaataaag agttggcagt tatataaagc 2100
acttaataat actatagaaa atagatgtgt tttttcttaa tatgattttg gtattttcca 2160
cagatcagaa gtgtaaacag agagataatg taacagtatt tggaaagat aatgacacaa 2220

```



ggatatagtg	atctgggagc	atgaattaga	aacagggtac	tatgtttctg	gtgtaaaatc	2280
taaattgtgc	tttctactag	cgttactttt	tcaaattgga	tgatataaag	cactgtgggc	2340
tataagcaac	aatcttgggt	tgctaggcaa	atagaccaat	tgatctttat	tattattatt	2400
attattatta	ttattttttt	ttgagatgaa	gtcttgctct	tgctgcccag	gctgggtgca	2460
gtggcatgat	cttggtctac	tgcaacctct	gcctcctggg	ttcaagcacc	tgagcctccc	2520
gagtagctgg	gattacaggc	atctgccacc	acacctggct	aatttttgta	ttttttgtag	2580
agacagatgt	ttcaccatgt	tggccaggct	ggtctcaaac	tcctgacctc	aggatgatccg	2640
cccgcctttg	catcccaaaa	tgctgggatt	acagggtgtga	gccacagcac	ccggtcccag	2700
ttggtctttt	aatattaaat	ttgtgacta	ttactgggtc	tgaggttaat	gatttcaaat	2760
agtttctaaa	aataactgat	taaatgtaag	aaattataac	taattatcaa	ggtgattctc	2820
ttttgtttct	tcaatggaga	gtttctcttt	ctcttttctc	cctctaataa	aaatatttct	2880
ttttttcctg	tcctttttat	cattatatta	tgaaccttag	gttttaggaa	acaccttaag	2940
cgtcatttta	atgaagcaca	acattgatat	tttacctgaa	taataacggt	tggtatttta	3000
aatatacttc	aagggggtaa	taagccacaa	taactgtacc	aaaaaaactt	aaaaatgggg	3060
acataattcat	cccttggtg	tgcatatttt	accacttggt	gacaagatac	aattgtgacc	3120
tactttgagg	ggatgaataa	cgacttatca	ctttaagaca	ctttgcaaac	atgttactaa	3180
aaaaagggtc	ctagccaagg	aaaaaaccat	tcacttggaa	ttaaaattgt	ggatgtcact	3240
tcagagatga	ctttaacata	aatgctgaaa	gttcattcac	ctcacaatg	tggcagtttt	3300
ctctgtggag	aatgggtggtc	tccgtggcag	actggctctc	caaattaaat	gaaactcatt	3360
gacagacctg	ggacctttta	tgtgagtgga	cagacaagat	cttgggttgg	cttcattgtac	3420
tgttttctag	agagagtgtc	acgaaaaact	tatgatgctt	ttatgtgata	accaatataa	3480
tgctttaata	tgtaattctc	ttgtgatgct	atatacatag	tttttatagt	tttatgaaac	3540
cactttgtta	aacttatctg	gattttaaga	cacttgtaaa	caaattggtt	gttagtaaaa	3600
ttggggcatt	aagagtttta	cagagcaaat	aaagaagatt	ttgacaaaag	tcattttgag	3660
gctaagggtg	ttttacctgg	gttaacttct	gttaaaaatag	ctattgagtg	cccattgact	3720
tataaaaatac	gatactatga	ccataaaata	actttttact	tcattattctt	ctctatgacc	3780
ttaggatgac	tttatttttt	ttaagacatt	tttctatat	gtttttgggg	gaatgttagg	3840
ttgccacact	catagggaaa	gtgtgatgct	atcatgcctc	ctgtttttat	gtaaagggtg	3900
gaattcttgc	tatgtggtgt	gtgaagacag	aactatccca	tacatacgtg	gttcagagtgc	3960
agatatctct	aggctcacag	ttgtgaaccc	atattaatat	ggattatttc	ctgccaaactc	4020
ttccaattta	tagctcataa	actaacatcc	taaacattgt	cattgaatga	cctaccttat	4080
acacaaagga	taaagttcat	tcacctagaa	aaaaaatctg	tgcatttaaa	ttagtggccg	4140
caagacaaca	ggaagctttc	tttcattttt	tgttcaacaa	accttgcaaa	agcaaaagttt	4200
aaaaagtaga	ttaattcatc	aacagaaagc	atcacatgga	aactgtggcc	aatctgaaga	4260
gaaatatagc	atgtagacat	agatatgtat	caaatactta	tacagatgca	ctcacacact	4320
ttaaaacatt	aaaaaggcct	cctgaggcac	agcgttatta	ataaaaacaag	gctcttttgg	4380
gtgaagttag	gagaagcaat	gagttaaaac	gtgagaggaa	atgctaagaa	atgatataata	4440
ttatggtgct	tttaactctg	atttcctaag	actttaagag	atttaaaatt	cttctccaaa	4500
taagaaaacca	gcatgtcaat	gaaaaatgta	ttctaggagg	gtgttgaaac	aaatccggtt	4560
tttaaaatgt	gatatatcac	ataaaaccaa	acagaaacca	agacatatct	tgttttcctg	4620
aagtaactac	agagcatggt	tcctttccat	caaccttaag	cacgatacat	ttcagggtgta	4680
gattctttta	taccaatata	gattctgtta	ttactgtttg	tgacctgtg	tgtgcatgtg	4740
tgatttacat	agatgtgtca	ggactctttt	tcataccagt	tagccggggg	atcacaaata	4800
gaatgaaaga	ctgacttatt	ggtccattag	tttatataat	gttcagggtc	agtgcggaag	4860
catttttgga	ttcttcagga	atgaaaacat	ttttaaaagg	ttagtctggt	actctaagat	4920
gatgaacaca	tacagttctt	tgctattaaa	tatcattttt	gtaaatacca	caagattttt	4980
cctctttaaa	acatatcggt	acatttagat	gggactgatt	tttgttctcc	ctacatgaaa	5040
tttgtatatt	tcctcccatg	aagtttgagt	gacatgaatg	gggaatacaa	gagtgttccc	5100
ttatgttgat	aaggaaaaag	atactgtttt	ttgaagaggc	ataacatcct	gtaggagatg	5160
gggagttagg	acagttttta	aaaatgcctg	gattaccata	aggcatttat	aaaatgagga	5220
ggtgtaacca	gtggagctct	gttgacttaa	cgccaacaac	gacttcagct	ttactctaag	5280
aatgggacca	gatgaattct	ctgtagtttc	atcagcttga	acgatatagt	ttgtttcatt	5340
tattgtcacg	aatgcaatga	catatggaaa	gagggaatga	ttgtagtcat	tccttaggaga	5400
attttcgaga	aagcctgttt	tgtcttttgc	ttcagtgttt	tttcttgtgc	cttaaatctt	5460
taatgggtac	aatgataatg	ggtgattgtt	gatgtaagta	aagattaaat	tgaaggccag	5520
cacggtggtt	cacacctgta	atcccagcac	gttgggaggc	tgaggcgggt	ggatcacgag	5580
gtcaggagat	cgagaccatc	ctggctaaca	tggtgaaacc	ccgtctctac	tacaaatata	5640
aaaaattagc	caggcgtggt	ggcgggtgcc	tgtagtccca	gctactcaag	aggctgaggc	5700

176

aggagaatgg cgtgaagcca ggaggcggag cttgctgtga gccgagatcg cgccactgca 5760  
ctccagcctg ggcgacagag cgagactccg tctc 5794

<210> 163  
<211> 224  
<212> PRT  
<213> Homo sapiens

<400> 163  
Ser Gly Asn Asp Arg His Ser Lys Ser Thr Val Gly Ser Ser Asp Asn  
1 5 10 15  
Ser Ser Pro Gln Pro Leu Lys Arg Lys Gly Lys Lys Glu Asp Val Asn  
20 25 30  
Ser Glu Lys Leu Thr Lys Leu Lys Gln Asn Val Lys Leu Lys Asn Ser  
35 40 45  
Gln Glu Thr Ile Pro Asn Ser Asp Glu Gly Ile Phe Lys Ala Gly Ala  
50 55 60  
Glu Arg Ser Glu Thr Arg Gly Ala Ala Glu Val Gln Glu Asp Glu Asp  
65 70 75 80  
Thr Gln Val Glu Val Pro Val Asp Gln Arg Pro Ala Glu Ile Val Asp  
85 90 95  
Glu Glu Glu Asp Gly Glu Lys Ala Asn Lys Asp Ala Glu Gln Lys Glu  
100 105 110  
Asp Phe Ser Gly Met Asn Gly Asp Leu Glu Glu Glu Gly Gly Arg Glu  
115 120 125  
Ala Thr Asp Ala Pro Glu Gln Val Glu Glu Ile Leu Asp His Ser Glu  
130 135 140  
Gln Gln Ala Arg Pro Ala Arg Val Asn Gly Gly Thr Asp Glu Glu Asn  
145 150 155 160  
Gly Glu Glu Leu Gln Gln Val Asn Asn Glu Leu Gln Leu Val Leu Asp  
165 170 175  
Lys Glu Arg Lys Ser Gln Gly Ala Gly Ser Gly Gln Asp Glu Ala Asp  
180 185 190  
Val Asp Pro Gln Arg Pro Pro Arg Pro Glu Val Lys Ile Thr Ser Pro  
195 200 205  
Glu Glu Asn Glu Asn Asn Gln Gln Asn Lys Asp Tyr Ala Ala Val Ala  
210 215 220

<210> 164  
<211> 5759  
<212> DNA  
<213> Homo sapiens

<400> 164  
gtcttggtta gttaaaaaaa aaaaaaaagt tggccaggca cagtggcttg cacctgtaat 60  
cccagcactt tgggaggccg aggcaggcgg atcacctgag gttgggagtt cgagaccaac 120  
ctgaccaaca tggagaaacc catctctact aaaaatacaa aattatccgg tcatggtggc 180  
acgcgcctat gatccacact actcgggagg ctaaggcaag agaattgctt gaaccctgta 240  
ggcagagggt gcagtgaacc gagattgcgc cactgcactc cagcctgggt gactgaggga 300  
gactctgtct caaaataaat aaataaataa aagggttaatt atatttcttg ttatgagaca 360  
aatgaagtat ttcacatattt ccattgacga tagcatgtaa cgcagggtttt tctcttatag 420  
gttgtgggac tggaaaatat cttaaagtga acagccagggt acataccgtg ggctgtgact 480  
actgtgggcc actggtagag attgcccggg atagaggatg tgaagccatg gtatgtgaca 540  
accttaatct cccctttagg gatgagggct tcgatgccat catctccata ggagtcatac 600  
atcatttttc tacaaaaaaa agaagaatca gagcaataaa agaaatggcc aggttcttag 660  
ttcccgagg ccaactgatg atttacgttt gggcaatgga acaaaagaac cgtcgctttg 720  
agaagcaaga cgtgcttggt ccatggaaca gggccctgtg ttcccagctc ttctcagagt 780

ccagccagtc	tgggaggaag	aggcagtggt	gataccacaga	aagaggccat	ccctaccatc	840
ctccttgctc	tgaagtgtagc	tggtctgttt	gttttaaaga	gcagggtggt	tcaaaacggt	900
cccacagcgt	gggctatgaa	cctgctatgg	caagaacctg	ttttgcaa	atttctaagg	960
aaggcgagga	agaatatgga	ttttacagca	cattaggaaa	atcgtttcgt	tcctgggttt	1020
tctccagatc	tttgatgaa	tcgactctga	ggaagcaaat	tgaagagta	agacccttga	1080
aaaacacaga	agtgtgggcc	agtagcactg	taacagtcca	gccttccaga	cactctagtc	1140
tagactttga	tcaccaagag	ccattttcaa	caaaagagca	aagtttagat	gaggaagtgt	1200
ttgtggaatc	ttcttctgga	aaacacttgg	agtggctgag	agcaccaggc	actctgaaac	1260
atttaaattg	agaccatcaa	ggggaaatga	ggagaaatgg	agggggaaat	tttctggata	1320
gcactaatat	tggtgtgaat	tggtgtgatg	caggcaacat	agaagatgat	aatccttctg	1380
ctagtaaaat	attgagaagg	atttctgcag	tcgattccac	agatttcaac	ccagatgata	1440
caatgtctgt	cgaagatcca	cagactgatg	ttttggactc	cacagccttt	atgcgctact	1500
accatgtgtt	tcgagaaggg	gagctctgca	gtctgctcaa	ggagaatgtg	tcagagctcc	1560
gtatcctgag	ttctgggaat	gatcatggta	actggtgtat	cattgcagag	aaaaagggag	1620
gttgtgattg	attggatcct	tttagacaac	tcctccaaaa	gatgaaccac	attcttttct	1680
cttggtttga	tatggttacc	tgaatttgca	ttcagtggtta	tttgttaatc	catttacgct	1740
ttggtctgca	gagactatta	attatttgg	tggttttgtt	ttcatgtttg	aataagcaca	1800
gattctggca	ttgaaagcac	ttgacaaagg	gtatttgtgc	ttaaatgtta	atataaaaga	1860
tctgaagaag	caacagaaag	tacccttcag	tacacctcag	actttttttt	aacccagag	1920
agataaaata	catgtatagt	gttttctcag	attacacatt	gatttaaaaa	gattatgctg	1980
ttaaataatc	tttttaaacg	gtatttttat	aaagtgagg	gataatttct	ggttctcagg	2040
ttataactga	gagcagtggt	caagataata	ggtaaatttg	atccattgca	cagatatact	2100
ttgaaccatg	tgatgagtta	tcttggtgcc	aaggccttgc	ttctacttaa	agttttcaga	2160
aaactgagtg	acagtggaga	gaaccaagaa	gttttacaag	gactttacta	aattataagc	2220
aaacttgctt	caaaataagt	tgacatgtga	taataagggt	ttcaatgtag	cccaggaggt	2280
ttttaaaggc	actgttaggc	tgagcatggt	ggctcatgcc	tgtaatccca	gcactttggg	2340
aggccaaggc	agaagcatca	cttgaaccca	ggagttcaag	aatagcctgg	gcaacatagc	2400
gagacctcat	ctctataaaa	attagcaaga	tggtggtggt	catgcctgtc	atccaagcta	2460
ctcaggagac	tgaggcagga	ggatcacgtg	agcccaggaa	ttcaaggctg	cagtgaacta	2520
tgattgcata	agctgcactg	agcctgggca	acatagcaag	actctgtctc	aaaataataa	2580
taataataat	aataaaggca	ttgttagctt	gtaaggagtg	gagtatgtag	gtagtaggag	2640
ttatatgcaa	gtacccaagt	ggtattcttc	caatcttatt	agaagcatga	atattcaaga	2700
ttgatattac	tattgcttat	tagcaagatt	gttatcaatc	atgcttatta	gaaggatgaa	2760
tatccaagac	caagattgac	taatgatgag	tctgcatcaa	gaactaggca	tttcttctga	2820
gttgacggac	tctttaggaa	aggagaatct	aagtgaagca	ctgattttag	ctctgagaac	2880
aaacaaatta	aggtacagca	tagttagcct	tggtagaggt	atgacttgga	tttgctgtat	2940
cctttaaaaa	agtatctggg	cattttattt	attgaagggt	actacatttt	attagttata	3000
ttaggaaatt	aggtagaatc	aacttctact	gattacaggt	tgaatttctg	tcactttgta	3060
gagaaacgaa	tagactggac	actgtgtggt	cactgtttag	atttgcccat	gggtctgttt	3120
aaatctatgt	catggatcct	gagacacaaa	tataattaag	acaggtctag	agacaggaga	3180
agcagaaata	agttgaccca	ggagtacagt	ctcaagtagt	tcattaatga	gaaaattgac	3240
atctgacaag	agtcttttta	ctttatgctg	gatgaaaatc	caaactctgt	tttatttttt	3300
ccactaaaag	tgaactaaaat	aataacgaat	ttcatttgtt	cttggttctt	tttttctctt	3360
aatgattgtg	ctataactta	aaataatgat	gttacttttg	aacaaactta	aagaaatatt	3420
tttaaagcgt	atctgaaaac	gattgatgtt	tataactctc	ttttggcttc	aaaataagat	3480
tgtgttatca	ccattttggt	agatgaggtt	gtctggtgaa	aatgatgcat	atgagttgta	3540
ctgttcagtg	tacatcctgc	agtagtggtt	gattgaaaac	atatataagt	ggagtataaa	3600
ttaaaaatta	atttggtttc	ttctatttct	tttttttttt	tttttttttt	ttttgagaca	3660
gagtctcgct	ctgtcgccca	ggctggagtg	cactggcgcg	atctcggtct	actgtaagct	3720
ccgcctcccg	ggttcacgcc	atcctcctgc	ctcagcctcc	caagtagctg	ggactactgg	3780
caccaccac	gacgcccggc	tggttttttg	tatttttagg	agagacgggg	tttcgcccgt	3840
ttggccagga	tggtctcgat	ctcctgacgt	cgtgatccac	ccgcctcggc	ccccacagt	3900
gctgggatta	caggcatgag	ccaccgcgcc	cggcctgttc	cttttatttc	ttaattcagg	3960
acactaaacc	atgactgcaa	gggattttct	tggtaaaaag	aaaagattct	cagagtcaaa	4020
atgttcttac	aactcgggct	tgacggcctt	tgaattatga	atggattgtt	cctctctctg	4080
aagcctattg	tcacatgggt	ttttaatcct	ggccttgctg	ctagaaatct	gtgcttgaag	4140
tcctctcttt	ctgctggtag	cctaccagtt	aaaagtcaag	acttgggtga	actcagttta	4200
ccagactctt	tagcctttga	gctaaactgt	ctgagcaacc	tcttagatgt	gcacacacca	4260

```

ctttgtatga aagggttctc tagaacggtt ctttggagag aaatatatttc atgtacgttt 4320
gacaggggtg taaataaagc atgctgacta ataagtcctt tactcttcat ctaatgaaca 4380
taagaatcta tgcattccaga tattattttg tatacaaata tttaatttgg tgattgataa 4440
tctctctttg gggtagtcac atggaaagct cttttaaatt taacttccgc ctttggattt 4500
tttttaaaaa gccattgaag agcaaaaact atgtaaagct cttgatcatt taaaaagctt 4560
gcttgtcctc gaaaggaaac acagggtcatc agtgagtata aacgtagaca gttgatttgt 4620
gaatgctgtc ggctcaact tgcttgatga tagattctac tgacctagct ggagtaatct 4680
gatcacttac ttccttatta atactagatc acacagtgtc tttcttattc cttcttcttt 4740
acttactggc atcagcacag agtcccacta tctgaaatag aaggagaggt ttgggggttt 4800
attggaggag tcttaaaaac ttggttggca gctgggtacg gtgactcaca cctgtactcc 4860
cagcacttca ggaagctgag gtgggtggat cagctgaggt caggagtttg ggaccagcct 4920
gaccaacatg gtgaaacccc gtctttatta aatacaaaaa attagccagg ttggtggcgc 4980
atgcctgtgg tcccagctac ttgggaggct gaggcaggag aatcgcttga acctgggagg 5040
cggagggttg agtgagccga gattgtgccca ttgcaactca acctgggcaa caagagtga 5100
actccatctc caacaaaaca aaactttgct ggcttctctga tgcctcactg tctatttgag 5160
gaattccaca gaatttcaa aggatttggg ggaaagcgca ttaacatgga caaaggatgg 5220
aatcaaaaata atgttatagt gagaatcatt caagcaccta tttaaatttt ttccaattgc 5280
cagtatatgt atgatatgac accagcatat caaagtaact aacaaactag ctacacaaac 5340
gtcttggagt ttggtttcgt tctcttttct catcatagat ctccgtgcag aatagtgcta 5400
attcttattt tctgtttgcc tttctatttc cttccaaatt ctacatgcca gtaattcctc 5460
tgtcttttaa gtgaccatca attcaatagg caaaaatttg gagtaatcca gagaaaaaac 5520
catccaaata taaaccagct aggaacatga atgcccctga ttattaatgg ccaaaaaaaa 5580
aagcactggg ggattttaaa ttaaattaat acatatatac gagtttggag gagaacagaa 5640
gttctaactc agtacttgaa cttggtgggg gagggcacag gttaaatatg agctgtgagc 5700
ccccagtttt ggaggaagga ggaaatggga accaaccacc agacaagcag ctgcagctc 5759

```

&lt;210&gt; 165

&lt;211&gt; 421

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 165

```

Ser Ile Ser His Phe Pro Leu Thr Ile Ala Cys Asn Ala Gly Phe Ser
1           5           10           15
Leu Ile Gly Cys Gly Thr Gly Lys Tyr Leu Lys Val Asn Ser Gln Val
20           25           30
His Thr Val Gly Cys Asp Tyr Cys Gly Pro Leu Val Glu Ile Ala Arg
35           40           45
Asn Arg Gly Cys Glu Ala Met Val Cys Asp Asn Leu Asn Leu Pro Phe
50           55           60
Arg Asp Glu Gly Phe Asp Ala Ile Ile Ser Ile Gly Val Ile His His
65           70           75           80
Phe Ser Thr Lys Gln Arg Arg Ile Arg Ala Ile Lys Glu Met Ala Arg
85           90           95
Val Leu Val Pro Gly Gly Gln Leu Met Ile Tyr Val Trp Ala Met Glu
100          105          110
Gln Lys Asn Arg Arg Phe Glu Lys Gln Asp Val Leu Val Pro Trp Asn
115          120          125
Arg Ala Leu Cys Ser Gln Leu Phe Ser Glu Ser Ser Gln Ser Gly Arg
130          135          140
Lys Arg Gln Cys Gly Tyr Pro Glu Arg Gly His Pro Tyr His Pro Pro
145          150          155          160
Cys Ser Glu Cys Ser Cys Ser Val Cys Phe Lys Glu Gln Gly Gly Ser
165          170          175
Lys Arg Ser His Ser Val Gly Tyr Glu Pro Ala Met Ala Arg Thr Cys
180          185          190
Phe Ala Asn Ile Ser Lys Glu Gly Glu Glu Glu Tyr Gly Phe Tyr Ser
195          200          205

```

Thr Leu Gly Lys Ser Phe Arg Ser Trp Phe Phe Ser Arg Ser Leu Asp  
 210 215 220  
 Glu Ser Thr Leu Arg Lys Gln Ile Glu Arg Val Arg Pro Leu Lys Asn  
 225 230 235 240  
 Thr Glu Val Trp Ala Ser Ser Thr Val Thr Val Gln Pro Ser Arg His  
 245 250 255  
 Ser Ser Leu Asp Phe Asp His Gln Glu Pro Phe Ser Thr Lys Glu Gln  
 260 265 270  
 Ser Leu Asp Glu Glu Val Phe Val Glu Ser Ser Ser Gly Lys His Leu  
 275 280 285  
 Glu Trp Leu Arg Ala Pro Gly Thr Leu Lys His Leu Asn Gly Asp His  
 290 295 300  
 Gln Gly Glu Met Arg Arg Asn Gly Gly Gly Asn Phe Leu Asp Ser Thr  
 305 310 315 320  
 Asn Thr Gly Val Asn Cys Val Asp Ala Gly Asn Ile Glu Asp Asp Asn  
 325 330 335  
 Pro Ser Ala Ser Lys Ile Leu Arg Arg Ile Ser Ala Val Asp Ser Thr  
 340 345 350  
 Asp Phe Asn Pro Asp Asp Thr Met Ser Val Glu Asp Pro Gln Thr Asp  
 355 360 365  
 Val Leu Asp Ser Thr Ala Phe Met Arg Tyr Tyr His Val Phe Arg Glu  
 370 375 380  
 Gly Glu Leu Cys Ser Leu Leu Lys Glu Asn Val Ser Glu Leu Arg Ile  
 385 390 395 400  
 Leu Ser Ser Gly Asn Asp His Gly Asn Trp Cys Ile Ile Ala Glu Lys  
 405 410 415  
 Lys Gly Gly Cys Asp  
 420

&lt;210&gt; 166

&lt;211&gt; 1454

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 166

accagcggca gaccacaggc agggcagagc cacgtctggg tcccctccct ccttctctatc 60  
 ggcgactccc agatcctggc catgagagct ccgcaoctcc acctctccgc cgctctggc 120  
 gcccgggctc tggcgaagct gctgccgctg ctgatggcgc aactctgggc cgagaggcg 180  
 gcgctgctcc cccaaaacga cagcgcttg gacccgaag cctatggcgc ccgctgcgcg 240  
 cgcggtcgc agccctggca ggtctcgctc ttcaacggcc tctcggtcca ctgcgcgggt 300  
 gtcctgggtg accagagttg ggtgctgacg gccgcgcaact gcggaacaa gccactgtg 360  
 gctcgagtag gggatgatca cctgctgctt ctccaggcg agcagctccg ccggacgact 420  
 cgctctgttg tccatcccaa gtaccaccag ggctcaggcc ccatcctgcc aaggcgaacg 480  
 gatgagcacg atctcatgtt gctaaagctg gccaggccc tagtgccggg gccccgcgc 540  
 cgggccctgc agcttcccta cgctgtgct cagcccgag accagtcca ggttgctggc 600  
 tggggcacca cggccgccc gagagtgaag tacaacaagg gcctgacctg ctccagcatc 660  
 actatcctga gccctaaaga gtgtgaggtc ttctaccctg gcgtgggtcac caacaacatg 720  
 atatgtgctg gactggaccg gggccaggac ccttgccaga gtgactctgg agggccctg 780  
 gtctgtgacg agaccctcca aggcattctc tcgtggggtg ttaccctg tggctctgcc 840  
 cagcatccag ctgtctacac ccagatctgc aaatacatgt cctggatcaa taaagtcata 900  
 cgctccaact gatccagatg ctacgctcca gctgatccag atgttatgct cctgctgac 960  
 cagatgccca gaggtcccat cgtccatcct ctctctcccc agtcggctga actctcccc 1020  
 tgtctgcact gttcaaacct ctgccgccct ccacacctct aaacatctcc cctctcacct 1080  
 cattccccca cctatccca ttctctgcct gtactgaagc tgaaatgcag gaagtgggtg 1140  
 caaagggtta ttccagagaa gccaggaagc cgggtcatcac ccagcctctg agagcagtta 1200  
 ctggggtcac ccaacctgac ttctctgccc actccccgct gtgtgacttt gggcaagcca 1260  
 agtgccctct ctgaacctca gtttctctat ctgcaaaatg ggaacaatga cgtgcctacc 1320

180

tcttagacat gttgtgagga gactatgata taacatgtgt atgtaaatct tcatgtgatt 1380  
 gtcattgtaag gcttaacaca gtgggtggtg agttctgact aaagggtacc tgttgcgtg 1440  
 aaaaaaaaaa aaaa 1454

<210> 167  
 <211> 276  
 <212> PRT  
 <213> Homo sapiens

<400> 167  
 Met Arg Ala Pro His Leu His Leu Ser Ala Ala Ser Gly Ala Arg Ala  
 1 5 10 15  
 Leu Ala Lys Leu Leu Pro Leu Leu Met Ala Gln Leu Trp Ala Ala Glu  
 20 25 30  
 Ala Ala Leu Leu Pro Gln Asn Asp Thr Arg Leu Asp Pro Glu Ala Tyr  
 35 40 45  
 Gly Ala Pro Cys Ala Arg Gly Ser Gln Pro Trp Gln Val Ser Leu Phe  
 50 55 60  
 Asn Gly Leu Ser Phe His Cys Ala Gly Val Leu Val Asp Gln Ser Trp  
 65 70 75 80  
 Val Leu Thr Ala Ala His Cys Gly Asn Lys Pro Leu Trp Ala Arg Val  
 85 90 95  
 Gly Asp Asp His Leu Leu Leu Leu Gln Gly Glu Gln Leu Arg Arg Thr  
 100 105 110  
 Thr Arg Ser Val Val His Pro Lys Tyr His Gln Gly Ser Gly Pro Ile  
 115 120 125  
 Leu Pro Arg Arg Thr Asp Glu His Asp Leu Met Leu Leu Lys Leu Ala  
 130 135 140  
 Arg Pro Val Val Pro Gly Pro Arg Val Arg Ala Leu Gln Leu Pro Tyr  
 145 150 155 160  
 Arg Cys Ala Gln Pro Gly Asp Gln Cys Gln Val Ala Gly Trp Gly Thr  
 165 170 175  
 Thr Ala Ala Arg Arg Val Lys Tyr Asn Lys Gly Leu Thr Cys Ser Ser  
 180 185 190  
 Ile Thr Ile Leu Ser Pro Lys Glu Cys Glu Val Phe Tyr Pro Gly Val  
 195 200 205  
 Val Thr Asn Asn Met Ile Cys Ala Gly Leu Asp Arg Gly Gln Asp Pro  
 210 215 220  
 Cys Gln Ser Asp Ser Gly Gly Pro Leu Val Cys Asp Glu Thr Leu Gln  
 225 230 235 240  
 Gly Ile Leu Ser Trp Gly Val Tyr Pro Cys Gly Ser Ala Gln His Pro  
 245 250 255  
 Ala Val Tyr Thr Gln Ile Cys Lys Tyr Met Ser Trp Ile Asn Lys Val  
 260 265 270  
 Ile Arg Ser Asn  
 275

<210> 168  
 <211> 1506  
 <212> DNA  
 <213> Homo sapiens

<400> 168  
 agcgagacaa agcccgattg ttctctgggc ctttcccat cgcgctggg cctgctcccc 60  
 agcccggggc agggcgggg gccagtgtg tgacacacgc ttagctgtc tccccggctg 120  
 gctggctgc tctctctgg ggaacacag gtcggcaggc agcacacaga gggacctacg 180  
 ggcagctgtt ctttccccg actcaagaat ccccgaggc ccggaggcct gcagcaggag 240

```

cggccatgaa gaagctgatg gtggtgctga gtctgattgc tgcagcctgg gcagaggagc 300
agaataagtt ggtgcatggc ggaccctgcg acaagacatc tcaccctac caagctgcc 360
tctacacctc gggccacttg ctctgtggtg gggtccttat ccatccactg tgggtcctca 420
cagctgcccc ctgcaaaaaa ccgaatcttc aggtcttcct ggggaagcat aaccttcggc 480
aaagggagag ttcccaggag cagagttctg ttgtccgggc tgtgatccac cctgactatg 540
atgccgccag ccatgaccag gacatcatgc tgttgccgct ggcacgcca gccaaactct 600
ctgaactcat ccagcccctt cccctggaga gggactgctc agccaacacc accagctgcc 660
acatcctggg ctggggcaag acagcagatg gtgatttccc tgacaccatc cagtgtgcat 720
acatccacct ggtgtcccgt gaggagtgtg agcatgccta ccctggccag atcaccaga 780
acatgttgtg tgctgggatg gagaagtacg ggaaggattc ctgccagggt gattctgggg 840
gtccgctggt atgtggagac cacctccgag gccttgtgtc atggggtaac atcccctgtg 900
gatcaaagga gaagccagga gtctacacca acgtctgcag atacacgaac tggatccaaa 960
aaaccattca ggccaagtga ccctgacatg tgacatctac ctcccagact accacccac 1020
tggtctggtc cagaacgtct ctcacctaga ccttgccctc cctcctctcc tgcccagctc 1080
tgaccctgat gcttaataaa cgcagcgacg tgagggctct gattctccct ggttttacc 1140
cagctccatc cttgcatcac tggggaggac gtgatgagtg aggacttggg tcctcggtct 1200
tacccccacc actaagagaa tacaggaaaa tcccttctag gcctctctc tccccaaccc 1260
ttccacacgt ttgatttctt cctgcagagg cccagccacg tgtctggaat cccagctccg 1320
ctgcttactg tcggtgtccc cttgggatgt accttcttc actgcagatt tctcacctgt 1380
aagatgaaga taaggtgat acagtctcca tcaggcagtg gctgttgaa agatttaaga 1440
tttcacacct atgacatata tgggatagca cctgggcccgc catgcactca ataaagaatg 1500
tattttt                                     1506

```

&lt;210&gt; 169

&lt;211&gt; 244

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 169

```

Met Lys Lys Leu Met Val Val Leu Ser Leu Ile Ala Ala Ala Trp Ala
 1          5          10          15
Glu Glu Gln Asn Lys Leu Val His Gly Gly Pro Cys Asp Lys Thr Ser
 20          25          30
His Pro Tyr Gln Ala Ala Leu Tyr Thr Ser Gly His Leu Leu Cys Gly
 35          40          45
Gly Val Leu Ile His Pro Leu Trp Val Leu Thr Ala Ala His Cys Lys
 50          55          60
Lys Pro Asn Leu Gln Val Phe Leu Gly Lys His Asn Leu Arg Gln Arg
 65          70          75          80
Glu Ser Ser Gln Glu Gln Ser Ser Val Val Arg Ala Val Ile His Pro
 85          90          95
Asp Tyr Asp Ala Ala Ser His Asp Gln Asp Ile Met Leu Leu Arg Leu
100          105          110
Ala Arg Pro Ala Lys Leu Ser Glu Leu Ile Gln Pro Leu Pro Leu Glu
115          120          125
Arg Asp Cys Ser Ala Asn Thr Thr Ser Cys His Ile Leu Gly Trp Gly
130          135          140
Lys Thr Ala Asp Gly Asp Phe Pro Asp Thr Ile Gln Cys Ala Tyr Ile
145          150          155          160
His Leu Val Ser Arg Glu Glu Cys Glu His Ala Tyr Pro Gly Gln Ile
 165          170          175
Thr Gln Asn Met Leu Cys Ala Gly Asp Glu Lys Tyr Gly Lys Asp Ser
 180          185          190
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Asp His Leu Arg
195          200          205
Gly Leu Val Ser Trp Gly Asn Ile Pro Cys Gly Ser Lys Glu Lys Pro
210          215          220
Gly Val Tyr Thr Asn Val Cys Arg Tyr Thr Asn Trp Ile Gln Lys Thr

```

225  
Ile Gln Ala Lys

230

235

240

<210> 170  
<211> 1641  
<212> DNA  
<213> Homo sapiens

<400> 170  
agcgagtgcg cgctcctcct cgcccgcgcg taggtccatc ccggcccagc caccatgtcc 60  
atccacttca gctccccggt attcacctcg cgctcagccg ccttctcggg ccgcggcgcc 120  
cagggtgcgc tgagctccgc tcgccccggc ggccttggca gcagcagcct ctacggcctc 180  
ggcgccctcg ggccgcgcgt ggccgtgcgc tctgcctatg ggggcccggg gggcgccggc 240  
atccgcgcagg tcaccattaa ccagagcctg ctggccccgc tgcggctgga cgccgacccc 300  
tccctccagc ggggtgcgca ggaggagagc gagcagatca agaccctcaa caacaagttt 360  
gcctccttca tcgacaaggt gcggtttctg gagcagcaga acaagctgct ggagaccaag 420  
tggagcgtgc tcgaggagca gaagtcggcc aagagcagcc gcctcccaga catctttgag 480  
gccagattg ctggccttcg gggtcagctt gaggcactgc aggtggatgg gggccgcctg 540  
gaggcgagc tgcggagcat gcaggatgtg gtggaggact tcaagaataa gtacgaagat 600  
gaaattaacc gccgcacagc tgctgagaat gaggttgtgg tgctgaagaa ggatgtggat 660  
gctgcctaca cgagcaaggt ggagctggag gccaaagtgg atgccctgaa tgatgagatc 720  
aacttcctca ggaccctcaa tgagacggag ttgacagagc tgcagtccca gatctccgac 780  
acatctgtgg tgctgtccat ggacaacagt cgctccctgg acctggacgg catcatcgct 840  
gagggtcaagg cacagtatga ggagatggcc aaatgcagcc gggctgaggc tgaagcctgg 900  
taccagacca agtttgagac cctccaggcc caggctggga agcatgggga cgacctccgg 960  
aatacccgga atgagatttc agagatgaac cgggccatcc agaggctgca ggctgagatc 1020  
gacaacatca agaaccagcg tgccaagtgg gaggcgcgca ttgccgaggc tgaggagcgt 1080  
ggggagctgg cgctcaagga tgctcgtgcc aagcaggagg agctggaagc cgccctgcag 1140  
cgggccaagc aggatatggc acggcagctg cgtgagtacc aggaactcat gagcgtgaag 1200  
ctggccctgg acatcgagat cgccacctac cgcaagctgc tggaggcgca ggagagccgg 1260  
ttggctggag atggagtggg agccgtgaat atctctgtga tgaattccac tgggtggcagt 1320  
agcagtggcg gtggcattgg gctgacctc gggggaacca tgggcagcaa tgccctgagc 1380  
ttctccagca gtgcgggtcc tgggctcctg aaggcttatt ccatccggac cgcacctgcc 1440  
agtcgcagga gtgcccgcga ctgagccgcc tcccaccact ccactcctcc agccaccacc 1500  
cacaatcaca agaagattcc caccctgccc tcccatgcct ggtcccaaga cagtgaaca 1560  
gtctggaag tgatgtcaga atagcttcca ataaagcagc ctcattctga ggcctgagt 1620  
atccaaaaaa aaaaaaaaaa a 1641

<210> 171  
<211> 469  
<212> PRT  
<213> Homo sapiens

<400> 171  
Met Ser Ile His Phe Ser Ser Pro Val Phe Thr Ser Arg Ser Ala Ala  
1 5 10 15  
Phe Ser Gly Arg Gly Ala Gln Val Arg Leu Ser Ser Ala Arg Pro Gly  
20 25 30  
Gly Leu Gly Ser Ser Ser Leu Tyr Gly Leu Gly Ala Ser Arg Pro Arg  
35 40 45  
Val Ala Val Arg Ser Ala Tyr Gly Gly Pro Val Gly Ala Gly Ile Arg  
50 55 60  
Glu Val Thr Ile Asn Gln Ser Leu Leu Ala Pro Leu Arg Leu Asp Ala  
65 70 75 80  
Asp Pro Ser Leu Gln Arg Val Arg Gln Glu Glu Ser Glu Gln Ile Lys  
85 90 95



183

Ala Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu  
 100 105 110  
 Glu Gln Gln Asn Lys Leu Leu Glu Thr Lys Trp Thr Leu Leu Gln Glu  
 115 120 125  
 Gln Lys Ser Ala Lys Ser Ser Arg Leu Pro Asp Ile Phe Glu Ala Gln  
 130 135 140  
 Ile Ala Gly Leu Arg Gly Gln Leu Glu Ala Leu Gln Val Asp Gly Gly  
 145 150 155 160  
 Arg Leu Glu Gln Gly Leu Arg Thr Met Gln Asp Val Val Glu Asp Phe  
 165 170 175  
 Lys Asn Lys Tyr Glu Asp Glu Ile Asn Arg Arg Thr Ala Ala Glu Asn  
 180 185 190  
 Glu Phe Val Val Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Ser Lys  
 195 200 205  
 Val Glu Leu Glu Ala Lys Val Asp Ala Leu Asn Asp Glu Ile Asn Phe  
 210 215 220  
 Leu Arg Thr Leu Asn Glu Thr Glu Leu Thr Glu Leu Gln Ser Gln Ile  
 225 230 235 240  
 Ser Asp Thr Ser Val Val Leu Ser Met Asp Asn Ser Arg Ser Leu Asp  
 245 250 255  
 Leu Asp Gly Ile Ile Ala Glu Val Lys Ala Gln Tyr Glu Glu Met Ala  
 260 265 270  
 Lys Cys Ser Arg Ala Glu Ala Glu Ala Trp Tyr Gln Thr Lys Phe Glu  
 275 280 285  
 Thr Leu Gln Ala Gln Ala Gly Lys His Gly Asp Asp Leu Arg Asn Thr  
 290 295 300  
 Arg Asn Glu Ile Ser Glu Met Asn Arg Ala Ile Gln Arg Leu Gln Ala  
 305 310 315 320  
 Glu Ile Asp Asn Ile Lys Asn Gln Arg Ala Lys Leu Glu Ala Ala Ile  
 325 330 335  
 Ala Glu Ala Glu Glu Cys Gly Glu Leu Ala Leu Lys Asp Ala Arg Ala  
 340 345 350  
 Lys Gln Glu Glu Leu Glu Ala Ala Leu Gln Arg Ala Lys Gln Asp Met  
 355 360 365  
 Ala Arg Gln Leu Arg Glu Tyr Gln Glu Leu Met Ser Val Lys Leu Ala  
 370 375 380  
 Leu Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Glu Gly Glu Glu  
 385 390 395 400  
 Ser Arg Leu Ala Gly Asp Gly Val Gly Ala Val Asn Ile Ser Val Met  
 405 410 415  
 Asn Ser Thr Gly Gly Ser Ser Ser Gly Gly Gly Ile Gly Leu Thr Leu  
 420 425 430  
 Gly Gly Thr Met Gly Ser Asn Ala Leu Ser Phe Ser Ser Ser Ala Gly  
 435 440 445  
 Pro Gly Leu Leu Lys Ala Tyr Ser Ile Arg Thr Ala Ser Ala Ser Arg  
 450 455 460  
 Arg Ser Ala Arg Asp  
 465

&lt;210&gt; 172

&lt;211&gt; 1640

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 172

ggcagtgccg gctcctcctc gcccgccgct aggtccatcc cggcccagcc accatgtcca 60  
 tccacttcag ctccccggta ttcacctcgc gctcagccgc cttctcgggc cgcggcgcc 120

```

aggtgcgct gagctccgct cgccccggcg gccttggcag cagcagcctc tacggcctcg 180
gcgccctcgcg gccgcgcgtg gccgtgcgct ctgcctatgg gggcccggtg ggcgccgca 240
tccgcgaggt caccattaac cagagcctgc tggccccgct gcggctggac gccgaccct 300
ccctccagcg ggtgcgccag gaggagagcg agcagatcaa gacctcaac aacaagtttg 360
cctccttcat cgacaaggtg cggtttctgg agcagcagaa caagctgctg gagaccaagt 420
ggacgctgct gcaggagcag aagtcggcca agagcagccg cctcccagac atctttgagg 480
cccagattgc tggccttcg ggtcagcttg aggcaactgca ggtggatggg ggccgctgg 540
aggcggagct gcggagcatg caggatgtgg tggaggactt caagaataag tacgaagatg 600
aaattaaccg ccgcacagct gctgagaatg agtttgtggt gctgaagaag gatgtggatg 660
ctgcctacat gagcaaggtg gagctggagg ccaaggtgga tgcctgaat gatgagatca 720
acttccctcag gacctcaat gagacggagt tgacagagct gcagtcccag atctccgaca 780
catctgtggt gctgtccatg gacaacagtc gctccctgga cctggacggc atcatcgctg 840
aggtcaaggc acagtatgag gagatggcca aatgcagccg ggctgaggct gaagcctggt 900
accagaccaa gtttgagacc ctccaggccc aggtctggga gcatggggac gacctccgga 960
ataccggaa tgagatttca gagatgaacc gggccatcca gaggctgcag gctgagatcg 1020
acaacatcaa gaaccagcgt gccaaagttg aggcgcctat tgccgaggct gaggagcgtg 1080
gggagctggc gctcaaggat gctcgtgcca agcaggagga gctggaagcc gccctgcagc 1140
gggccaagca ggatatggca cggcagctgc gtgagtacca ggaactcatg agcgtgaagc 1200
tggccctgga catcgagatc gccacctacc gcaagctgct ggagggcgag gagagccggt 1260
tggctggaga tggagtggga gccgtgaata tctctgtgat gaattccact ggtggcagta 1320
gcagtggcgg tggcattggg ctgaccctcg ggggaaccat gggcagcaat gccctgagct 1380
tctccagcag tgcgggtcct gggctcctga aggcttattc catccggacc gcatccgcca 1440
gtcgcaggag tgcgcgcgac tgagccgcct cccaccactc cactcctcca gccaccaccc 1500
acaatcacia gaagattccc acccctgcct cccatgcctg gtccaagac agtgagacag 1560
tctggaaagt gatgtcagaa tagcttccaa taaagcagcc tcattctgag gcctgagtga 1620
tccaaaaaaa aaaaaaaaaa 1640

```

&lt;210&gt; 173

&lt;211&gt; 469

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 173

```

Met Ser Ile His Phe Ser Ser Pro Val Phe Thr Ser Arg Ser Ala Ala
1          5          10          15
Phe Ser Gly Arg Gly Ala Gln Val Arg Leu Ser Ser Ala Arg Pro Gly
20          25          30
Gly Leu Gly Ser Ser Ser Leu Tyr Gly Leu Gly Ala Ser Arg Pro Arg
35          40          45
Val Ala Val Arg Ser Ala Tyr Gly Gly Pro Val Gly Ala Gly Ile Arg
50          55          60
Glu Val Thr Ile Asn Gln Ser Leu Leu Ala Pro Leu Arg Leu Asp Ala
65          70          75          80
Asp Pro Ser Leu Gln Arg Val Arg Gln Glu Ser Glu Gln Ile Lys
85          90          95
Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu
100         105         110
Glu Gln Gln Asn Lys Leu Leu Glu Thr Lys Trp Thr Leu Leu Gln Glu
115         120         125
Gln Lys Ser Ala Lys Ser Ser Arg Leu Pro Asp Ile Phe Glu Ala Gln
130         135         140
Ile Ala Gly Leu Arg Gly Gln Leu Glu Ala Leu Gln Val Asp Gly Gly
145         150         155         160
Arg Leu Glu Ala Glu Leu Arg Ser Met Gln Asp Val Val Glu Asp Phe
165         170         175
Lys Asn Lys Tyr Glu Asp Glu Ile Asn Arg Arg Thr Ala Ala Glu Asn
180         185         190
Glu Phe Val Val Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Ser Lys

```

185

195	200	205
Val Glu Leu Glu Ala Lys	Val Asp Ala Leu Asn	Asp Glu Ile Asn Phe
210	215	220
Leu Arg Thr Leu Asn Glu Thr	Glu Leu Thr Glu Leu Gln Ser Gln Ile	
225	230	235
Ser Asp Thr Ser Val Val Leu Ser Met Asp Asn Ser Arg Ser Leu Asp		240
245	250	255
Leu Asp Gly Ile Ile Ala Glu Val Lys Ala Gln Tyr Glu Glu Met Ala		260
260	265	270
Lys Cys Ser Arg Ala Glu Ala Glu Ala Trp Tyr Gln Thr Lys Phe Glu		275
275	280	285
Thr Leu Gln Ala Gln Ala Gly Lys His Gly Asp Asp Leu Arg Asn Thr		290
290	295	300
Arg Asn Glu Ile Ser Glu Met Asn Arg Ala Ile Gln Arg Leu Gln Ala		305
305	310	315
Glu Ile Asp Asn Ile Lys Asn Gln Arg Ala Lys Leu Glu Ala Ala Ile		320
325	330	335
Ala Glu Ala Glu Glu Arg Gly Glu Leu Ala Leu Lys Asp Ala Arg Ala		340
340	345	350
Lys Gln Glu Glu Leu Glu Ala Ala Leu Gln Arg Ala Lys Gln Asp Met		355
355	360	365
Ala Arg Gln Leu Arg Glu Tyr Gln Glu Leu Met Ser Val Lys Leu Ala		370
370	375	380
Leu Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu		385
385	390	395
Ser Arg Leu Ala Gly Asp Gly Val Gly Ala Val Asn Ile Ser Val Met		400
405	410	415
Asn Ser Thr Gly Gly Ser Ser Ser Gly Gly Gly Ile Gly Leu Thr Leu		420
420	425	430
Gly Gly Thr Met Gly Ser Asn Ala Leu Ser Phe Ser Ser Ala Gly		435
435	440	445
Pro Gly Leu Leu Lys Ala Tyr Ser Ile Arg Thr Ala Ser Ala Ser Arg		450
450	455	460
Arg Ser Ala Arg Asp		
465		

&lt;210&gt; 174

&lt;211&gt; 2186

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 174

```

acacggacca aggagtctaa cacgtgcgcg agtcgggggc tcgcacgaaa gcgcgcgtgg 60
cgcaatgaag gtgaaggccg gcgcgctcgc cgcccgaggt gggatcccga ggcctctcca 120
gtccgcccag ggcgaccac cggcccgtct cgcccgcgc gccggggagg tggagcacga 180
gcgcacgtgt taggaccga aagatggtga actatgcctg ggcagggcga agccagagga 240
aactctggtg gaggtccgta gcggtcctga cgtgcaaata ggtcgtccga cctgggtata 300
ggggcgggct ccaggcgagg cggtcgacgc tcctgaaaac ttgcgcgcgc gctcgcgcca 360
ctgcgcccgg agcgatgaag atggtcgcgc cctggacgcg gttctactcc aacagctgct 420
gcttggtgctg ccatgtccgc accggcacca tcctgctcgg cgtctggtat ctgatcatca 480
atgctgtggt actgttgatt ttattgagtg ccctggctga tccggatcag tataactttt 540
caagttctga actgggaggt gactttgagt tcatggatga tgccaacatg tgcattgcca 600
ttgcgatttc tcttctcatg atcctgatat gtgctatggc tacttacgga gcgtacaagc 660
aacgcgcagc ctggatcatc ccattcttct gttaccagat ctttgacttt gccctgaaca 720
tggttggttg aatcactgtg cttattttat caaactccat tcaggaatac atacggcaac 780
tgcctcctaa ttttcctac agagatgatg tcatgtcagt gaatcctacc tgtttggtcc 840
ttattattct tctgtttatt agcattatct tgacttttaa gggttacttg attagctgtg 900

```

```

tttggaaactg ctaccgatac atcaatggta ggaactcctc tgatgtcctg gtttatgtta 960
ccagcaatga cactacgggtg ctgctacccc cgtatgatga tgccactgtg aatgggtgctg 1020
ccaaggagcc accgccacct tacgtgtctg cctaagcctt caagtgggag gagctgagg 1080
cagcagcttg actttgcaga catctgagca atagtctctg tatttcactt ttgccatgag 1140
cctctctgag cttgtttgtt gctgaaatgc tactttttta aatttagatg ttagattgaa 1200
aactgtagtt ttcaacatat gctttgctag aacactgtga tagattaact gtagaattct 1260
tcctgtacga ttggggatat aatgggcttc actaaccttc cctaggcatt gaaacttccc 1320
ccaaatctga tggacctaga agtctgcttt tgtacctgct gggcccccataa gttgggcatt 1380
tttctctctg ttccctctct tttgaaaatg taaaataaaa ccaaaaatag acaacttttt 1440
cttcagccat tccagcatag agaacaaaac cttatggaaa caggaatgtc aattgtgtaa 1500
tcattgttct attaggtaa atagaagtcc ttatgtatgt gttacaagaa tttccccac 1560
aacatccttt atgactgaag ttcaatgaca gtttgtgttt ggggtgtaaa ggattttctc 1620
catggcctga attaagacca ttagaaagca ccaggccgtg ggagcagtga ccatctgctg 1680
actgttcttg tggatcttgt gtccagggtg atggggtgac atgcctcgta tgtgttagag 1740
gggtggaatg atgtgtttgg cgctgcatgg gatctggtgc cctcttctc ctggattcac 1800
atccccaccc agggcccgct ttactaagt gttctgccct agattggttc aaggaggtca 1860
tccaactgac tttatcaagt ggaattggga tatatttgat atacttctgc ctaacaacat 1920
ggaaaagggt tttcttttcc ctgcaagcta catcctactg ctttgaactt ccaagtatgt 1980
ctagtcacct tttaaaatgt aaacattttc agaaaaatga ggattgcctt ccttgtatgc 2040
gctttttacc tctactacct gaattgcaag ggatttttat atattcatat gttacaaagt 2100
cagcaactct cctgttggtt cattattgaa tgtgctgtaa attaatgtgt ttgcaattaa 2160
aacaagggtt gccacaaaa aaaaaa 2186

```

&lt;210&gt; 175

&lt;211&gt; 283

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 175

```

Met Val Asn Tyr Ala Trp Ala Gly Arg Ser Gln Arg Lys Leu Trp Trp
1          5          10          15
Arg Ser Val Ala Val Leu Thr Cys Lys Ser Val Val Arg Pro Gly Tyr
20          25          30
Arg Gly Gly Leu Gln Ala Arg Arg Ser Thr Leu Leu Lys Thr Cys Ala
35          40          45
Arg Ala Arg Ala Thr Ala Pro Gly Ala Met Lys Met Val Ala Pro Trp
50          55          60
Thr Arg Phe Tyr Ser Asn Ser Cys Cys Leu Cys Cys His Val Arg Thr
65          70          75          80
Gly Thr Ile Leu Leu Gly Val Trp Tyr Leu Ile Ile Asn Ala Val Val
85          90          95
Leu Leu Ile Leu Leu Ser Ala Leu Ala Asp Pro Asp Gln Tyr Asn Phe
100          105          110
Ser Ser Ser Glu Leu Gly Gly Asp Phe Glu Phe Met Asp Asp Ala Asn
115          120          125
Met Cys Ile Ala Ile Ala Ile Ser Leu Leu Met Ile Leu Ile Cys Ala
130          135          140
Met Ala Thr Tyr Gly Ala Tyr Lys Gln Arg Ala Ala Trp Ile Ile Pro
145          150          155          160
Phe Phe Cys Tyr Gln Ile Phe Asp Phe Ala Leu Asn Met Leu Val Ala
165          170          175
Ile Thr Val Leu Ile Tyr Pro Asn Ser Ile Gln Glu Tyr Ile Arg Gln
180          185          190
Leu Pro Pro Asn Phe Pro Tyr Arg Asp Asp Val Met Ser Val Asn Pro
195          200          205
Thr Cys Leu Val Leu Ile Ile Leu Leu Phe Ile Ser Ile Ile Leu Thr
210          215          220
Phe Lys Gly Tyr Leu Ile Ser Cys Val Trp Asn Cys Tyr Arg Tyr Ile

```

<400> 176						
atgccoctag	gtctcctgtg	gctggggccta	gccctgttg	gggctctgca	tgcccaggcc	60
caggactcca	cctcagacct	gatcccagcc	ccacctctga	gcaagggtccc	tctgcagcag	120
aacttcagg	acaaccaatt	ccaggggaag	tggtatgtgg	taggcctggc	agggaatgca	180
attctcagag	aagacaaaga	cccgcaaaag	atgtatgcc	ccatctatga	gctgaaagaa	240
gacaagagct	acaatgtcac	ctccgtcctg	tttaggaaaa	agaagtgtga	ctactggatc	300
aggacttttg	ttccagggtt	ccagcccggc	gagttcacgc	tgggcaacat	taagagttac	360
cctggatttaa	cgagttacct	cgtccgagtg	gtgagcacca	actacaacca	gcatgctatg	420
gtgttcttca	agaaagtttc	tcaaaacagg	gagtaacttca	agatcacccct	ctacggggaga	480
accaaggagc	tgactttcgg	actaaaggag	aacttcatcc	gcttctccaa	atatctgggc	540
ctccctgaaa	accacatcgt	cttccctgtc	ccaatcgacc	agtgtatcga	cggtctga	597

<400>	177
Met Pro Leu Gly Leu Leu Trp Leu Gly Leu Ala Leu Leu Gly Ala Leu 1 5 10 15	
His Ala Gln Ala Gln Asp Ser Thr Ser Asp Leu Ile Pro Ala Pro Pro 20 25 30	
Leu Ser Lys Val Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe Gln 35 40 45	
Gly Lys Trp Tyr Val Val Gly Leu Ala Gly Asn Ala Ile Leu Arg Glu 50 55 60	
Asp Lys Asp Pro Gln Lys Met Tyr Ala Thr Ile Tyr Glu Leu Lys Glu 65 70 75 80	
Asp Lys Ser Tyr Asn Val Thr Ser Val Leu Phe Arg Lys Lys Lys Cys 85 90 95	
Asp Tyr Trp Ile Arg Thr Phe Val Pro Gly Cys Gln Pro Gly Glu Phe 100 105 110	
Thr Leu Gly Asn Ile Lys Ser Tyr Pro Gly Leu Thr Ser Tyr Leu Val 115 120 125	
Arg Val Val Ser Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys 130 135 140	
Lys Val Ser Gln Asn Arg Glu Tyr Phe Lys Ile Thr Leu Tyr Gly Arg 145 150 155 160	
Thr Lys Glu Leu Thr Ser Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser 165 170 175	
Lys Tyr Leu Gly Leu Pro Glu Asn His Ile Val Phe Pro Val Pro Ile 180 185 190	
Asp Gln Cys Ile Asp Gly 195	

<210> 178  
 <211> 1518  
 <212> DNA  
 <213> Homo sapiens

<400> 178  
 gcctgagacc ctctgcagc cttctcaagg gacagcccca ctctgcctct tgctcctcca 60  
 gggcagcacc atgcagcccc tgtggtctctg ctgggcactc tgggtgttgc ccctggccag 120  
 ccccggggcc gccctgaccg gggagcagct cctgggcagc ctgctgcggc agctgcagct 180  
 caaagagggtg cccaccctgg acagggccga catggaggag ctggatcatc ccaccacgt 240  
 gagggcccag tacgtggccc tgctgcagcg cagccacggg gaccgctccc gcggaagag 300  
 gttcagccag agcttccgag aggtggccgg caggttctctg gcgttgagg ccagcacaca 360  
 cctgctggtg ttccgcatgg agcagcggct gccgcccaac agcagctgg tgaggccgt 420  
 gctgcggctc ttccaggagc cggccccaa ggccgcgctg cacaggcacg ggcggctgtc 480  
 cccgcgcagc gcccgggccc gggtgaccgt cgagtggctg cgcgtccgag acgacggctc 540  
 caaccgcacc tccctcatcg actccaggct ggtgtccgtc cacgagagcg gctggaaggc 600  
 cttcgacgtg accgaggccg tgaacttctg gcagcagctg agccggcccc ggcagccgt 660  
 gctgctacag gtgtcgggtg agaggagca tctgggcccg ctggcgtccg gcgccacaa 720  
 gctgggtccgc tttgcctcgc agggggcgcc agccgggctt ggggagcccc agctggagct 780  
 gcacaccctg gaccttgggg actatggagc tcaggggcagc tgtgaccctg aagaccaat 840  
 gaccgagggc acccgctgct gccgccagga gatgtacatt gacctgcagg ggatgaagt 900  
 ggccgagaac tgggtgctgg agccccggg cttcctggct tatgagtgtg tgggcacctg 960  
 ccggcagccc ccggaggccc tggccttcaa gtggccgttt ctggggcctc gacagtgc 1020  
 cgctcggag actgactcgc tgcccattgat cgtcagcatc aaggaggag gcaggaccag 1080  
 gccccagggtg gtcagcctgc ccaacatgag ggtgcagaag tgcagctgtg cctcggtatg 1140  
 tgcgctcgtg ccaaggaggc tccagccata ggcgcctagt gtagccatcg agggacttga 1200  
 cttgtgtgtg tttctgaagt gttcagggt accaggagag ctggcgatga ctgaactgct 1260  
 gatggacaaa tgctctgtgc tctctagtga gccctgaatt tgcttctct gacaagtta 1320  
 ctcacctaatt tttgtcttct cagggaatgag aatctttggc cactggagag cccttgctca 1380  
 gttttctcta ttcttattat tcaactgact atattctaag cacttacatg tggagatact 1440  
 gtaacctgag ggcagaaagc ccaatgtgtc attgtttact tgtcctgtca ctggatctgg 1500  
 gctaaagtcc tccaccac 1518

<210> 179  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 179  
 Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala  
 1 5 10 15  
 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
 20 25 30  
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
 35 40 45  
 Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
 50 55 60  
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
 65 70 75 80  
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
 85 90 95  
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
 100 105 110  
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
 115 120 125  
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg

189

130		135		140
Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr				
145		150		155
Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys				160
		165		170
Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg				175
		180		185
Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu				190
		195		200
Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln				205
		210		215
Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu				220
		225		230
Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro				235
		245		250
Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu				255
		260		265
Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe				270
		275		280
Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu				285
		290		295
Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu				300
		305		310
Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr				315
		325		330
Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser				335
		340		345
Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro				350
		355		360
				365

&lt;210&gt; 180

&lt;211&gt; 444

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 180

```

aattctagaa gtccaaatca ctcattgttt gtgaaagctg agctcacagc aaaacaagcc 60
accatgaagc tgtcgggtgtg tctcctgctg gtcacgctgg ccctctgctg ctaccaggcc 120
aatgccgagt tctgcccagc tcttgtttct gagctgttag acttcttctt cattagttaa 180
cctctgttca agttaagtct tgccaaattt gatgccctc cggaagctgt tgcagccaag 240
ttaggagtga agagatgcac ggatcagatg tcccttcaga aacgaagcct cattgcggaa 300
gtcctggtga aaatattgaa gaaatgtagt gtgtgacatg taaaaacttt catcctggtt 360
tccactgtct ttcaatgaca ccctgatctt cactgcagaa tgtaaagggt tcaacgtctt 420
gctttaataa atcacttgct ctac                                     444

```

&lt;210&gt; 181

&lt;211&gt; 90

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 181

Met Lys Leu Ser Val Cys Leu Leu Leu Val Thr Leu Ala Leu Cys Cys	
1	5
Tyr Gln Ala Asn Ala Glu Phe Cys Pro Ala Leu Val Ser Glu Leu Leu	10
	15
	20
Asp Phe Phe Phe Ile Ser Glu Pro Leu Phe Lys Leu Ser Leu Ala Lys	25
	30
	35
	40
	45

190

Phe Asp Ala Pro Pro Glu Ala Val Ala Ala Lys Leu Gly Val Lys Arg  
 50 55 60  
 Cys Thr Asp Gln Met Ser Leu Gln Lys Arg Ser Leu Ile Ala Glu Val  
 65 70 75 80  
 Leu Val Lys Ile Leu Lys Lys Cys Ser Val  
 85 90

<210> 182  
 <211> 754  
 <212> DNA  
 <213> Homo sapiens

<400> 182  
 ggagtatgag atgaaacgaa tggcagagaa tgagctgagc cggtcagtaa atgagtttct 60  
 gtccaagctg caagatgacc tcaaggaggc aatgaatact atgatgtgta gccgatgcc 120  
 aggaaagcat aggaggtttg aaatggaccg ggaacctaa agtgccagat actgtgctga 180  
 gtgtaatagg ctgcatcctg ctgaggaagg agacttttgg gcagagtcaa gcatgttggg 240  
 cctcaagatc acctactttg cactgatgga tggaaagggtg tatgacatca cagagtgggc 300  
 tggatgccag cgtgtaggta tctccccaga taccacaga gtcccctatc acatctcatt 360  
 tggttctcgg attccaggca ccagagggcg gcagagagcc accccagatg cccctcctgc 420  
 tgatcttcag gatttcttga gtcggatctt tcaagtaccc ccagggcaga tgccaatggg 480  
 aacttctttg cagctcctca gcctgcccct ggagccgctg cagcctctaa gcccaacagc 540  
 acagtaccca agggagaagc caaacctaag cggcggaaga aagtgaggag gcccttccaa 600  
 cgttgatgcc ctttctcttt cttcaaatca atgtcagggg gtcaaaaggg ctgtagcaca 660  
 ggatggagtt tgatttatcc ctctccccc aacacctagg aactgaatct ttttcttttt 720  
 attttttgag atggagtctt gctctgttgc ccag 754

<210> 183  
 <211> 191  
 <212> PRT  
 <213> Homo sapiens

<400> 183  
 Met Lys Arg Met Ala Glu Asn Glu Leu Ser Arg Ser Val Asn Glu Phe  
 1 5 10 15  
 Leu Ser Lys Leu Gln Asp Asp Leu Lys Glu Ala Met Asn Thr Met Met  
 20 25 30  
 Cys Ser Arg Cys Gln Gly Lys His Arg Arg Phe Glu Met Asp Arg Glu  
 35 40 45  
 Pro Lys Ser Ala Arg Tyr Cys Ala Glu Cys Asn Arg Leu His Pro Ala  
 50 55 60  
 Glu Glu Gly Asp Phe Trp Ala Glu Ser Ser Met Leu Gly Leu Lys Ile  
 65 70 75 80  
 Thr Tyr Phe Ala Leu Met Asp Gly Lys Val Tyr Asp Ile Thr Glu Trp  
 85 90 95  
 Ala Gly Cys Gln Arg Val Gly Ile Ser Pro Asp Thr His Arg Val Pro  
 100 105 110  
 Tyr His Ile Ser Phe Gly Ser Arg Ile Pro Gly Thr Arg Gly Arg Gln  
 115 120 125  
 Arg Ala Thr Pro Asp Ala Pro Pro Ala Asp Leu Gln Asp Phe Leu Ser  
 130 135 140  
 Arg Ile Phe Gln Val Pro Pro Gly Gln Met Pro Met Gly Thr Ser Leu  
 145 150 155 160  
 Gln Leu Leu Ser Leu Pro Leu Glu Pro Leu Gln Pro Leu Ser Pro Thr  
 165 170 175  
 Ala Gln Tyr Pro Arg Glu Lys Pro Asn Leu Ser Gly Gly Arg Lys  
 180 185 190



<210> 184  
 <211> 2511  
 <212> DNA  
 <213> Homo sapiens

<400> 184  
 cttttcacac tggccttaaa gaggatatat tagaagttga agtaggaagg gagccagaga 60  
 ggccgatggc gcaaaggtag gacgatctac cccattacgg gggcatggat ggagtaggca 120  
 tcccctccac gatgtatggg gaccgcgatg cagccagggtc catgcagccg gtccaccacc 180  
 tgaaccacgg gcctcctctg cactcgcacg agtaccgcga cacagctcat accaacgcca 240  
 tggcccccag catgggctcc tctgtcaatg acgctttaaa gagagataaa gatgccattt 300  
 atggacaccc cctcttccct ctcttagcac tgatttttga gaaatgtgaa ttagctactt 360  
 gtaccccccg cgagccgggg gtggcggggc gggacgtctg ctcgtcagag tcattcaatg 420  
 aagatatagc cgtgttcgcc aaacagattc gcgcagaaaa acctctattt tcttctaata 480  
 cagaactgga taacttgatg attcaagcca tacaagtatt aaggtttcat ctattggaat 540  
 tagagaaggt acacgaatta tgtgacaatt tctgccaccg gtatattagc tgtttgaaag 600  
 ggaaaatgcc tatcgatttg gtgatagacg atagagaagg aggatcaaaa tcagacagtg 660  
 aagatataac aagatcagca aatctaactg accagccctc ttggaacaga gatcatgatg 720  
 acacggcatc tactcgttca ggaggaaacc caggcccttc cagcgggtggc cacacgtcac 780  
 acagtgggga caacagcagt gagcaagggt atggccttga caacagtgtg gcttcccca 840  
 gcacagggtg cgatgatgac cctgataagg acaaaaagcg tcacaaaaag cgtggcatct 900  
 ttcccaaagt agccacaaat atcatgaggg cgtggctgtt ccagcatcta acacaccctt 960  
 acccttctga agaacagaaa aagcagttgg cacaagacac gggactcacc atccttcaag 1020  
 tgaacaattg gtttattaat gcccgagaa gaatagtgc gccatgata gaccagtcca 1080  
 accgagcagt aagtcaagga acacettata atcctgatgg acagcccatg ggaggtttcg 1140  
 taatggacgg tcagcaacat atgggaatta gagcaccagg acctatgagt ggaatgggca 1200  
 tgaatatggg cagtggcact acatgtaacc ttcactagt taaccaactg 1260  
 caaagcaagg gggaaggctg caaagtatgc caggggagta tgtagcccg ggtggtccaa 1320  
 tgggtgtgag tatgggacag ccaagttata cccaacccca gatgcccccc catcctgctc 1380  
 agctgcgtca tgggcccccc atgcatacgt acattcctgg acaccctcac caccacaacag 1440  
 tgatgatgca tggaggaccg cccaccctg gaatgccaat gtcagcatca agccccacag 1500  
 ttcttaatac aggagacca acaatgagtg gacaagtcac ggacattcat gctcagtagc 1560  
 ttaagggaat atgcattgtc tgcaatgggt actgatttca aatcatgttt tttctgcaat 1620  
 gactgtggag ttccattctt ggcatctact ctggaccaag gagcatccct aattcttcat 1680  
 agggaccttt aaaaagcagg aaataccaac tgaagtcaat ttgggggaca tgctaaataa 1740  
 ctatataaga cattaaagag acaaagagt aaatattgta aatgctatta tactgttata 1800  
 catattacgt tgtttcttat agatttttta aaaaaaatgt gaaatttttc cacactatgt 1860  
 gtgtgttttc catagctctt cacttctctc agaagcctcc ttacattaaa aagccttaca 1920  
 gttatcctgc aaggacagc aaggtctgat ttgcaggatt tttagagcat taaaataact 1980  
 atcaggcaga agaactcttc ttctcgccta ggatttcagc catgcgcgcg ctctctctct 2040  
 ttctctctct tttcctctct ctocctcttt ctagcctggg gcttgaattt gcattgtctaa 2100  
 ttcatctact caccatattt gaattggcct gaacagatgt aaatcgggaa ggatgggaaa 2160  
 aactgcagtc atcaacaatg attaatcagc tgttgaggc agtgtcttaa ggagactggg 2220  
 aggaggaggc atggaacca aaaggccgtg tgtttagaag cctaattgtc acatcaagca 2280  
 tcattgtccc catgcaacaa ccaccacctt atacatcact tctgtttta agcagctcta 2340  
 aaacatagac tgaagattta tttttaatat gttgacttta tttctgagca aagcatcggg 2400  
 catgtgtgta ttttttcata gtcccacctt ggagcattta tgtagacatt gtaaataaat 2460  
 tttgtgcaaa aaggactgga aaaatgaact gtattattgc aatttttttt t 2511

<210> 185  
 <211> 390  
 <212> PRT  
 <213> Homo sapiens

<400> 185  
 Met Ala Gln Arg Tyr Asp Asp Leu Pro His Tyr Gly Gly Met Asp Gly

192

1	5	10	15
Val Gly Ile Pro Ser Thr Met Tyr Gly Asp Pro His Ala Ala Arg Ser			
20		25	30
Met Gln Pro Val His His Leu Asn His Gly Pro Pro Leu His Ser His			
35		40	45
Gln Tyr Pro His Thr Ala His Thr Asn Ala Met Ala Pro Ser Met Gly			
50		55	60
Ser Ser Val Asn Asp Ala Leu Lys Arg Asp Lys Asp Ala Ile Tyr Gly			
65	70	75	80
His Pro Leu Phe Pro Leu Leu Ala Leu Ile Phe Glu Lys Cys Glu Leu			
85		90	95
Ala Thr Cys Thr Pro Arg Glu Pro Gly Val Ala Gly Gly Asp Val Cys			
100		105	110
Ser Ser Glu Ser Phe Asn Glu Asp Ile Ala Val Phe Ala Lys Gln Ile			
115		120	125
Arg Ala Glu Lys Pro Leu Phe Ser Ser Asn Pro Glu Leu Asp Asn Leu			
130		135	140
Met Ile Gln Ala Ile Gln Val Leu Arg Phe His Leu Leu Glu Leu Glu			
145	150	155	160
Lys Val His Glu Leu Cys Asp Asn Phe Cys His Arg Tyr Ile Ser Cys			
165		170	175
Leu Lys Gly Lys Met Pro Ile Asp Leu Val Ile Asp Asp Arg Glu Gly			
180		185	190
Gly Ser Lys Ser Asp Ser Glu Asp Ile Thr Arg Ser Ala Asn Leu Thr			
195		200	205
Asp Gln Pro Ser Trp Asn Arg Asp His Asp Asp Thr Ala Ser Thr Arg			
210		215	220
Ser Gly Gly Thr Pro Gly Pro Ser Ser Gly Gly His Thr Ser His Ser			
225	230	235	240
Gly Asp Asn Ser Ser Glu Gln Gly Asp Gly Leu Asp Asn Ser Val Ala			
245		250	255
Ser Pro Ser Thr Gly Asp Asp Asp Asp Pro Asp Lys Asp Lys Lys Arg			
260		265	270
His Lys Lys Arg Gly Ile Phe Pro Lys Val Ala Thr Asn Ile Met Arg			
275		280	285
Ala Trp Leu Phe Gln His Leu Thr His Pro Tyr Pro Ser Glu Glu Gln			
290		295	300
Lys Lys Gln Leu Ala Gln Asp Thr Gly Leu Thr Ile Leu Gln Val Asn			
305	310	315	320
Asn Trp Phe Ile Asn Ala Arg Arg Arg Ile Val Gln Pro Met Ile Asp			
325		330	335
Gln Ser Asn Arg Ala Val Ser Gln Gly Thr Pro Tyr Asn Pro Asp Gly			
340		345	350
Gln Pro Met Gly Gly Phe Val Met Asp Gly Gln Gln His Met Gly Ile			
355		360	365
Arg Ala Pro Gly Pro Met Ser Gly Met Gly Met Asn Met Gly Met Glu			
370		375	380
Gly Gln Trp His Tyr Met			
385	390		

&lt;210&gt; 186

&lt;211&gt; 517

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 186

cctccacagc aacttccttg atccctgccg cgcacgactg aacacagaca gcagccgcct 60

193

cgccatgaag ctgctgatgg tctcatgctt ggccggccctc ctctgcact gctatgcaga 120  
 ttctggctgc aaactcctgg aggacatggg tgaaaagacc atcaattccg acatatctat 180  
 acctgaatac aaagagcttc ttcaagagtt catagacagt gatgccgctg cagaggctat 240  
 ggggaaattc aagcagtgtt tctcaacca gtcacataga actctgaaa actttggact 300  
 gatgatgcat acagtgtacg acagcatttg gtgtaatatg aagagtaatt aactttaccc 360  
 aaggcgtttg gctcagaggg ctacagacta tggccagaac tcactgtgtg attgctagaa 420  
 accacttttc tttcttgtgt tgtcttttta tgtggaaact gctagacaac tgttgaaacc 480  
 tcaaattcat ttccatttca ataactaact gcaaatc 517

&lt;210&gt; 187

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 187

Met Lys Leu Leu Met Val Leu Met Leu Ala Ala Leu Leu Leu His Cys  
 1 5 10 15  
 Tyr Ala Asp Ser Gly Cys Lys Leu Leu Glu Asp Met Val Glu Lys Thr  
 20 25 30  
 Ile Asn Ser Asp Ile Ser Ile Pro Glu Tyr Lys Glu Leu Leu Gln Glu  
 35 40 45  
 Phe Ile Asp Ser Asp Ala Ala Ala Glu Ala Met Gly Lys Phe Lys Gln  
 50 55 60  
 Cys Phe Leu Asn Gln Ser His Arg Thr Leu Lys Asn Phe Gly Leu Met  
 65 70 75 80  
 Met His Thr Val Tyr Asp Ser Ile Trp Cys Asn Met Lys Ser Asn  
 85 90 95

&lt;210&gt; 188

&lt;211&gt; 2048

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 188

ctctgcaaac gccgcgttc ccgggtcccg cggctccgc gcgcgatctg ccgcccgcgg 60  
 ctgctgggca aaaatcagag ccgcctccgc cccattacc atcatggaaa ccctccagga 120  
 aaaagtggcc ccggacgcgc gagcctgagg attctgcaca aaagaggtgc ccaaaatgaa 180  
 gacctgatg cgccatggtc tggcagtgtg tttagcgctc accaccatgt gcaccagctt 240  
 gttgctagtg tacagcagcc tcggcggcca gaaggagcgg ccccccagc agcagcagca 300  
 gcagcagcaa cagcagcagc aggcgtcggc caccggcagc tcgcagccgg cggcggagag 360  
 cagcaccag cagcgcgccg gggcctccgc gggaccgcgg cactggacg gatacctcgg 420  
 agtggcggac cacaagcccc tgaaaatgca ctgcagggac tgtgccctgg tgaccagctc 480  
 agggcatctg ctgcacagtc ggcaaggctc ccagattgac cagacagagt gtgtcatccg 540  
 catgaatgac gccccacac gcggctatgg gcgtgacgtg ggcaatcgca ccagcctgag 600  
 ggtcatcgcg cattccagca tccagaggat cctccgcaac cgccatgacc tgctcaacgt 660  
 gagccagggc accgtgttca tcttctgggg ccccgagcgc tacatgcggc gggacggcaa 720  
 gggccaggtc tacaacaacc tgcattctct gagccagggt ctgccccggc tgaaggcctt 780  
 catgattact cgccacaaga tgctgcagtt tgatgagctc ttcaagcagg agactggcaa 840  
 agacaggaag atatccaaca cttggctcag cactggctgg tttacaatga caattgcact 900  
 ggagctctgt gacaggatca atgtttatgg catggtgccc ccagacttct gcagggatcc 960  
 caatcaccct tcagtacctt atcattatta tgaacctttt ggacctgatg aatgtacaat 1020  
 gtacctctcc catgagcgag gacgcaaggg cagtcacac cgctttatca cagagaaacg 1080  
 agtctttaag aactgggcac ggacattcaa tattcacttt tttcaaccag actggaaacc 1140  
 agaatacatt gctataaatc atcctgagaa taaacctgtg ttctaaggaa tgagcatgcc 1200  
 agactgtaat cccaggtatt cactgcatca gacacggaga cactgaactt cctgagccac 1260  
 cagacaggaa agggtagcag aaaacagctt cactcctcag gaagtaccat ggacagacgc 1320  
 ctaccagggg tgacaaagca gtgcagttgg attgtaagga aaaattccgg aattaatgca 1380

```

tcctaataagaa tgttgtcccc ttcaatgggt ttaccttagg agctgaacat tcaattcagt 1440
tacaccacta tgactaaaaa cagtttggat ctcttagtat tgcctttgaa actgcaacat 1500
aagcaactca acaatattag ttgcattcct ttatagacat accatgtcaa agacgttttt 1560
ctatcaagtt gtattctttc ctgttctata acctttgtca tctgttagac tctgtatgtg 1620
tgatttgtaa aaagcaggct gaaactatgg acatgatttc tgaagagcac atctccactg 1680
actttcataa agcaaatgtc caatatttat ttattgagag ttttttagtg caatctgggc 1740
cagtattttt atagattatg attatgtggt aatttatcct tcctaactct ttaatcctga 1800
atgatgggtg gaaatggcct agaattaggt tactctgttc acaatgctca ttgttagcat 1860
gcaattggta ttgacttgg aagtgttgtg ttgtattttt tgaacccta ggcttcagga 1920
aaactgctct ttgtaaaaa gaatagcgat gacattttct aatgtgcaga aatgttccaa 1980
aaggacaaaa ttgaaaacca aaaactatgt tattaataca aaaaaatgct aaaaaaaaaa 2040
aaaaaaaaa 2048

```

&lt;210&gt; 189

&lt;211&gt; 336

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 189

```

Met Lys Thr Leu Met Arg His Gly Leu Ala Val Cys Leu Ala Leu Thr
 1          5          10          15
Thr Met Cys Thr Ser Leu Leu Leu Val Tyr Ser Ser Leu Gly Gly Gln
 20          25          30
Lys Glu Arg Pro Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 35          40          45
Gln Ala Ser Ala Thr Gly Ser Ser Gln Pro Ala Ala Glu Ser Ser Thr
 50          55          60
Gln Gln Arg Pro Gly Val Pro Ala Gly Pro Arg Pro Leu Asp Gly Tyr
 65          70          75          80
Leu Gly Val Ala Asp His Lys Pro Leu Lys Met His Cys Arg Asp Cys
 85          90          95
Ala Leu Val Thr Ser Ser Gly His Leu Leu His Ser Arg Gln Gly Ser
100          105          110
Gln Ile Asp Gln Thr Glu Cys Val Ile Arg Met Asn Asp Ala Pro Thr
115          120          125
Arg Gly Tyr Gly Arg Asp Val Gly Asn Arg Thr Ser Leu Arg Val Ile
130          135          140
Ala His Ser Ser Ile Gln Arg Ile Leu Arg Asn Arg His Asp Leu Leu
145          150          155          160
Asn Val Ser Gln Gly Thr Val Phe Ile Phe Trp Gly Pro Ser Ser Tyr
165          170          175
Met Arg Arg Asp Gly Lys Gly Gln Val Tyr Asn Asn Leu His Leu Leu
180          185          190
Ser Gln Val Leu Pro Arg Leu Lys Ala Phe Met Ile Thr Arg His Lys
195          200          205
Met Leu Gln Phe Asp Glu Leu Phe Lys Gln Glu Thr Gly Lys Asp Arg
210          215          220
Lys Ile Ser Asn Thr Trp Leu Ser Thr Gly Trp Phe Thr Met Thr Ile
225          230          235          240
Ala Leu Glu Leu Cys Asp Arg Ile Asn Val Tyr Gly Met Val Pro Pro
245          250          255
Asp Phe Cys Arg Asp Pro Asn His Pro Ser Val Pro Tyr His Tyr Tyr
260          265          270
Glu Pro Phe Gly Pro Asp Glu Cys Thr Met Tyr Leu Ser His Glu Arg
275          280          285
Gly Arg Lys Gly Ser His His Arg Phe Ile Thr Glu Lys Arg Val Phe
290          295          300
Lys Asn Trp Ala Arg Thr Phe Asn Ile His Phe Phe Gln Pro Asp Trp

```

305                      310                      315                      320  
Lys Pro Glu Ser Leu Ala Ile Asn His Pro Glu Asn Lys Pro Val Phe  
                                325                      330                      335

<400> 190					
aagaacaatt	gtctctggac	ggcagctatg	cgactcaccg	tgtgtgtgtgc	tgtgtgcctg 60
ctgcctggca	gcttggcoct	gccgctgcct	caggaggcgg	gaggcatgag	tgagctacag 120
tgggaacagg	ctcaggacta	tctcaagaga	ttttatctct	atgactcaga	aacaaaaaat 180
gccaacagtt	tagaagccaa	actcaaggag	atgcaaaaat	tctttggcct	acctataact 240
ggaatgttaa	actcccgcgt	catagaaata	atgcagaagc	ccagatgtgg	agtgccagat 300
gttgacagat	actcactatt	tccaaatagc	ccaaaatgga	cttccaaagt	ggtcacctac 360
aggatcgtat	catatactcg	agactttaccg	catattacag	tggatcgatt	agtgctaaag 420
gctttaaaca	tgtggggcaa	agagatcccc	ctgcatttca	ggaaagtgtt	atggggaaact 480
gctgacatca	tgattggctt	tgcgcgagga	gctcatgggg	actcctaccc	atttgatggg 540
ccaggaaaca	cgctggctca	tgccttttgcg	cctgggacag	gtctcggagg	agatgctcac 600
ttcgatgagg	atgaacgctg	gacggatggt	agcagtctag	ggattaactt	cctgtatgct 660
gcaactcatg	aacttggcca	ttctttgggt	atgggacatt	cctctgatcc	taatgcagtg 720
atgtatccaa	cctatggaaa	tggagatccc	caaaatttta	aactttccca	ggatgatatt 780
aaaggcattc	agaaactata	tggaaagaga	agtaattcaa	gaaagaaata	gaaacttcag 840
tcagaaacac	cattcattca	tctattggat	tgtatatcat	tgttgaccaa	tcagaattga 900
taagcactgt	tctccactc	catttagcaa	ttatgtcacc	cttttttatt	gcagttgggt 960
tttgaatgtc	tttactcct	tttattgggt	aaactccttt	atgggtgtgac	tgtgtcttat 1020
tccatctatg	agctttgtca	gtgcgcgtag	atgtcaataa	atgttacata	cacaaata 1078

<400> 191															
Met	Arg	Leu	Thr	Val	Leu	Cys	Ala	Val	Cys	Leu	Leu	Pro	Gly	Ser	Leu
1				5					10					15	
Ala	Leu	Pro	Leu	Pro	Gln	Glu	Ala	Gly	Gly	Met	Ser	Glu	Leu	Gln	Trp
			20					25					30		
Glu	Gln	Ala	Gln	Asp	Tyr	Leu	Lys	Arg	Phe	Tyr	Leu	Tyr	Asp	Ser	Glu
		35					40					45			
Thr	Lys	Asn	Ala	Asn	Ser	Leu	Glu	Ala	Lys	Leu	Lys	Glu	Met	Gln	Lys
	50					55					60				
Phe	Phe	Gly	Leu	Pro	Ile	Thr	Gly	Met	Leu	Asn	Ser	Arg	Val	Ile	Glu
65					70					75				80	
Ile	Met	Gln	Lys	Pro	Arg	Cys	Gly	Val	Pro	Asp	Val	Ala	Glu	Tyr	Ser
				85					90					95	
Leu	Phe	Pro	Asn	Ser	Pro	Lys	Trp	Thr	Ser	Lys	Val	Val	Thr	Tyr	Arg
			100					105					110		
Ile	Val	Ser	Tyr	Thr	Arg	Asp	Leu	Pro	His	Ile	Thr	Val	Asp	Arg	Leu
		115					120					125			
Val	Ser	Lys	Ala	Leu	Asn	Met	Trp	Gly	Lys	Glu	Ile	Pro	Leu	His	Phe
		130				135					140				
Arg	Lys	Val	Val	Trp	Gly	Thr	Ala	Asp	Ile	Met	Ile	Gly	Phe	Ala	Arg
145					150					155					160
Gly	Ala	His	Gly	Asp	Ser	Tyr	Pro	Phe	Asp	Gly	Pro	Gly	Asn	Thr	Leu
				165					170					175	

196

Ala His Ala Phe Ala Pro Gly Thr Gly Leu Gly Gly Asp Ala His Phe  
 180 185 190  
 Asp Glu Asp Glu Arg Trp Thr Asp Gly Ser Ser Leu Gly Ile Asn Phe  
 195 200 205  
 Leu Tyr Ala Ala Thr His Glu Leu Gly His Ser Leu Gly Met Gly His  
 210 215 220  
 Ser Ser Asp Pro Asn Ala Val Met Tyr Pro Thr Tyr Gly Asn Gly Asp  
 225 230 235 240  
 Pro Gln Asn Phe Lys Leu Ser Gln Asp Asp Ile Lys Gly Ile Gln Lys  
 245 250 255  
 Leu Tyr Gly Lys Arg Ser Asn Ser Arg Lys Lys  
 260 265

&lt;210&gt; 192

&lt;211&gt; 2217

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 192

```

ggcgggccac tccggtctgc tgtgacgcgc ggacagagag ctaccggtgg acccacggtg 60
cctccctccc tgggatctac acagaccatg gccttgccaa cggctcgacc cctgttgggg 120
tcctgtggga ccccgccct cggcagcctc ctgttcctgc tcttcagcct cggatgggtg 180
cagccctcga ggacctggc tggagagaca gggcaggagg ctgcaccctt ggacggagtc 240
ctggccaacc cacctaaccat ttccagcctc tccctcgcc aactccttgg cttcccggtg 300
gcgagggtgt ccggcctgag cacggagcgt gtccgggagc tggctgtggc cttggcacag 360
aagaatgtca agctotcaac agagcagctg cgctgtctgg ctacccggct ctctgagccc 420
cccaggagacc tggacgccc cccattggac ctgctgctat tcctcaacc agatgcgttc 480
tcggggcccc aggcctgcac ccgtttcttc tccgcacat cgaaggccaa tgtggacctg 540
ctcccgaggg ggcctcccga gcgacagcgg gctgtgcctg cggtctgggc ctgctggggg 600
gtgcgggggg ctctgtgtag cgaggctgat gtgcgggctc tgggaggcct ggcttgcgac 660
ctgcttgggc gctttgtggc cgagtcggcc gaagtgtgct taccctggct ggtgagctgc 720
ccgggacccc tggaccagga ccagcaggag gcagccaggg cggctctgca gggcggggga 780
ccccctacg gccccccgtc gacatggtct gtctccacga tggacgctct gcggggcctg 840
ctgcccgtgc tgggccagcc catcatccgc agcatccgc agggcatcgt ggccgcgtgg 900
cggcaacgct cctctcgga cccatcctgg cggcagcctg aacggaccat cctccggccg 960
cggttccggc ggaagtggga gaagacagcc tgtccttcag gcaagaaggc ccgcgagata 1020
gacgagacc tcattctcta caagaagtgg gagctggaag cctgcgtgga tgcggccctg 1080
ctggccaccc atatggaccg cgtgaacgcc atcccctca cctacgagca gctggacgta 1140
ctaaagcata aactggatga gctctacca caaggttacc ccgagtctgt gatccagcac 1200
ctgggtacc tcttctcaa gatgagccct gaggacattc gcaagtggaa tgtgacgtcc 1260
ctggagacc tgaaggcttt gcttgaagtc aacaaagggc acgaaatgag tcctcaggct 1320
cctcgggcgc ccctcccaca ggtggccacc ctgatcgacc gctttgtgaa gggaaggggc 1380
cagctagaca aagacaccct agacaccctg accgccttct accctgggta cctgtgctcc 1440
ctcagccccg aggagctgag ctccgtgccc ccagcagca tctgggaggg caggccccag 1500
gacctggaca cgtgtgacct aaggcagctg gacgtcctct atcccaaggc ccgccttgtc 1560
ttccagaaca tgaacgggtc cgaatacttc gtgaagatcc agtccttcct ggtgggggccc 1620
cccacggagg atttgaaggc gctcagtcag cagaatgtga gcatggactt ggccacgttc 1680
atgaagctgc ggacggatgc ggtgctgccc ttgactgtgg ctgagggtgca gaaacttctg 1740
ggacccacg tggagggcct gaaggcggag gaggcgacc gcccggtgcg ggactggatc 1800
ctacggcagc ggcaggacga cctggacacg ctggggctgg ggctacaggg cggcatcccc 1860
aacggctacc tggctcctaga cctcagcgtg caaggtgggc ggggcggcca ggccagggct 1920
gggggcagag ctgggggcgt ggaggtgggc gctctgagtc acccctctct ctgtagaggc 1980
cctctcgggg acgccctgcc tcctaggacc tggacctgtt ctacccgtcc tggcactgct 2040
cctagcctcc accctggcct gagggcccc ctccttgcct ggccccagcc ctgctgggga 2100
tccccgcctg gccaggagca ggcacgggtg atcccgttc caccacaaga gaactcgcgc 2160
tcagtaaacg ggaacatgcc cctgcagac acgtaaaaaa aaaaaaaaaa aaaaaaa 2217

```

<210> 193  
 <211> 702  
 <212> PRT  
 <213> Homo sapiens

<400> 193

Met	Ala	Leu	Pro	Thr	Ala	Arg	Pro	Leu	Leu	Gly	Ser	Cys	Gly	Thr	Pro
1				5					10					15	
Ala	Leu	Gly	Ser	Leu	Leu	Phe	Leu	Leu	Phe	Ser	Leu	Gly	Trp	Val	Gln
			20					25					30		
Pro	Ser	Arg	Thr	Leu	Ala	Gly	Glu	Thr	Gly	Gln	Glu	Ala	Ala	Pro	Leu
		35					40					45			
Asp	Gly	Val	Leu	Ala	Asn	Pro	Pro	Asn	Ile	Ser	Ser	Leu	Ser	Pro	Arg
	50					55					60				
Gln	Leu	Leu	Gly	Phe	Pro	Cys	Ala	Glu	Val	Ser	Gly	Leu	Ser	Thr	Glu
65					70					75					80
Arg	Val	Arg	Glu	Leu	Ala	Val	Ala	Leu	Ala	Gln	Lys	Asn	Val	Lys	Leu
				85				90						95	
Ser	Thr	Glu	Gln	Leu	Arg	Cys	Leu	Ala	His	Arg	Leu	Ser	Glu	Pro	Pro
			100					105					110		
Glu	Asp	Leu	Asp	Ala	Leu	Pro	Leu	Asp	Leu	Leu	Leu	Phe	Leu	Asn	Pro
	115						120					125			
Asp	Ala	Phe	Ser	Gly	Pro	Gln	Ala	Cys	Thr	Arg	Phe	Phe	Ser	Arg	Ile
	130					135					140				
Thr	Lys	Ala	Asn	Val	Asp	Leu	Leu	Pro	Arg	Gly	Ala	Pro	Glu	Arg	Gln
145					150					155					160
Arg	Leu	Leu	Pro	Ala	Leu	Ala	Cys	Trp	Gly	Val	Arg	Gly	Ser	Leu	
				165				170					175		
Leu	Ser	Glu	Ala	Asp	Val	Arg	Ala	Leu	Gly	Gly	Leu	Ala	Cys	Asp	Leu
		180						185					190		
Pro	Gly	Arg	Phe	Val	Ala	Glu	Ser	Ala	Glu	Val	Leu	Leu	Pro	Arg	Leu
		195					200					205			
Val	Ser	Cys	Pro	Gly	Pro	Leu	Asp	Gln	Asp	Gln	Gln	Glu	Ala	Ala	Arg
	210					215				220					
Ala	Ala	Leu	Gln	Gly	Gly	Gly	Pro	Pro	Tyr	Gly	Pro	Pro	Ser	Thr	Trp
225				230						235					240
Ser	Val	Ser	Thr	Met	Asp	Ala	Leu	Arg	Gly	Leu	Leu	Pro	Val	Leu	Gly
				245					250					255	
Gln	Pro	Ile	Ile	Arg	Ser	Ile	Pro	Gln	Gly	Ile	Val	Ala	Ala	Trp	Arg
		260						265					270		
Gln	Arg	Ser	Ser	Arg	Asp	Pro	Ser	Trp	Arg	Gln	Pro	Glu	Arg	Thr	Ile
		275					280					285			
Leu	Arg	Pro	Arg	Phe	Arg	Arg	Glu	Val	Glu	Lys	Thr	Ala	Cys	Pro	Ser
	290					295					300				
Gly	Lys	Lys	Ala	Arg	Glu	Ile	Asp	Glu	Ser	Leu	Ile	Phe	Tyr	Lys	Lys
305					310					315					320
Trp	Glu	Leu	Glu	Ala	Cys	Val	Asp	Ala	Ala	Leu	Leu	Ala	Thr	Gln	Met
				325				330						335	
Asp	Arg	Val	Asn	Ala	Ile	Pro	Phe	Thr	Tyr	Glu	Gln	Leu	Asp	Val	Leu
			340					345					350		
Lys	His	Lys	Leu	Asp	Glu	Leu	Tyr	Pro	Gln	Gly	Tyr	Pro	Glu	Ser	Val
		355					360					365			
Ile	Gln	His	Leu	Gly	Tyr	Leu	Phe	Leu	Lys	Met	Ser	Pro	Glu	Asp	Ile
	370					375					380				
Arg	Lys	Trp	Asn	Val	Thr	Ser	Leu	Glu	Thr	Leu	Lys	Ala	Leu	Leu	Glu
385					390					395					400
Val	Asn	Lys	Gly	His	Glu	Met	Ser	Pro	Gln	Ala	Pro	Arg	Arg	Pro	Leu
				405					410					415	

Pro Gln Val Ala Thr Leu Ile Asp Arg Phe Val Lys Gly Arg Gly Gln  
 420 425 430  
 Leu Asp Lys Asp Thr Leu Asp Thr Leu Thr Ala Phe Tyr Pro Gly Tyr  
 435 440 445  
 Leu Cys Ser Leu Ser Pro Glu Glu Leu Ser Ser Val Pro Pro Ser Ser  
 450 455 460  
 Ile Trp Ala Val Arg Pro Gln Asp Leu Asp Thr Cys Asp Pro Arg Gln  
 465 470 475 480  
 Leu Asp Val Leu Tyr Pro Lys Ala Arg Leu Ala Phe Gln Asn Met Asn  
 485 490 495  
 Gly Ser Glu Tyr Phe Val Lys Ile Gln Ser Phe Leu Gly Gly Ala Pro  
 500 505 510  
 Thr Glu Asp Leu Lys Ala Leu Ser Gln Gln Asn Val Ser Met Asp Leu  
 515 520 525  
 Ala Thr Phe Met Lys Leu Arg Thr Asp Ala Val Leu Pro Leu Thr Val  
 530 535 540  
 Ala Glu Val Gln Lys Leu Leu Gly Pro His Val Glu Gly Leu Lys Ala  
 545 550 555 560  
 Glu Glu Arg His Arg Pro Val Arg Asp Trp Ile Leu Arg Gln Arg Gln  
 565 570 575  
 Asp Asp Leu Asp Thr Leu Gly Leu Gly Leu Gln Gly Gly Ile Pro Asn  
 580 585 590  
 Gly Tyr Leu Val Leu Asp Leu Ser Val Gln Gly Gly Arg Gly Gly Gln  
 595 600 605  
 Ala Arg Ala Gly Gly Arg Ala Gly Gly Val Glu Val Gly Ala Leu Ser  
 610 615 620  
 His Pro Ser Leu Cys Arg Gly Pro Leu Gly Asp Ala Leu Pro Pro Arg  
 625 630 635 640  
 Thr Trp Thr Cys Ser His Arg Pro Gly Thr Ala Pro Ser Leu His Pro  
 645 650 655  
 Gly Leu Arg Ala Pro Leu Pro Cys Trp Pro Gln Pro Cys Trp Gly Ser  
 660 665 670  
 Pro Pro Gly Gln Glu Gln Ala Arg Val Ile Pro Val Pro Pro Gln Glu  
 675 680 685  
 Asn Ser Arg Ser Val Asn Gly Asn Met Pro Pro Ala Asp Thr  
 690 695 700

&lt;210&gt; 194

&lt;211&gt; 2135

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 194

ggccggccac tcccgtctgc tgtgacgcgc ggacagagag ctaccggtgg acccaccggtg 60  
 cctccctccc tgggatctac acagaccatg gccttgccaa cggctcgacc cctgttgggg 120  
 tctgtggga ccccgcct cggcagcctc ctgttctctgc tcttcagcct cggatgggtg 180  
 cagccctcga ggaccctggc tggagagaca gggcaggagg ctgcaccctt ggacggagtc 240  
 ctggccaacc caccatacat ttccagcctc tcccctcgcc aactccttgg cttcccggtg 300  
 gcgagggtgt ccggcctgag cacggagcgt gtccgggagc tggctgtggc cttggcacag 360  
 aagaatgtca agctctcaac agagcagctg cgctgtcttg ctcaccggct ctctgagccc 420  
 cccgaggacc tggacgcct cccattggac ctgctgctat tctcaaccc agatgcgttc 480  
 tgggggcccc aggcctgcac ccgtttcttc tcccgcatca cgaaggccaa tgtggacctg 540  
 ctcccagggg gggctcccga gcgacagcgg ctgctgcctg cggctctggc ctgctggggg 600  
 gtgccccggg ctctgctgag cgaggctgat gtgcgggctc tgggaggcct ggcttgcgac 660  
 ctgctggggt gctttgtggc cgagtcggcc gaagtgcctg taccocggct ggtgagctgc 720  
 ccgggacccc tggaccagga ccagcaggag cggtcttgca gggcggggga 780  
 cccccctacg gcccccgctc gacatggtct gtctccacga tggacgtctt gcggggcctg 840



```

ctgcccgtgc tgggccagcc catcatccgc agcatcccgc agggcatcgt ggccgcgtgg 900
cggcaacgct cctctcggga cccatcctgg cggcagcctg aacggaccat cctccggccg 960
cggttccggc gggaagtggg gaagacagcc tgtccttcag gcaagaaggc ccgcgagata 1020
gacgagagcc tcatcttcta caagaagtgg gagctggaag cctgcgtgga tgcggccctg 1080
ctggccaccc agatggaccg cgtgaacgcc atccccttca cctacgagca gctggacgtc 1140
ctaaagcata aactggatga gctctacca caaggttacc ccgagtctgt gatccagcac 1200
ctgggctacc tcttcctcaa gatgagccct gaggacattc gcaagtggaa tgtgacgtcc 1260
ctggagaccc tgaaggcttt gcttgaagtc aacaaagggc acgaaatgag tcctcaggct 1320
cctcggcggc ccctcccaca ggtggccacc ctgatcgacc gctttgtgaa gggaaggggc 1380
cagctagaca aagacaccct agacaccctg accgccttct accctgggta cctgtgctcc 1440
ctcagccccg aggagctgag ctccgtgccc cccagcagca tctgggcggg caggccccag 1500
gacctggaca cgtgtgaccc aaggcagctg gagctcctct atcccaaggc ccgccttgc 1560
ttccagaaca tgaacgggtc cgaatacttc gtgaagatcc agtccttcct ggggtggggc 1620
cccacggagg atttgaaggc gctcagtcag cagaatgtga gcatggactt ggccacgttc 1680
atgaagctgc ggacggatgc ggtgctgccg ttgactgtgg ctgaggtgca gaaacttctg 1740
ggacccccac tggagggcct gaaggcggag gagcggcacc gcccggtgcg ggactggatc 1800
ctacggcagc ggcaggacga cctggacacg ctggggctgg ggctacaggg cggcatcccc 1860
aacggctacc tggctcctaga cctcagcgtg caagaggccc tctcggggac gccctgcctc 1920
ctaggacctg gacctgttct caccgtcctg gcactgctcc tagcctccac cctggcctga 1980
gggccccact ccttgtctgg cccagccct gctggggatc cccgcctggc caggagcagg 2040
cacgggtgat ccccgttcca cccaagaga actcgcgtc agtaaacggg aacatgcccc 2100
ctgcagacac gtaaaaaaaaa aaaaaaaaaa aaaaaa 2135

```

&lt;210&gt; 195

&lt;211&gt; 630

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 195

```

Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro
1          5          10          15
Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln
20          25          30
Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
35          40          45
Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
50          55          60
Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
65          70          75          80
Arg Val Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu
85          90          95
Ser Thr Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro
100         105         110
Glu Asp Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro
115         120         125
Asp Ala Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile
130         135         140
Thr Lys Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln
145         150         155         160
Arg Leu Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu
165         170         175
Leu Ser Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu
180         185         190
Pro Gly Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu
195         200         205
Val Ser Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg
210         215         220
Ala Ala Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp

```

200

225		230		235		240
Ser Val Ser Thr Met	Asp Ala Leu Arg Gly	Leu Leu Pro Val	Leu Gly			
	245		250			255
Gln Pro Ile Ile Arg	Ser Ile Pro Gln Gly	Ile Val Ala Ala	Trp Arg			
	260		265			270
Gln Arg Ser Ser Arg	Asp Pro Ser Trp Arg	Gln Pro Glu Arg	Thr Ile			
	275		280			285
Leu Arg Pro Arg Phe	Arg Arg Glu Val Glu	Lys Thr Ala Cys	Pro Ser			
	290		295			300
Gly Lys Lys Ala Arg	Glu Ile Asp Glu Ser	Leu Ile Phe Tyr	Lys Lys			
305		310		315		320
Trp Glu Leu Glu Ala	Cys Val Asp Ala Ala	Leu Leu Ala Thr	Gln Met			
	325		330			335
Asp Arg Val Asn Ala	Ile Pro Phe Thr Tyr	Glu Gln Leu Asp	Val Leu			
	340		345			350
Lys His Lys Leu Asp	Glu Leu Tyr Pro	Gln Gly Tyr Pro	Glu Ser Val			
	355		360			365
Ile Gln His Leu Gly	Tyr Leu Phe Leu Lys	Met Ser Pro Glu	Asp Ile			
	370		375			380
Arg Lys Trp Asn Val	Thr Ser Leu Glu Thr	Leu Lys Ala Leu	Leu Glu			
385		390		395		400
Val Asn Lys Gly His	Glu Met Ser Pro	Gln Ala Pro Arg	Arg Pro Leu			
	405		410			415
Pro Gln Val Ala Thr	Leu Ile Asp Arg	Phe Val Lys Gly	Arg Gly Gln			
	420		425			430
Leu Asp Lys Asp Thr	Leu Asp Thr Leu Thr	Ala Phe Tyr Pro	Gly Tyr			
	435		440			445
Leu Cys Ser Leu Ser	Pro Glu Leu Ser Ser	Val Pro Pro Ser	Ser Ser			
	450		455			460
Ile Trp Ala Val Arg	Pro Gln Asp Leu Asp	Thr Cys Asp Pro	Arg Gln			
465		470		475		480
Leu Asp Val Leu Tyr	Pro Lys Ala Arg	Leu Ala Phe Gln	Asn Met Asn			
	485		490			495
Gly Ser Glu Tyr Phe	Val Lys Ile Gln Ser	Phe Leu Gly Gly	Ala Pro			
	500		505			510
Thr Glu Asp Leu Lys	Ala Leu Ser Gln	Gln Asn Val Ser	Met Asp Leu			
	515		520			525
Ala Thr Phe Met Lys	Leu Arg Thr Asp	Ala Val Leu Pro	Leu Thr Val			
	530		535			540
Ala Glu Val Gln Lys	Leu Leu Gly Pro	His Val Glu Gly	Leu Lys Ala			
545		550		555		560
Glu Glu Arg His Arg	Pro Val Arg Asp	Trp Ile Leu Arg	Gln Arg Gln			
	565		570			575
Asp Asp Leu Asp Thr	Leu Gly Leu Gly	Leu Gln Gly Gly	Ile Pro Asn			
	580		585			590
Gly Tyr Leu Val Leu	Asp Leu Ser Val	Gln Glu Ala Leu	Ser Gly Thr			
	595		600			605
Pro Cys Leu Leu Gly	Pro Gly Pro Val	Leu Thr Val Leu	Ala Leu Leu			
	610		615			620
Leu Ala Ser Thr Leu	Ala					
625		630				

&lt;210&gt; 196

&lt;211&gt; 2105

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 196

```

ggccggccac tcccgctctgc tgtgacgcgc ggacagagag ctaccgggtgg acccacggtg 60
cctccctccc tgggatctac acagaccatg gccttgccaa cggctcgacc cctgttgggg 120
tctgtgggga ccccgccct cggcagcctc ctgttctctgc tcttcagcct cggatgggtg 180
cagccctcga ggaccctggc tggagagaca gggcaggagg ctgcacccct ggacggagtc 240
ctggccaacc cacctaacat ttccagcctc tccctcgcc aactccttgg cttcccgtgt 300
gcgaggtgt cgggcctgag cacggagcgt gtccgggagc tggctgtggc cttggcacag 360
aagaatgtca agctctcaac agagcagctg cgctgtctgg ctacccggct ctctgagccc 420
cccaggagacc tggacgcctt cccattggac ctgctgctat tcctcaaccc agatgcgttc 480
tcggggcccc aggcctgcac ccgtttcttc tcccgcatca cgaaggccaa tgtggacctg 540
ctcccaggag gggctcccga gcgacagcgg ctgctgcctg cggctctggc ctgctggggt 600
gtgcgggggt ctctgctgag cgaggctgat gtgcgggctc tgggaggcct ggcttgcgac 660
ctgctggggt gctttgtggc cgagtcggcc gaagtgtctc taccgggtgt ggtgagctgc 720
ccgggacccc tggaccagga ccagcaggag gcagccaggg cggctctgca gggcggggga 780
ccccctacg gcccccgctc gacatggtct gtctccacga tggacgctct gcggggcctg 840
ctgcccgtgc tggggccagcc catcatccgc agcatcccgc agggcatcgt ggccgctgg 900
cggcaacgct cctctcgggg cccatcctgg cggcagcctg aacggaccat cctccggccg 960
cggttccggc ggggaagtga gaagacagcc tgtccttcag gcaagaaggc ccgcgagata 1020
gacgagagcc tcatcttcta caagaagtgg gagctggaag cctgcgtgga tgcggccctg 1080
ctggccaccc agatggaccg cgtgaacgcc atccccttca cctacgagca gctggacgtc 1140
ctaaagcata aactggatga gctctaccca caaggttacc ccgagtctgt gatccagcac 1200
ctgggctacc tcttctctca gatgagccct gaggacattc gcaagtggaa tgtgacgtcc 1260
ctggagaccc tgaaggcttt gcttgaagtc aacaaagggc acgaaatgag tcctcaggct 1320
cctcggcggc cctcccaca ggtggccacc ctgacgcacc gctttgtgaa ggggaaggggc 1380
cagctagaca aagacaccct agacaccctg accgccttct accctgggta cctgtgctcc 1440
ctcagccccg aggagctgag ctccgtgccc cccagcagca tctggggcgt caggccccag 1500
gacctggaca cgtgtgaccc aaggcagctg gacgtcctct atcccaaggc ccgccttgtc 1560
ttccagaaca tgaacgggtc cgaatacttc gtgaagatcc agtccttctt ggggtggggcc 1620
cccacggagg atttgaaggc gctcagtcag cagaatgtga gcatggactt ggccacgttc 1680
atgaagctgc ggacggatgc ggtgtgccc ttgactgtgg ctgagggtga gaaacttctg 1740
ggacccacg tggagggcct gaaggcggag gagcggcacc gcccgggtgc ggactggatc 1800
ctacggcagc ggcaggacga cctggacacg ctggggctgg ggctacaggg cggcatcccc 1860
aacggctacc tggctcctaga cctcagcgtg caaggacctg gacctgttct caccgtcctg 1920
gcaactgtcc tagcctccac cctggcctga gggccccact cccttgcctg cccagccct 1980
gctggggatc cccgcctggc caggagcagg cacgggtgat ccccgttcca cccaagaga 2040
actcgcgctc agtaaaccgg aacatgcccc ctgcagacac gtaaaaaaaaa aaaaaaaaaa 2100
aaaaa 2105

```

&lt;210&gt; 197

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 197

```

Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro
1          5          10          15
Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln
20          25          30
Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
35          40          45
Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
50          55          60
Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
65          70          75          80
Arg Val Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu
85          90          95
Ser Thr Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro
100          105          110

```

Glu Asp Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro  
 115 120 125  
 Asp Ala Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile  
 130 135 140  
 Thr Lys Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln  
 145 150 155 160  
 Arg Leu Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu  
 165 170 175  
 Leu Ser Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu  
 180 185 190  
 Pro Gly Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu  
 195 200 205  
 Val Ser Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg  
 210 215 220  
 Ala Ala Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp  
 225 230 235 240  
 Ser Val Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly  
 245 250 255  
 Gln Pro Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg  
 260 265 270  
 Gln Arg Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile  
 275 280 285  
 Leu Arg Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser  
 290 295 300  
 Gly Lys Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys  
 305 310 315 320  
 Trp Glu Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met  
 325 330 335  
 Asp Arg Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu  
 340 345 350  
 Lys His Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val  
 355 360 365  
 Ile Gln His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile  
 370 375 380  
 Arg Lys Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu  
 385 390 395 400  
 Val Asn Lys Gly His Glu Met Ser Pro Gln Ala Pro Arg Arg Pro Leu  
 405 410 415  
 Pro Gln Val Ala Thr Leu Ile Asp Arg Phe Val Lys Gly Arg Gly Gln  
 420 425 430  
 Leu Asp Lys Asp Thr Leu Asp Thr Leu Thr Ala Phe Tyr Pro Gly Tyr  
 435 440 445  
 Leu Cys Ser Leu Ser Pro Glu Glu Leu Ser Ser Val Pro Pro Ser Ser  
 450 455 460  
 Ile Trp Ala Val Arg Pro Gln Asp Leu Asp Thr Cys Asp Pro Arg Gln  
 465 470 475 480  
 Leu Asp Val Leu Tyr Pro Lys Ala Arg Leu Ala Phe Gln Asn Met Asn  
 485 490 495  
 Gly Ser Glu Tyr Phe Val Lys Ile Gln Ser Phe Leu Gly Gly Ala Pro  
 500 505 510  
 Thr Glu Asp Leu Lys Ala Leu Ser Gln Gln Asn Val Ser Met Asp Leu  
 515 520 525  
 Ala Thr Phe Met Lys Leu Arg Thr Asp Ala Val Leu Pro Leu Thr Val  
 530 535 540  
 Ala Glu Val Gln Lys Leu Leu Gly Pro His Val Glu Gly Leu Lys Ala  
 545 550 555 560  
 Glu Glu Arg His Arg Pro Val Arg Asp Trp Ile Leu Arg Gln Arg Gln  
 565 570 575

<400> 198						
ggccggccac	tcccgctctgc	tgtgacgcgc	ggacagagag	ctaccggtgg	accacggtg	60
cctccctccc	tgggatctac	acagaccatg	gccttgccaa	cggctcgacc	cctgttgggg	120
tctgttggga	cccccgccct	cggcagcctc	ctgttcctgc	tcttcagcct	cggatgggtg	180
cagccctcga	ggaccctggc	tggagagaca	gggcaggagg	ctgcacccct	ggacggagtc	240
ctggccaac	cacctaacat	ttccagcctc	tccctcgc	aactccttg	cttcccgtgt	300
gcgagctgt	cggcgctgag	cacggagcgt	gtccgggagc	tggctgtggc	cttggcacag	360
agaatgtca	agctctcaac	agagcagctg	cgtgtcttgg	ctcacggct	ctctgagccc	420
cccaggacc	tggacgcct	ccattggac	ctgtgtctat	tcctcaaccc	agatgcgttc	480
tccggggccc	aggcctgcac	ccgtttcttc	tcccgcatca	cgaaggccaa	tgtggacctg	540
ctcccgagg	gggctcccga	gcgacagcgg	ctgctgcctg	cggctctggc	ctgctgggg	600
gtgcgggggt	ctctgctgag	cagagctgat	gtgcgggctc	tggaggccct	ggcttgcgac	660
ctgcctggg	gctttgtgg	cgagtcggcc	gaagtgtgc	taccccggt	ggtgagctgc	720
ccgggacccc	tggacaggga	ccagcaggag	gcagccagg	cggctctgca	ggcgggggga	780
ccccctacg	gcccccgtc	gacatggtct	gtctccacga	tggacgctct	gcggggcttg	840
ctgcccgtgc	tgggccagcc	catcatccgc	agcatccgc	aggcatcgt	ggcgcgctg	900
cggcaacgct	cctctcgga	ccatcctgg	cggcagcctg	aacggaccat	cctccggccg	960
cggttccggc	gggaagtga	gaagacagcc	tgtccttcag	gcaagaaggc	ccgcgagata	1020
gacgagagcc	tcatcttcta	caagaagtgg	gagctggaag	cctgcgtgga	tgcggccctg	1080
ctggccaccc	agatggaccg	cgtgaacgcc	atccccttca	cctacgagca	gctggacgtc	1140
ctaaagcata	aactggatga	gctctaccca	caaggttacc	ccgagtctgt	gtaccagcac	1200
ctgggtctacc	tcttctctaa	gatgagccct	gaggacattc	gcaagtggaa	tgtgacgtcc	1260
ctggagaccc	tgaaggtctt	gcttgaagtc	aacaaagggc	acgaatgag	tcctcaggtg	1320
gccaccctga	tcgaccgctt	tgtgaaggga	aggggccagc	tagacaaaga	caccctagac	1380
accctgaccg	ccttctaccc	tgggtacctg	tgtcctctca	gccccgagga	gctgagctcc	1440
gtcccccca	gcagcatctg	ggcggtcagg	ccccaggacc	tggacacgtg	tgacccaagg	1500
cagctggacg	tcctctatcc	caaggcccg	cttgctttcc	agaacatgaa	cgggtccgaa	1560
tacttctgtg	agatccagtc	cttctctgggt	ggggccccc	cggaggattt	gaaggcgctc	1620
agtgcagaga	atgtgagcat	ggacttggcc	acgttcatga	agctgcggac	ggatgcggtg	1680
ctgccgttga	ctgtggctga	ggtgcagaaa	cttctgggac	ccacgttgg	gggcctgaag	1740
gcggaggagc	ggcacccgcc	gggtcgggac	tggatcctac	ggcagcggca	ggacgacctg	1800
gacacgctgg	ggctggggct	acaggggcgc	atccccaacg	gctacctggt	cctagacctc	1860
agcgtgcaag	gtgggcgggg	cggccaggcc	agggtgggg	gcagagctgg	gggctgggag	1920
gtgggcgctc	tgagtcaccc	ctctctctgt	agaggccctc	tcggggacgc	cctgcctcct	1980
aggacctgga	cctgtttctc	ccgtcctggc	actgctccta	gcctccaccc	tggcctgagg	2040
gccccactcc	cttgtgtgcc	ccagccctgc	tggggatccc	cgcttgcca	ggagcaggca	2100
cgggtagtcc	ccgttccacc	ccaagagaac	tcgcgctcag	taaacgggaa	catgccccct	2160
ggaacacgt	aaaaaaaaaa	aaaaaaaaaa	aaa			2193

<400> 199

204

Met	Ala	Leu	Pro	Thr	Ala	Arg	Pro	Leu	Leu	Gly	Ser	Cys	Gly	Thr	Pro	1	5	10	15
Ala	Leu	Gly	Ser	Leu	Leu	Phe	Leu	Leu	Phe	Ser	Leu	Gly	Trp	Val	Gln	20	25	30	
Pro	Ser	Arg	Thr	Leu	Ala	Gly	Glu	Thr	Gly	Gln	Glu	Ala	Ala	Pro	Leu	35	40	45	
Asp	Gly	Val	Leu	Ala	Asn	Pro	Pro	Asn	Ile	Ser	Ser	Leu	Ser	Pro	Arg	50	55	60	
Gln	Leu	Leu	Gly	Phe	Pro	Cys	Ala	Glu	Val	Ser	Gly	Leu	Ser	Thr	Glu	65	70	75	80
Arg	Val	Arg	Glu	Leu	Ala	Val	Ala	Leu	Ala	Gln	Lys	Asn	Val	Lys	Leu	85	90	95	
Ser	Thr	Glu	Gln	Leu	Arg	Cys	Leu	Ala	His	Arg	Leu	Ser	Glu	Pro	Pro	100	105	110	
Glu	Asp	Leu	Asp	Ala	Leu	Pro	Leu	Asp	Leu	Leu	Leu	Phe	Leu	Asn	Pro	115	120	125	
Asp	Ala	Phe	Ser	Gly	Pro	Gln	Ala	Cys	Thr	Arg	Phe	Phe	Ser	Arg	Ile	130	135	140	
Thr	Lys	Ala	Asn	Val	Asp	Leu	Leu	Pro	Arg	Gly	Ala	Pro	Glu	Arg	Gln	145	150	155	160
Arg	Leu	Leu	Pro	Ala	Ala	Leu	Ala	Cys	Trp	Gly	Val	Arg	Gly	Ser	Leu	165	170	175	
Leu	Ser	Glu	Ala	Asp	Val	Arg	Ala	Leu	Gly	Gly	Leu	Ala	Cys	Asp	Leu	180	185	190	
Pro	Gly	Arg	Phe	Val	Ala	Glu	Ser	Ala	Glu	Val	Leu	Leu	Pro	Arg	Leu	195	200	205	
Val	Ser	Cys	Pro	Gly	Pro	Leu	Asp	Gln	Asp	Gln	Gln	Glu	Ala	Ala	Arg	210	215	220	
Ala	Ala	Leu	Gln	Gly	Gly	Gly	Pro	Pro	Tyr	Gly	Pro	Pro	Ser	Thr	Trp	225	230	235	240
Ser	Val	Ser	Thr	Met	Asp	Ala	Leu	Arg	Gly	Leu	Leu	Pro	Val	Leu	Gly	245	250	255	
Gln	Pro	Ile	Ile	Arg	Ser	Ile	Pro	Gln	Gly	Ile	Val	Ala	Ala	Trp	Arg	260	265	270	
Gln	Arg	Ser	Ser	Arg	Asp	Pro	Ser	Trp	Arg	Gln	Pro	Glu	Arg	Thr	Ile	275	280	285	
Leu	Arg	Pro	Arg	Phe	Arg	Arg	Glu	Val	Glu	Lys	Thr	Ala	Cys	Pro	Ser	290	295	300	
Gly	Lys	Lys	Ala	Arg	Glu	Ile	Asp	Glu	Ser	Leu	Ile	Phe	Tyr	Lys	Lys	305	310	315	320
Trp	Glu	Leu	Glu	Ala	Cys	Val	Asp	Ala	Ala	Leu	Leu	Ala	Thr	Gln	Met	325	330	335	
Asp	Arg	Val	Asn	Ala	Ile	Pro	Phe	Thr	Tyr	Glu	Gln	Leu	Asp	Val	Leu	340	345	350	
Lys	His	Lys	Leu	Asp	Glu	Leu	Tyr	Pro	Gln	Gly	Tyr	Pro	Glu	Ser	Val	355	360	365	
Ile	Gln	His	Leu	Gly	Tyr	Leu	Phe	Leu	Lys	Met	Ser	Pro	Glu	Asp	Ile	370	375	380	
Arg	Lys	Trp	Asn	Val	Thr	Ser	Leu	Glu	Thr	Leu	Lys	Ala	Leu	Leu	Glu	385	390	395	400
Val	Asn	Lys	Gly	His	Glu	Met	Ser	Pro	Gln	Val	Ala	Thr	Leu	Ile	Asp	405	410	415	
Arg	Phe	Val	Lys	Gly	Arg	Gly	Gln	Leu	Asp	Lys	Asp	Thr	Leu	Asp	Thr	420	425	430	
Leu	Thr	Ala	Phe	Tyr	Pro	Gly	Tyr	Leu	Cys	Ser	Leu	Ser	Pro	Glu	Glu	435	440	445	
Leu	Ser	Ser	Val	Pro	Pro	Ser	Ser	Ile	Trp	Ala	Val	Arg	Pro	Gln	Asp	450	455	460	

Leu Asp Thr Cys Asp Pro Arg Gln Leu Asp Val Leu Tyr Pro Lys Ala  
 465 470 475 480  
 Arg Leu Ala Phe Gln Asn Met Asn Gly Ser Glu Tyr Phe Val Lys Ile  
 485 490 495  
 Gln Ser Phe Leu Gly Gly Ala Pro Thr Glu Asp Leu Lys Ala Leu Ser  
 500 505 510  
 Gln Gln Asn Val Ser Met Asp Leu Ala Thr Phe Met Lys Leu Arg Thr  
 515 520 525  
 Asp Ala Val Leu Pro Leu Thr Val Ala Glu Val Gln Lys Leu Leu Gly  
 530 535 540  
 Pro His Val Glu Gly Leu Lys Ala Glu Glu Arg His Arg Pro Val Arg  
 545 550 555 560  
 Asp Trp Ile Leu Arg Gln Arg Gln Asp Asp Leu Asp Thr Leu Gly Leu  
 565 570 575  
 Gly Leu Gln Gly Gly Ile Pro Asn Gly Tyr Leu Val Leu Asp Leu Ser  
 580 585 590  
 Val Gln Gly Gly Arg Gly Gly Gln Ala Arg Ala Gly Gly Arg Ala Gly  
 595 600 605  
 Gly Val Glu Val Gly Ala Leu Ser His Pro Ser Leu Cys Arg Gly Pro  
 610 615 620  
 Leu Gly Asp Ala Leu Pro Pro Arg Thr Trp Thr Cys Ser His Arg Pro  
 625 630 635 640  
 Gly Thr Ala Pro Ser Leu His Pro Gly Leu Arg Ala Pro Leu Pro Cys  
 645 650 655  
 Trp Pro Gln Pro Cys Trp Gly Ser Pro Pro Gly Gln Glu Gln Ala Arg  
 660 665 670  
 Val Ile Pro Val Pro Pro Gln Glu Asn Ser Arg Ser Val Asn Gly Asn  
 675 680 685  
 Met Pro Pro Ala Asp Thr  
 690

&lt;210&gt; 200

&lt;211&gt; 2081

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 200

ggccggccac tcccgtctgc tgtgacgcgc ggacagagag ctaccggtgg acccacggtg 60  
 cctccctccc tgggatctac acagaccatg gccttgccaa cggctcgacc cctgttgggg 120  
 tctgtggga ccccgccct cggcagcctc ctgttctctgc tcttcagcct cggatgggtg 180  
 cagccctcga ggaccctggc tggagagaca gggcaggagg ctgcacccct ggacggagtc 240  
 ctggccaacc cacctaacat ttccagcctc tcccctcgcc aactccttgg cttcccgtgt 300  
 gcggaggtgt ccggcctgag cacggagcgt gtccgggagc tggctgtggc cttggcacag 360  
 aagaatgtca agctctcaac agagcagctg cgctgtctgg ctacccggct ctctgagccc 420  
 cccgaggacc tggacgcct cccattggag ctgctgctat tcctcaacc agatgcgttc 480  
 tcggggcccc aggcctgcac ccgtttcttc tccgcacat cgaaggccaa tgtggacctg 540  
 ctcccagggg gggctcccga gcgacagcgg ctgctgcctg cggtcttggc ctgctgggtg 600  
 gtgcgggggt ctctgctgag cgaggctgat gtgcgggctc tgggaggcct ggcttgcgac 660  
 ctgcttgggc gctttgtggc cgagtgcggc gaagtgtctc taccocggct ggtgagctgc 720  
 ccgggacccc tggaccagga ccagcaggag gcagccaggg cggctctgca gggcggggga 780  
 cccccctacg gcccccgct gacatggtct gtctccacga tggacgtctc gcggggcctg 840  
 ctgcccgctg tgggccagcc catcatccgc agcatcccgc agggcatcgt ggccgcgtgg 900  
 cggcaacgct cctctcggga cccatcctgg cggcagcctg aacggaccat cctccggccg 960  
 cggttccggc gggaagtggg gaagacagcc tgtccttcag gcaagaagge ccgcgagata 1020  
 gatgagagcc tcatcttcta caagaagtgg gacttggaag cctgcgtgga tgcggccctg 1080  
 ctggccaccc agatggaccg cgtgaacgcc atcccctca cctacgagca gctggacgtc 1140  
 ctaaagcata aactgatga gctctaccca caaggttacc ccgagtctgt gatccagcac 1200

```

ctgggctacc tcttcctcaa gatgagccct gaggacattc gcaagtggaa tgtgacgtcc 1260
ctggagaccc tgaaggcttt gcttgaagtc aacaaagggc acgaaatgag tcctcaggtg 1320
gccaccctga tcgaccgctt tgtgaagggg agggggccagc tagacaaaga caccctagac 1380
accctgaccg ccttctaccc tgggtacctg tgctccctca gccccgagga gctgagctcc 1440
gtgcccccca gcagcatctg ggcggtcagg ccccgaggac tggacacgtg tgacccaagg 1500
cagctggacg tcctctatcc caaggcccgc cttgctttcc agaacatgaa cgggtccgaa 1560
tacttcgtga agatccagtc cttcctgggt ggggccccca cggaggattt gaaggcgctc 1620
agtcagcaga atgtgagcat ggacttgccc acgttcatga agctgcggac ggatgcgggtg 1680
ctgccgttga ctgtggctga ggtgcagaaa cttctgggac cccacgtgga gggcctgaag 1740
gcgaggagac ggcaccgccc ggtgcgggac tggatcctac ggcagcggca ggacgacctg 1800
gacacgctgg ggctggggct acagggcggc atccccaacg gctacctggt cctagacctc 1860
agcgtgcaag gacctggacc tgttctcacc gtcctggcac tgctcctagc ctccaccctg 1920
gcctgagggc cccactccct tgctggcccc agccctgctg gggatccccg cctggccagg 1980
agcaggcacg ggtgatcccc gttccacccc aagagaactc gcgctcagta aacgggaaca 2040
tgccccctgc agacacgtaa aaaaaaaaaa aaaaaaaaaa a 2081

```

&lt;210&gt; 201

&lt;211&gt; 612

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 201

```

Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro
  1          5          10          15
Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln
  20          25          30
Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
  35          40          45
Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
  50          55          60
Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
  65          70          75          80
Arg Val Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu
  85          90          95
Ser Thr Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro
  100         105         110
Glu Asp Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro
  115         120         125
Asp Ala Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile
  130         135         140
Thr Lys Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln
  145         150         155         160
Arg Leu Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu
  165         170         175
Leu Ser Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu
  180         185         190
Pro Gly Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu
  195         200         205
Val Ser Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg
  210         215         220
Ala Ala Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp
  225         230         235         240
Ser Val Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly
  245         250         255
Gln Pro Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg
  260         265         270
Gln Arg Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile
  275         280         285

```



207

Leu Arg Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser  
 290 295 300  
 Gly Lys Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys  
 305 310 315 320  
 Trp Glu Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met  
 325 330 335  
 Asp Arg Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu  
 340 345 350  
 Lys His Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val  
 355 360 365  
 Ile Gln His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile  
 370 375 380  
 Arg Lys Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu  
 385 390 395 400  
 Val Asn Lys Gly His Glu Met Ser Pro Gln Val Ala Thr Leu Ile Asp  
 405 410 415  
 Arg Phe Val Lys Gly Arg Gly Gln Leu Asp Lys Asp Thr Leu Asp Thr  
 420 425 430  
 Leu Thr Ala Phe Tyr Pro Gly Tyr Leu Cys Ser Leu Ser Pro Glu Glu  
 435 440 445  
 Leu Ser Ser Val Pro Pro Ser Ser Ile Trp Ala Val Arg Pro Gln Asp  
 450 455 460  
 Leu Asp Thr Cys Asp Pro Arg Gln Leu Asp Val Leu Tyr Pro Lys Ala  
 465 470 475 480  
 Arg Leu Ala Phe Gln Asn Met Asn Gly Ser Glu Tyr Phe Val Lys Ile  
 485 490 495  
 Gln Ser Phe Leu Gly Gly Ala Pro Thr Glu Asp Leu Lys Ala Leu Ser  
 500 505 510  
 Gln Gln Asn Val Ser Met Asp Leu Ala Thr Phe Met Lys Leu Arg Thr  
 515 520 525  
 Asp Ala Val Leu Pro Leu Thr Val Ala Glu Val Gln Lys Leu Leu Gly  
 530 535 540  
 Pro His Val Glu Gly Leu Lys Ala Glu Glu Arg His Arg Pro Val Arg  
 545 550 555 560  
 Asp Trp Ile Leu Arg Gln Arg Gln Asp Asp Leu Asp Thr Leu Gly Leu  
 565 570 575  
 Gly Leu Gln Gly Gly Ile Pro Asn Gly Tyr Leu Val Leu Asp Leu Ser  
 580 585 590  
 Val Gln Gly Pro Gly Pro Val Leu Thr Val Leu Ala Leu Leu Leu Ala  
 595 600 605  
 Ser Thr Leu Ala  
 610

&lt;210&gt; 202

&lt;211&gt; 1195

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 202

gtggagaaga cagcctgtcc ttcaggcaag aaggcccgcg agatagacga gagcctcatc 60  
 ttctacaaga agtgggagct ggaagcctgc gtggatgcgg ccctgctggc caccagatg 120  
 gaccgcgtga acgccatccc cttcacctac gagcagctgg acgtcctaaa gcataaactg 180  
 gatgagctct acccacaagg ttaccccgag tctgtgatcc agcacctggg ctacctcttc 240  
 ctcaagatga gccctgagga cattcgcaag tggaatgtga cgtccctgga gaccctgaag 300  
 gctttgcttg aagtcaacaa agggcacgaa atgagtcctc aggtggccac cctgatcgac 360  
 cgctttgtga agggaagggg ccagctagac aaagacaccc tagacaccct gaccgccttc 420  
 taccctgggt acctgtgtc cctcagcccc gaggagctga gctccgtgcc cccagcagc 480

```

atctgggagg tcaggcccca ggacctggac acgtgtgacc caaggcagct ggacgtcctc 540
tatcccaagg cccgccttgc tttccagaac atgaacgggt ccgaatactt cgtgaagatc 600
cagtccttcc tgggtggggc cccacaggag gatttgaagg cgctcagtca gcagaatgtg 660
agcatggact tggccacgtt catgaagctg cggacggatg cgggtgctgcc gttgactgtg 720
gctgaggtgc agaaacttct gggacccac gtggaggggc tgaaggcgga ggagcggcac 780
cgcccgggtgc gggactggat cctacggcag cggcaggacg acctggacac gctggggctg 840
gggctacagg gcggcatccc caacggctac ctggtcctag acctcagcgt gcaagggtggg 900
cgggggcggc aggccagggc tgggggcaga gctggggggc tggaggtggg cgctctgagt 960
caccctctc tctgtagagg ccctctcggg gacgccctgc ctctaggac ctggacctgt 1020
tctcaccgtc ctggcactgc tcctagcctc caccctggcc tgaggggccc actcccttgc 1080
tggccccagc cctgctgggg atccccgcct ggccaggagc aggcacgggt gatccccgtt 1140
ccaccccaag agaactcgcg ctacagtaaac ggaacatgc cccctgcaga cacgt 1195

```

&lt;210&gt; 203

&lt;211&gt; 398

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 203

```

Val Glu Lys Thr Ala Cys Pro Ser Gly Lys Lys Ala Arg Glu Ile Asp
 1          5          10          15
Glu Ser Leu Ile Phe Tyr Lys Lys Trp Glu Leu Glu Ala Cys Val Asp
          20          25          30
Ala Ala Leu Leu Ala Thr Gln Met Asp Arg Val Asn Ala Ile Pro Phe
          35          40          45
Thr Tyr Glu Gln Leu Asp Val Leu Lys His Lys Leu Asp Glu Leu Tyr
          50          55          60
Pro Gln Gly Tyr Pro Glu Ser Val Ile Gln His Leu Gly Tyr Leu Phe
          65          70          75          80
Leu Lys Met Ser Pro Glu Asp Ile Arg Lys Trp Asn Val Thr Ser Leu
          85          90          95
Glu Thr Leu Lys Ala Leu Leu Glu Val Asn Lys Gly His Glu Met Ser
          100          105          110
Pro Gln Val Ala Thr Leu Ile Asp Arg Phe Val Lys Gly Arg Gly Gln
          115          120          125
Leu Asp Lys Asp Thr Leu Asp Thr Leu Thr Ala Phe Tyr Pro Gly Tyr
          130          135          140
Leu Cys Ser Leu Ser Pro Glu Glu Leu Ser Ser Val Pro Pro Ser Ser
          145          150          155          160
Ile Trp Ala Val Arg Pro Gln Asp Leu Asp Thr Cys Asp Pro Arg Gln
          165          170          175
Leu Asp Val Leu Tyr Pro Lys Ala Arg Leu Ala Phe Gln Asn Met Asn
          180          185          190
Gly Ser Glu Tyr Phe Val Lys Ile Gln Ser Phe Leu Gly Gly Ala Pro
          195          200          205
Thr Glu Asp Leu Lys Ala Leu Ser Gln Gln Asn Val Ser Met Asp Leu
          210          215          220
Ala Thr Phe Met Lys Leu Arg Thr Asp Ala Val Leu Pro Leu Thr Val
          225          230          235          240
Ala Glu Val Gln Lys Leu Leu Gly Pro His Val Glu Gly Leu Lys Ala
          245          250          255
Glu Glu Arg His Arg Pro Val Arg Asp Trp Ile Leu Arg Gln Arg Gln
          260          265          270
Asp Asp Leu Asp Thr Leu Gly Leu Gly Leu Gln Gly Gly Ile Pro Asn
          275          280          285
Gly Tyr Leu Val Leu Asp Leu Ser Val Gln Gly Gly Arg Gly Gly Gln
          290          295          300
Ala Arg Ala Gly Gly Arg Ala Gly Gly Val Glu Val Gly Ala Leu Ser

```

209

305		310		315		320
His Pro Ser Leu Cys Arg Gly Pro Leu Gly Asp Ala Leu Pro Pro Arg						
	325		330		335	
Thr Trp Thr Cys Ser His Arg Pro Gly Thr Ala Pro Ser Leu His Pro						
	340		345		350	
Gly Leu Arg Ala Pro Leu Pro Cys Trp Pro Gln Pro Cys Trp Gly Ser						
	355		360		365	
Pro Pro Gly Gln Glu Gln Ala Arg Val Ile Pro Val Pro Pro Gln Glu						
	370		375		380	
Asn Ser Arg Ser Val Asn Gly Asn Met Pro Pro Ala Asp Thr						
385	390		395			

&lt;210&gt; 204

&lt;211&gt; 2085

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 204

tgccactcc	cgtctgctgt	gacgcgcgga	cagagagcta	ccggtggacc	cacggtgcct	60
ccctccctgg	gatctacaca	gaccatggcc	ttgccaaagg	ctcgaccctt	gttgggtgcc	120
tgtgggaccc	ccgccctcgg	cagcctcctg	ttcctgctct	tcagcctcgg	atgggtgcag	180
ccctcgagga	ccctggctgg	agagacaggg	caggaggctg	cacccctgga	cggagtcctg	240
gccaaccac	ctaacatttc	cagcctctcc	cctcgccaac	tccttggctt	cccgtgtgcg	300
gaggtgtccg	gcctgagcac	ggagcgtgtc	cgggagctgg	ctgtggcctt	ggcacagaag	360
aatgtcaagc	tctcaacaga	gcagctgcgc	tgtctggctc	accggtcttc	tgagccccc	420
gaggacctgg	acgccctccc	attggacctg	ctgctattcc	tcaaccacga	tgcgttctcg	480
gggccccagg	cctgcacccg	ttcttctctc	cgcctcacga	aggccaatgt	ggacctgtct	540
ccgagggggg	ctcccagcgg	acagcggctg	ctgcctgcgg	ctctggcctg	ctgggggtgtg	600
cgggggtctc	tgctgagcga	ggctgatgtg	cgggctctgg	gaggcctggc	ttgcgacctg	660
cctgggcgct	ttgtggccga	gtcggccgaa	gtgctgtctc	cccggctggg	gagctgcccc	720
ggacccctgg	accaggacca	gcaggaggca	gccaggcgcg	ctctgcaggg	cgggggaccc	780
ccctacggcc	ccccgtcgac	atgggtctgtc	tccacgatgg	acgctctgcg	gggcctgctg	840
cccgtgctgg	gccagcccat	catccgcagc	atcccgcagg	gcctcgtggc	cgcgtggcgg	900
caacgctcct	ctcgggaccc	atcctggcgg	cagcctgaac	ggaccatcct	ccggccgcgg	960
ttccggcggg	aagtggagaa	gacagcctgt	ccttcaggca	agaaggcccc	cgagatagac	1020
gagagcctca	tcttctacaa	gaagtgggag	ctggaagcct	gcgtggatgc	ggccctgctg	1080
gccaccacga	tggaccgcgt	gaacgccatc	cccttcacct	acgagcagct	ggacgtccta	1140
aagcataaac	tggatgagct	ctaccacaaa	ggttaccccc	agtctgtgat	ccagcacctg	1200
ggctacctct	tctcaagat	gagccctgag	gacattcgca	agtggaatgt	gacgtccctg	1260
gagacctga	aggctttgct	tgaagtcaac	aaagggcacg	aaatgagtcc	tcaggtggcc	1320
accctgatcg	accgctttgt	gaagggaagg	ggccagctag	acaaagacac	cctagacacc	1380
ctgaccgcct	tctaccctgg	gtacctgtgc	tccctcagcc	ccgaggagct	gagctccgtg	1440
ccccccagca	gcactctggc	ggtcaggccc	caggacctgg	acacgtgtga	cccaaggcag	1500
ctggacgtcc	tctatcccaa	ggcccgcctt	gctttccaga	acatgaacgg	gtccgaatac	1560
ttcgtgaaga	tccagtcctt	cctgggtggg	gccccacgg	aggatttgaa	ggcgctcagt	1620
cagcagaatg	tgagcatgga	cttggccacg	ttcatgaagc	tgcgagcggg	tgcggtgctg	1680
ccgttgactg	tggctgaggt	gcagaaactt	ctgggaaccc	acgtggaggg	cctgaaggcg	1740
gaggagcggc	accgcccggg	gcgggactgg	atcctacggc	agcggcagga	cgacctggac	1800
acgctggggc	tggggctaca	ggcgggcatc	cccaacggct	acctggctct	agacctcagc	1860
gtgcaagagg	ccctctcggg	gacgccctgc	ctcctaggac	ctggacctgt	tctcaccgtc	1920
ctggcactgc	tcttagcctc	caccctggcc	tgaggggccc	actcccttgc	tgcccccagc	1980
cctgctgggg	atccccgcct	ggccaggagc	aggcacgggt	gatccccgtt	ccaccccaag	2040
agaactcgcg	ctcagtaaac	gggaacatgc	cccctgcaga	cacgt		2085

&lt;210&gt; 205

&lt;211&gt; 622

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 205

```

Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro
 1      5      10      15
Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln
      20      25      30
Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
      35      40      45
Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
      50      55      60
Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
      65      70      75      80
Arg Val Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu
      85      90      95
Ser Thr Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro
      100      105      110
Glu Asp Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro
      115      120      125
Asp Ala Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile
      130      135      140
Thr Lys Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln
      145      150      155      160
Arg Leu Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu
      165      170      175
Leu Ser Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu
      180      185      190
Pro Gly Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu
      195      200      205
Val Ser Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg
      210      215      220
Ala Ala Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp
      225      230      235      240
Ser Val Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly
      245      250      255
Gln Pro Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg
      260      265      270
Gln Arg Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile
      275      280      285
Leu Arg Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser
      290      295      300
Gly Lys Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys
      305      310      315      320
Trp Glu Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met
      325      330      335
Asp Arg Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu
      340      345      350
Lys His Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val
      355      360      365
Ile Gln His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile
      370      375      380
Arg Lys Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu
      385      390      395      400
Val Asn Lys Gly His Glu Met Ser Pro Gln Val Ala Thr Leu Ile Asp
      405      410      415
Arg Phe Val Lys Gly Arg Gly Gln Leu Asp Lys Asp Thr Leu Asp Thr
      420      425      430
Leu Thr Ala Phe Tyr Pro Gly Tyr Leu Cys Ser Leu Ser Pro Glu Glu

```

211

435	440	445
Leu Ser Ser Val Pro Pro Ser Ser Ile Trp Ala Val Arg Pro Gln Asp		
450	455	460
Leu Asp Thr Cys Asp Pro Arg Gln Leu Asp Val Leu Tyr Pro Lys Ala		
465	470	475
Arg Leu Ala Phe Gln Asn Met Asn Gly Ser Glu Tyr Phe Val Lys Ile		
	485	490
Gln Ser Phe Leu Gly Gly Ala Pro Thr Glu Asp Leu Lys Ala Leu Ser		
	500	505
Gln Gln Asn Val Ser Met Asp Leu Ala Thr Phe Met Lys Leu Arg Thr		
	515	520
Asp Ala Val Leu Pro Leu Thr Val Ala Glu Val Gln Lys Leu Leu Gly		
	530	535
Pro His Val Glu Gly Leu Lys Ala Glu Glu Arg His Arg Pro Val Arg		
545	550	555
Asp Trp Ile Leu Arg Gln Arg Gln Asp Asp Leu Asp Thr Leu Gly Leu		
	565	570
Gly Leu Gln Gly Gly Ile Pro Asn Gly Tyr Leu Val Leu Asp Leu Ser		
	580	585
Val Gln Glu Ala Leu Ser Gly Thr Pro Cys Leu Leu Gly Pro Gly Pro		
	595	600
Val Leu Thr Val Leu Ala Leu Leu Leu Ala Ser Thr Leu Ala		
610	615	620

&lt;210&gt; 206

&lt;211&gt; 2111

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 206

```

ggcgggccac tcccgctctgc tgtgacgcgc ggacagagag ctaccggtgg acccacggtg 60
cctccctccc tgggatctac acagaccatg gccttgccaa cggctcgacc cctgttgggg 120
tcctgtggga ccccgccct cggcagcctc ctgttcctgc tcttcagcct cggatgggtg 180
cagccctcga ggacctggc tggagagaca gggcaggagg ctgcacccct ggacggagtc 240
ctggccaacc cacctaaccat ttccagcctc tccctcgcc aactccttgg cttcccgtgt 300
gcgagggtgt ccggcctgag cacggagcgt gtccgggagc tggctgtggc cttggcacag 360
aagaatgtca agctctcaac agagcagctg cgctgtctgg ctaccggct ctctgagccc 420
cccgaggacc tggacgcccct cccattggac ctgctgctat tcctcaacc agatgcgttc 480
tcggggcccc aggcctgcac ccgtttcttc tcccgcatca cgaaggccaa tgtggacctg 540
ctcccgaggg gggtcccgga gcgacagcgg ctgctgctg cggtcttggc ctgctggggg 600
gtgcgggggt ctctgctgag cgaggctgat gtgcgggctc tgggaggcct ggcttgcgac 660
ctgcctgggc gctttgtggc cgagtcggcc gaagtgtgc taccocggct ggtgagctgc 720
ccgggacccc tggaccagga ccagcaggag gcagccaggg cggctctgca gggcggggga 780
ccccctacg gcccccgctc gacatgggtct gtctccacga tggacgtctt gcggggcctg 840
ctgcccgtgc tgggccagcc catcatccgc agcatcccgc agggcatcgt ggccgcgtgg 900
cggcaacgct cctctcggga cccatcctgg cggcagcctg aacggaccat cctccggccg 960
cggttcggc ggggaagtga gaagacagcc tgtccttcag gcaagaaggc ccgcgagata 1020
gacgagagcc tcatcttcta caagaagtgg gagctggaag cctgcgtgga tgcggccctg 1080
ctggccaccc agatggaccg cgtgaacgcc atccccttca cctacgagca gctggacgtc 1140
ctaaagcata aactggatga gctctacca caaggttacc ccgagtctgt gatccagcac 1200
ctgggctacc tcttctcaa gatgagccct gaggacattc gcaagtggaa tgtgacgtcc 1260
ctggagaccc tgaaggcttt gcttgaagtc aacaaagggc acgaaatgag tcctcaggtg 1320
gccacctga tcgaccgctt tgtgaaggga aggggcccagc tagacaaaga caccctagac 1380
acctgaccg ccttctaccc tgggtacctg tgctccctca gcccggagga gctgagctcc 1440
cagctccccc gcagcatctg ggcggtcagg ccccgagacc tggacacgtg tgaccaagg 1500
ctgctggacc tccctatcc caaggcccgc cttgctttcc agaacatgaa cgggtccgaa 1560
tacttcgtga agatccagtc cttcctgggt ggggccccca cggaggattt gaaggcgctc 1620

```

212

```

agtcagcaga atgtgagcat ggacttggcc acgttcatga agctgcggac ggatgcggtg 1680
ctgccgttga ctgtggctga ggtgcagaaa cttctgggac cccacgtgga gggcctgaag 1740
gcggaggagc ggacccggcc ggtgcgggac tggatcctac ggacgcggca ggacgacctg 1800
gacacgctgg ggctggggct acaggggcgc atccccaacg gctacctggt cctagacctc 1860
agcgtgcaag aggccctctc ggggacgccc tgccctctag gacctggacc tgttctcacc 1920
gtcctggcac tgctcctagc ctccaccctg gcctgagggc cccactccct tgctggcccc 1980
agccctgctg gggatccccg cctggccagg agcaggcacg ggtgatcccc gttccacccc 2040
aagagaactc gcgctcagta aacgggaaca tgccccctgc agacacgtaa aaaaaaaaaa 2100
aaaaaaaaaa a 2111

```

&lt;210&gt; 207

&lt;211&gt; 2107

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

```

tgcccgccca ctcccgctct ctgtgacgcg cggacagaga gctaccggtg gaccacggt 60
gcctccctcc ctgggatcta cacagaccat ggccctgcaa cggctcgacc cctgttggtc 120
ctgtggggac cgccctggca gcctcctgtt cctgctcttc agcctcggtt ggggtgatcc 180
cgcgaggacc ctggctggag agacagggac ggagctgtgc ccctggggg gagtctgtac 240
aaccceccat aacatttcca gcctctcccc tcgccaactc cttggcttcc cgtgtgcgga 300
ggtgtccggc ctgagcacgg agcgtgtccg ggagctggct gtggccttgg cacagaagaa 360
tgtcaagctc tcaacagagc agctgcgctg tctggctcac cggctctctg agccccccga 420
ggacctggac gccctcccat tggacctgct gctattcttc aaccagatg cgttctcggg 480
gccccaggcc tgcacccggt tcttctcccc catcacgaag gccaatgtgg acctgctccc 540
gaggggggct cccgagcgac agcggctgct gcctgcggct ctggcctgct ggggtgtgcg 600
ggggtctctg ctgagcgagg ctgatgtgcg ggctctggga ggctgtggtt ggcacctgcc 660
tgggcgcttt gtggccgagt cggccgaagt gctgctaccc cggctggtga gctgcccggg 720
accctggac caggaccagc agggagcagc cagggcggtc ctgcaggcg ggggacccc 780
ctacggcccc ccgtcgacat ggtctgtctc caagatggac gctctgcggg gcctgctgcc 840
cgtgctgggc cagcccatca tccgcagcat cccgcagggc atcgtggccg cgtggcggca 900
acgtcctctc cgggacccat cctggcgga gcctgaacgg accatcctcc ggccgcggtt 960
ccggcgggaa gtggagaaga cagcctgtcc ttcaggcaag aaggcccgcg agatagacga 1020
gagcctcatc ttctacaaga agtgggagct ggaagcctgc gtggatgcgg ccctgctggc 1080
caccagatg gaccgcgtga acgccatccc ctacacctac gagcagctgg acgtcctaaa 1140
gcataaactg gatgagctct accacaagg ttaccccgag tctgtgatcc agcacctggg 1200
ctacctcttc ctcaagatga gccctgagga cattcgcaag tggaaatgtga cgtccctgga 1260
gacctgaag gctttgcttg aagtcgacaa agggcacgaa atgagtcctc aggtcctcg 1320
gcggcccttc ccacagggtg ccaccctgat cgaccgcttt gtgaaggga ggggccagct 1380
agacaaagac accctagaca ccctgaccgc cttctacctt gggtaacctg gctccctcag 1440
ccccgaggag ctgagctccg tgccccccag cagcatctgg gcggtcaggc ccaggacct 1500
ggacacgtgt gacccaaggc agctggacgt cctctatccc aaggcccgcc ttgctttcca 1560
gaacatgaac gggctccgaat acttcgtgaa gatccagtc ttcttgggtg gggcccccac 1620
ggaggatttg aaggcgctca gtcagcagaa tgtgagcatg gacttggcca cgttcatgaa 1680
gctgcggacg gatgcggtgc tgccgttgac tgtggctgag gtgcagaaac ttctgggacc 1740
ccacgtggag ggctgaagg cggaggagcg gcaccgccc gtgcgggact ggatcctacg 1800
gcagcggcag gacgacctgg acacgctggg gctggggcta cagggcggca tccccaacgg 1860
ctacctggtc ctagacctca gcgtgcaaga gacctctcgg gggacgccc gcctcctagg 1920
acctggacct gttctcacgg tcttggcact gctcctagcc tccaccttgg cctgagggcc 1980
ccactccctt gctggcccca gccctgctgg ggatccccgc ctggccagga gcaggcacgg 2040
gtgatccccg ttccaccca agagaactcg cgctcagtaa acgggaacat gccccctgca 2100
gacacgt 2107

```

&lt;210&gt; 208

&lt;211&gt; 628

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 208

```

Met Ala Leu Gln Arg Leu Asp Pro Cys Trp Ser Cys Gly Asp Arg Pro
 1           5           10           15
Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val His Pro Ala
          20           25           30
Arg Thr Leu Ala Gly Glu Thr Gly Thr Glu Ser Ala Pro Leu Gly Gly
          35           40           45
Val Leu Thr Thr Pro His Asn Ile Ser Ser Leu Ser Pro Arg Gln Leu
          50           55           60
Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu Arg Val
65           70           75           80
Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu Ser Thr
          85           90           95
Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro Glu Asp
          100          105          110
Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro Asp Ala
          115          120          125
Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile Thr Lys
          130          135          140
Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln Arg Leu
145          150          155          160
Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu Leu Ser
          165          170          175
Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu Pro Gly
          180          185          190
Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu Val Ser
          195          200          205
Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg Ala Ala
          210          215          220
Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp Ser Val
225          230          235          240
Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly Gln Pro
          245          250          255
Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg Gln Arg
          260          265          270
Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile Leu Arg
          275          280          285
Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser Gly Lys
          290          295          300
Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys Trp Glu
305          310          315          320
Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met Asp Arg
          325          330          335
Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu Lys His
          340          345          350
Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val Ile Gln
          355          360          365
His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile Arg Lys
          370          375          380
Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu Val Asp
385          390          395          400
Lys Gly His Glu Met Ser Pro Gln Ala Pro Arg Arg Pro Leu Pro Gln
          405          410          415
Val Ala Thr Leu Ile Asp Arg Phe Val Lys Gly Arg Gly Gln Leu Asp
          420          425          430
Lys Asp Thr Leu Asp Thr Leu Thr Ala Phe Tyr Pro Gly Tyr Leu Cys
          435          440          445
Ser Leu Ser Pro Glu Glu Leu Ser Ser Val Pro Pro Ser Ser Ile Trp

```

214

450	455	460
Ala Val Arg Pro Gln Asp	Leu Asp Thr Cys Asp	Pro Arg Gln Leu Asp
465	470	475
Val Leu Tyr Pro Lys Ala	Arg Leu Ala Phe Gln	Asn Met Asn Gly Ser
485	490	495
Glu Tyr Phe Val Lys Ile	Gln Ser Phe Leu Gly	Gly Ala Pro Thr Glu
500	505	510
Asp Leu Lys Ala Leu Ser	Gln Gln Asn Val Ser	Met Asp Leu Ala Thr
515	520	525
Phe Met Lys Leu Arg Thr	Asp Ala Val Leu Pro	Leu Thr Val Ala Glu
530	535	540
Val Gln Lys Leu Leu Gly	Pro His Val Glu Gly	Leu Lys Ala Glu Glu
545	550	555
Arg His Arg Pro Val Arg	Asp Trp Ile Leu Arg	Gln Arg Gln Asp Asp
565	570	575
Leu Asp Thr Leu Gly Leu	Gly Leu Gln Gly Gly	Ile Pro Asn Gly Tyr
580	585	590
Leu Val Leu Asp Leu Ser	Val Gln Glu Thr Leu	Ser Gly Thr Pro Cys
595	600	605
Leu Leu Gly Pro Gly Pro	Val Leu Thr Val Leu	Ala Leu Leu Leu Ala
610	615	620
Ser Thr Leu Ala		
625		

&lt;210&gt; 209

&lt;211&gt; 2316

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 209

```

ctatagggag tgcacccacg cgtccgcccg gcgttagggg taaagctccc tacccaactg 60
cgcagaaggc ctcagaggcc tgggggctgg gcttcccctt tcacatcgcc ctttagaggc 120
ccacgtgtgg gcattggccs gcgatctgaa aggggctgtc ctgttcctca tgggcgctgc 180
cagcgccacg cactcctctt tctgcctggc cgccactcc cgtctgctgt gacgcgcgga 240
cagagagcta ccggtggacc caccgtgcct ccctccctgg gatctacaca gaccatggcc 300
ttgccaacgg ctgcaccctt gttggggctc tgtgggaccc ccgcctcgg cagcctcctg 360
ttcctgctct tcagcctcgg atgggtgcag ccctcgagga ccctggctgg agagacaggg 420
caggaggctg cgcctctgga cggagtcctg gccaacccac ctaacatttc cagcctctcc 480
cctcgccaac tccttggctt cccgtgtgcg gaggtgtccg gcctgagcac ggagcgtgtc 540
cgggagctgg ctgtggcctt ggcacagaag aatgtcaagc tctcaacaga gcagctgcgc 600
tgtctggctc accggtctct tgagccccc gaggacctgg acgcccctcc attggacctg 660
ctgtatttcc tyaacccaga tgcgttctcg gggcccagg cctgcacccg tttcttctcc 720
cgcattcacga aggccaatgt ggacctgtc ccgagggggg ctcccagagc acagcggctg 780
ctgcttgcgg ctctggcctg ctgggggtgt cgggggtctc tgctgagcga ggctgatgtg 840
cgggctctgg gaggcctggc ttgcgacctg cctgggcgct ttgtggccga gtcggccgaa 900
gtgtgtctac cccggtcggg gagctgcccc ggaccctgg accaggacca gcaggaggca 960
gccaggggcg ctctgcaggg cgggggaccc ccctacggcc ccccgctcac atggtctgtc 1020
tccacgatgg acgctctgcg gggcctgtct cccgtgtctg gccagcccat catccgcagc 1080
atcccgcagg gcattcgtgg cgcgtggcgg caacgctcct ctccgggaccc atcctggcgg 1140
cagcctgaac ggaccatcct ccggccgcgg ttccggcggg aagtggagaa gacagcctgt 1200
ccttcaggca agaaggcccg cgagatagac gagagcctca tcttctacaa gaagtgggag 1260
ctggaagcct gcgtggatgc ggccctgtct gccaccaga tggaccgctg gaacgccatc 1320
cccttcacct acgagcagct ggacgtccta aagcataaac tggatgagct ctaccacaaa 1380
ggttaccocg agtctgtgat ccagcacctg ggtacctct tcctcaagat gagccctgag 1440
gacattcgca agtggaaatgt gacgtccctg gagaccctga aggttttct tgaagtcgac 1500
aaagggcacg aaatgagtc ttaggtcctc cggcgggccc tcccacaggt ggccaccctg 1560
atcgaccgct ttgtgaaggg aaggggccag ctagacaaag acaccctaga caccctgacc 1620

```



215

```

gccttctacc ctgggtacct gtgctccctc agccccgagg agctgagctc cgtgcccccc 1680
agcagcatct gggcggtcag gcccaggac ctggacacgt gtgaccaag gcagctggac 1740
gtcctctatc ccaaggcccg ccttgcttc cagaacatga acgggtccga atacttcgtg 1800
aagatccagt ccttctctggg tggggccccc acggaggatt tgaaggcgct cagtcagcag 1860
aatgtgagca tggacttggc cacgttcacg aagctgcgga cggatgcggt gctgccgttg 1920
actgtggctg aggtgcagaa acttctggga cccacgtgg agggcctgaa ggcggaggag 1980
cggcaccgcc cgggtgcgga ctggatccta cggcagcggc aggacgacct ggacacgtg 2040
gggctggggc tacagggcgg catccccaac ggctacctg tcctagacct cagcgtgcaa 2100
gasrccctct cggggacgcc ctgcctccta ggacctggac ctgttctcac cgtcctggca 2160
ctgctcctag cctccaccct ggctgaggg cccactccc ttgctggccc cagccctgct 2220
ggggatcccc gcctggccag gacgaggcac gggatgaccc cgttccaccc caagagaact 2280
cgcgctcagt aaacgggaac atgcccctg cagaca 2316

```

&lt;210&gt; 210

&lt;211&gt; 630

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(630)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 210

```

Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro
1          5          10          15
Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln
20          25          30
Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
35          40          45
Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
50          55          60
Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
65          70          75          80
Arg Val Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu
85          90          95
Ser Thr Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro
100         105         110
Glu Asp Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro
115         120         125
Asp Ala Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile
130         135         140
Thr Lys Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln
145         150         155         160
Arg Leu Leu Pro Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu
165         170         175
Leu Ser Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu
180         185         190
Pro Gly Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu
195         200         205
Val Ser Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg
210         215         220
Ala Ala Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp
225         230         235         240
Ser Val Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly
245         250         255
Gln Pro Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg
260         265         270

```

216

Gln Arg Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile  
 275 280 285  
 Leu Arg Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser  
 290 295 300  
 Gly Lys Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys  
 305 310 315 320  
 Trp Glu Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met  
 325 330 335  
 Asp Arg Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu  
 340 345 350  
 Lys His Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val  
 355 360 365  
 Ile Gln His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile  
 370 375 380  
 Arg Lys Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu  
 385 390 395 400  
 Val Asp Lys Gly His Glu Met Ser Pro Gln Ala Pro Arg Arg Pro Leu  
 405 410 415  
 Pro Gln Val Ala Thr Leu Ile Asp Arg Phe Val Lys Gly Arg Gly Gln  
 420 425 430  
 Leu Asp Lys Asp Thr Leu Asp Thr Leu Thr Ala Phe Tyr Pro Gly Tyr  
 435 440 445  
 Leu Cys Ser Leu Ser Pro Glu Glu Leu Ser Ser Val Pro Pro Ser Ser  
 450 455 460  
 Ile Trp Ala Val Arg Pro Gln Asp Leu Asp Thr Cys Asp Pro Arg Gln  
 465 470 475 480  
 Leu Asp Val Leu Tyr Pro Lys Ala Arg Leu Ala Phe Gln Asn Met Asn  
 485 490 495  
 Gly Ser Glu Tyr Phe Val Lys Ile Gln Ser Phe Leu Gly Gly Ala Pro  
 500 505 510  
 Thr Glu Asp Leu Lys Ala Leu Ser Gln Gln Asn Val Ser Met Asp Leu  
 515 520 525  
 Ala Thr Phe Met Lys Leu Arg Thr Asp Ala Val Leu Pro Leu Thr Val  
 530 535 540  
 Ala Glu Val Gln Lys Leu Leu Gly Pro His Val Glu Gly Leu Lys Ala  
 545 550 555 560  
 Glu Glu Arg His Arg Pro Val Arg Asp Trp Ile Leu Arg Gln Arg Gln  
 565 570 575  
 Asp Asp Leu Asp Thr Leu Gly Leu Gly Leu Gln Gly Gly Ile Pro Asn  
 580 585 590  
 Gly Tyr Leu Val Leu Asp Leu Ser Val Gln Xaa Xaa Leu Ser Gly Thr  
 595 600 605  
 Pro Cys Leu Leu Gly Pro Gly Pro Val Leu Thr Val Leu Ala Leu Leu  
 610 615 620  
 Leu Ala Ser Thr Leu Ala  
 625 630

&lt;210&gt; 211

&lt;211&gt; 1721

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 211

gaattccctg gctgcttgaa tctgttctgc cccctcccca cccatttcac caccaccatg 60  
 acaccgggca cccagtctcc tttcttctg ctgctgctcc tcacagtgtc tacagttgtt 120  
 acaggttctg gtcattgcaag ctctacccca ggtggagaaa aggagacttc ggctaccag 180  
 agaagttcag tgccagctc tactgagaag aatgctgtga gtatgaccag cagcgtactc 240

```

tccagccaca gccccggttc aggtctctcc accactcagg gacaggatgt cactctggcc 300
ccggccacgg aaccagcttc aggttcagct gccacctggg gacaggatgt cacctcggtc 360
ccagtaccca ggccagccct gggtccacc accccgccag cccacgatgt cacctcagcc 420
ccggacaaca agccagcccc gggtccacc gccccccag cccacggtgt cacctcggcc 480
ccggacacca ggccgcccc gggtccacc gccccccag cccacggtgt cacctcggcc 540
ccggacacca ggccgcccc gggtccacc gcgcccgcag cccacggtgt cacctcggcc 600
ccggacacca ggccgcccc gggtccacc gccccccag cccatggtgt cacctcggcc 660
ccggacaaca ggcccgctt gggtccacc gccctccag tccacaatgt cacctcggcc 720
tcaggctctg catcaggctc agcttctact ctggtgcaca acggcacctc tgccagggct 780
accacaaccc cagccagcaa gagcactcca ttctcaattc ccagccacca ctctgatact 840
cctaccacc ttgccagcca tagcaccaag actgatgcca gtagcactca ccatagcacg 900
gtacctctc tcacctctc caatcacagc acttctccc agttgtctac tggggtctct 960
ttctttttcc tgtcttttca catttcaaac ctccagttta attcctctct ggaagatccc 1020
agcaccgact actaccaaga gctgcagaga gacatttctg aaatgttttt gcagatttat 1080
aaacaagggg gttttctggg cctctccaat attaatgtta ggccaggatc tgtggtggta 1140
caattgactc tggccttcgg agaaggtacc atcaatgtcc acgacgtgga gacacagttc 1200
aatcagtata aaacggaagc agcctctcga tataacctga cgatctcaga cgtcagcggtg 1260
agtgatgtgc catttcttt ctctgccag tctggggctg ggggtgccagg ctggggcatc 1320
gcgctgctgg tgctggtctg tgttctggtt gcgctggcca ttgtctatct cattgccttg 1380
gctgtctgtc agtgccgccc aaagaactac gggcagctgg acatctttcc agcccgggat 1440
acctaccatc ctatgagcga gtacccacc taccacacc atgggcgcta tgtgccccct 1500
agcagtaccg atcgtagccc ctatgagaag gtttctgcag gtaatggtgg cagcagcctc 1560
tcttacacaa acccagcagt ggcagccact tctgccaaact tgtaggggca cgtcgccctc 1620
tgagctgagt ggccagccag tgccattcca ctccactcag ggctctctgg gccagtctc 1680
ctgggagccc ccaccacaac acttcccagg catggaattc c 1721

```

&lt;210&gt; 212

&lt;211&gt; 515

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 212

```

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr
  1          5          10          15
Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
  20          25          30
Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
  35          40          45
Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
  50          55          60
Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
  65          70          75          80
Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
  85          90          95
Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
  100          105          110
Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
  115          120          125
Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
  130          135          140
Arg Pro Pro Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
  145          150          155          160
Ala Pro Asp Thr Arg Pro Pro Pro Gly Ser Thr Ala Pro Ala Ala His
  165          170          175
Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
  180          185          190
Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Asn Arg Pro Ala Leu
  195          200          205

```

218

Ala	Ser	Thr	Ala	Pro	Pro	Val	His	Asn	Val	Thr	Ser	Ala	Ser	Gly	Ser
210						215					220				
Ala	Ser	Gly	Ser	Ala	Ser	Thr	Leu	Val	His	Asn	Gly	Thr	Ser	Ala	Arg
225				230						235					240
Ala	Thr	Thr	Thr	Pro	Ala	Ser	Lys	Ser	Thr	Pro	Phe	Ser	Ile	Pro	Ser
				245						250				255	
His	His	Ser	Asp	Thr	Pro	Thr	Thr	Leu	Ala	Ser	His	Ser	Thr	Lys	Thr
			260					265					270		
Asp	Ala	Ser	Ser	Thr	His	His	Ser	Thr	Val	Pro	Pro	Leu	Thr	Ser	Ser
		275					280					285			
Asn	His	Ser	Thr	Ser	Pro	Gln	Leu	Ser	Thr	Gly	Val	Ser	Phe	Phe	Phe
290						295					300				
Leu	Ser	Phe	His	Ile	Ser	Asn	Leu	Gln	Phe	Asn	Ser	Ser	Leu	Glu	Asp
305				310						315					320
Pro	Ser	Thr	Asp	Tyr	Tyr	Gln	Glu	Leu	Gln	Arg	Asp	Ile	Ser	Glu	Met
			325							330				335	
Phe	Leu	Gln	Ile	Tyr	Lys	Gln	Gly	Gly	Phe	Leu	Gly	Leu	Ser	Asn	Ile
		340					345						350		
Lys	Phe	Arg	Pro	Gly	Ser	Val	Val	Gln	Leu	Thr	Leu	Ala	Phe	Arg	
		355					360					365			
Glu	Gly	Thr	Ile	Asn	Val	His	Asp	Val	Glu	Thr	Gln	Phe	Asn	Gln	Tyr
		370				375					380				
Lys	Thr	Glu	Ala	Ala	Ser	Arg	Tyr	Asn	Leu	Thr	Ile	Ser	Asp	Val	Ser
385					390					395					400
Val	Ser	Asp	Val	Pro	Phe	Pro	Phe	Ser	Ala	Gln	Ser	Gly	Ala	Gly	Val
			405						410					415	
Pro	Gly	Trp	Gly	Ile	Ala	Leu	Leu	Val	Leu	Val	Cys	Val	Leu	Val	Ala
		420					425						430		
Leu	Ala	Ile	Val	Tyr	Leu	Ile	Ala	Leu	Ala	Val	Cys	Gln	Cys	Arg	Arg
		435					440					445			
Lys	Asn	Tyr	Gly	Gln	Leu	Asp	Ile	Phe	Pro	Ala	Arg	Asp	Thr	Tyr	His
		450				455					460				
Pro	Met	Ser	Glu	Tyr	Pro	Thr	Tyr	His	Thr	His	Gly	Arg	Tyr	Val	Pro
465					470					475					480
Pro	Ser	Ser	Thr	Asp	Arg	Ser	Pro	Tyr	Glu	Lys	Val	Ser	Ala	Gly	Asn
			485						490					495	
Gly	Gly	Ser	Ser	Leu	Ser	Tyr	Thr	Asn	Pro	Ala	Val	Ala	Ala	Thr	Ser
			500					505						510	
Ala	Asn	Leu													
		515													

&lt;210&gt; 213

&lt;211&gt; 5793

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 213

```

cctggactgg acagagagcg gctatactgg gagctgagcc agctgaccaa cagcatcaca 60
gagctggggac cctacaccct ggatagggac agtctctatg tcaatggcctt caacccttgg 120
agctctgtgc caaccaccag cactcctggg acctccacag tgcacctggc aacctctggg 180
actccatcct ccctgcctgg ccacacagcc cctgtccctc tcttgatacc attcaccctc 240
aactttacca tcaccaacct gcattatgaa gaaaacatgc aacaccctgg ttccaggaag 300
ttcaacacca cggagaggggt tctgcagggt ctgctcaagc ccttggttcaa gagcaccagc 360
gttgccctc tgtactctgg ctgcagactg accttgctca gacctgagaa acatggggca 420
gccactggag tggagcccat ctgcaccctc cgccttgatc ccactgggtcc tggactggac 480
agagagcggc tatactggga gctgagccag ctgaccaaca gcgttacaga gctggggccc 540
tacaccctgg acagggacag tctctatgtc aatggcttca cccatcggag ctctgtgcca 600

```

accaccagta	ttcctgggac	ctctgcagtg	cacctggaaa	cctctgggac	tccagcctcc	660
ctccctggcc	acacagcccc	tggccctctc	ctgggtgcat	tcaccctcaa	cttcactatc	720
accaacctgc	agtatgagga	ggacatgcgt	cacctgggtt	ccaggaagtt	caacaccacg	780
gagagagtcc	tgagggtct	gctcaagccc	ttgttcaaga	gcaccagtgt	tggccctctg	840
tactctggct	gcagactgac	cttgctcagg	cctgaaaaac	gtggggcagc	caccggcgctg	900
gacaccatct	gcactcaccg	ccttgaccct	ctaaaccctg	gactggacag	agagcagcta	960
tactgggagc	tgagcaaaact	gacccgtggc	atcatcgagc	tgggccccta	cctcctggac	1020
agaggcagtc	tctatgtcaa	tggtttcacc	catcggaact	ttgtgcccac	caccagcact	1080
cctgggacct	ccacagtaca	cctaggaacc	tctgaaactc	catcctccct	acctagaccc	1140
atagtgcctg	gccctctcct	ggtgccattc	accctcaact	tcaccatcac	caacttgacg	1200
tatgaggagg	ccatgcgaca	ccctggctcc	aggaagttca	ataccacgga	gagggtccta	1260
cagggctctg	tcaggccctt	gttcaagaat	accagtatcg	gccctctgta	ctccagctgc	1320
agactgacct	tgctcaggcc	agagaaggac	aaggcagcca	ccagagtgga	tgccatctgt	1380
accaccacc	ctgaccctca	aagccctgga	ctgaacagag	agcagctgta	ctgggagctg	1440
agccagctga	cccacggcat	cactgagctg	ggcccctaca	ccctggacag	ggacagtctc	1500
tatgtcgatg	gtttcactca	ttggagcccc	ataccaacca	ccagcactcc	tgggacctcc	1560
atagtgaacc	tgggaacctc	tgggatccca	ccttccctcc	ctgaaactac	agccaccggc	1620
cctctcctgg	tgccattcac	actcaacttc	accatcacta	acctacagta	tgaggagaac	1680
atgggtcacc	ctggctccag	gaagttcaac	atcacggaga	gtgttctgca	gggtctgctc	1740
aagcccttgt	tcaagagcac	cagtgttggc	cctctgtatt	ctggctgcag	actgaccttg	1800
ctcaggcctg	agaaggacgg	agtagccacc	agagtggacg	ccatctgcac	ccaccgacct	1860
gaccccaaaa	tccctgggct	agacagacag	cagctatact	gggagctgag	ccagctgacc	1920
cacagcatca	ctgagctggg	accctacacc	ctggataggg	acagtctcta	tgtcaatggg	1980
ttcaccacagc	ggagctctgt	gccaccacc	agcactcctg	ggactttcac	agtacagccg	2040
gaaacctctg	agactccatc	atccctccct	ggccccacag	ccactggccc	tgtcctgctg	2100
ccattcaccc	tcaattttac	catcattaac	ctgcagtatg	aggaggacat	gcacgcacct	2160
ggctccagga	agttcaaacac	cacggagagg	gtccttcagg	gtctgcttat	gcccttgttc	2220
aagaacacca	gtgtcagctc	tctgtactct	ggttgacagc	tgaccttgct	caggcctgag	2280
aaggatgggg	cagccaccag	agtggatgct	gtctgcaccc	atogtctga	ccccaaaagc	2340
cctggactgg	acagagagcg	gctgtactgg	aagctgagcc	agctgaccca	cggcatcact	2400
gagctggggc	cctacaccct	ggacaggcac	agtctctatg	tcaatggttt	cacccatcag	2460
agctctatga	cgaccaccag	aactcctgat	acctccacaa	tgacacctggc	aacctcgaga	2520
actccagcct	ccctgtctgg	acctacgacc	gccagccctc	tccctgggtgt	attcaccaatt	2580
aacttcacca	tcactaacct	gcggtatgag	gagaacatgc	atcaccctgg	ctctagaaag	2640
tttaacacca	cggagagagt	ccttcagggt	ctgctcaggc	ctgtgttcaa	gaacaccagt	2700
gttgccctc	tgtactctgg	ctgcagactg	accttgctca	ggcccaagaa	ggatggggca	2760
gccaccaaa	tggatgccat	ctgcacctac	cgcctgatc	ccaaaagccc	tggactggac	2820
agagcagcc	tatactggga	gctgagccag	ctaaccacac	gcactactga	gctgggcccc	2880
tacaccctgg	acagggacag	tctctatgtc	aatggtttca	cacagcggag	ctctgtgccc	2940
accactagca	ttcctgggac	ccccacagtg	gacctgggaa	catctgggac	tccagtttct	3000
aaacctggtc	cctcggctgc	cagccctctc	ctggtgctat	tcactctcaa	cttcaccatc	3060
accaacctgc	ggtatgagga	gaacatgcag	cacctgggct	ccaggaagtt	caacaccacg	3120
gagagggctc	ttcagggcct	gctcagggtc	ctgttcaaga	gcaccagtgt	tggccctctg	3180
tactctggct	gcagactgac	tttgctcagg	cctgaaaagg	atgggacagc	cactggagtg	3240
gatgccatct	gcaccaccca	ccctgacccc	aaaagcccta	ggctggacag	agagcagctg	3300
tattgggagc	tgagccagct	gaccacaaat	atcactgagc	tggggcacta	tggccctggac	3360
aacgacagcc	tctttgtcaa	tggtttcact	catcggagct	ctgtgtccac	caccagcact	3420
cctgggaccc	ccacagtgtc	tctgggagca	tctaagactc	cagcctcgat	atttggccct	3480
tcagctgcca	gccatctcct	gatactattc	accctcaact	tcaccatcac	taacctgcgg	3540
tatgaggaga	acatgtggcc	tggctccagg	aagttcaaca	ctacagagag	ggctccttcag	3600
ggcctgctaa	ggcccttggt	caagaacacc	agtgttgccc	ctctgtactc	tggctccagg	3660
ctgaccttgc	tcaggccaga	gaaagatggg	gaagccaccg	gagtggatgc	catctgcacc	3720
caccgccctg	acccacaggg	ccctgggctg	gacagagagc	agctgtattt	ggagctgagc	3780
cagctgaccc	acagcatcac	tgagctgggc	ccctacacac	tggacaggga	cagtctctat	3840
gtcaatgggt	tcaccatcgc	gagctctgta	cccaccacca	gcaccggggt	ggtcagcgag	3900
gagccattca	cactgaactt	caccatcaac	aacctgcgct	acatggcgga	catgggcca	3960
cccggtccc	tcaagttcaa	catcacagac	aacgtcatga	agcacctgct	cagtcctttg	4020
ttccagagga	gcagcctggg	tgcacggtac	acaggctgca	gggtcatcgc	actaaggctc	4080

220

```

gtgaagaacg gtgctgagac acgggtggac ctcctctgca cctacctgca gcccctcagc 4140
ggcccagggtc tgcctatcaa gcagggtgttc catgagctga gccagcagac ccatggcatc 4200
acccggctgg gcccctactc tctggacaaa gacagcctct accttaacgg ttacaatgaa 4260
cctggtctag atgagcctcc tacaactccc aagccagcca ccacattcct gcctcctctg 4320
tcagaagcca caacagccat ggggtaccac ctgaagaccc tcacactcaa cttcaccatc 4380
tccaatctcc agtattcacc agatatgggc aagggctcag ctacattcaa ctccaccgag 4440
ggggtccttc agcacctgct cagacccttg ttccagaaga gcagcatggg cccctcttac 4500
ttgggttgcc aactgatctc cctcaggcct gagaaggatg gggcagccac tgggtgtggac 4560
accacctgca cctaccaccc tgaccctgtg ggccccgggc tggacataca gcagctttac 4620
tgggagctga gtcagctgac ccatggtgtc acccaactgg gcttctatgt cctggacagg 4680
gatagcctct tcatcaatgg ctatgcacc cagaatttat caatccgggg cgagtaccag 4740
ataaatttcc acattgtcaa ctggaacctc agtaatccag accccacatc ctgagagtac 4800
atcacccctgc tgaggacat ccaggacaag gtcaccacac tctacaaagg cagtcaacta 4860
catgacacat tccgcttctg cctggtcacc aacttgacga tggactccgt gttggtcact 4920
gtcaaggcat tgttctctc caatttggac cccagcctgg tggagcaagt ctttctagat 4980
aagaccctga atgcctcatt ccattggctg ggctccacct accagttggt ggacatccat 5040
gtgacagaaa tggagtcata agtttatcaa ccaacaagca gctccagcac ccagcacttc 5100
taccygaatt tcaccatcac caacctacca tattccagg acaaagccca gccaggcacc 5160
accaattacc agaggaacaa aaggaatatt gaggatgcgg tgagaagggg gtgctcaacc 5220
aactcttccg aaacagcagc atcaagagtt attttctga ctgtcaagtt tcaacattca 5280
ggtctgtccc caacaggcac cacaccgggg tggactccct gtgtaacttc tcgccactgg 5340
ctcggagagt agacagagtt gccatctatg aggaatttct gcggatgacc cggaatggta 5400
cccagctgca gaacttcacc ctggacagga gcagtgtcct tgtggatggg tatttctcca 5460
acagaaatga gcccttaact gggaattctg acctccctt ctgggctgtc atcttcatcg 5520
gcttggcagg actcctggga ctcatcacat gcctgatctg cgggtgtcctg gtgaccacc 5580
gccggcggaa gaaggaagga gaatacaacg tccagcaaca gtgccaggc tactaccagt 5640
cacacctaga cctggaggat ctgcaatgac tggaacttgc cgggtgcctgg gytgcctttc 5700
ccccagccag ggtccaaaga agcttggctg gygcagaaat aaacctatatt ggtcggaaaa 5760
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 5793

```

&lt;210&gt; 214

&lt;211&gt; 1783

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(1783)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 214

```

Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 1           5           10           15
Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu
 20           25           30
Tyr Val Asn Gly Phe Asn Pro Trp Ser Ser Val Pro Thr Ser Thr
 35           40           45
Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser
 50           55           60
Leu Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu
 65           70           75           80
Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro
 85           90           95
Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu
100          105          110
Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
115          120          125
Arg Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val

```

130	135	140
Asp Ala Ile Cys Thr	Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp	
145	150	155
Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr		160
	165	170
Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly		175
	180	185
Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser		190
	195	200
Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His		205
	210	215
Thr Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile		220
225	230	235
Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys		240
	245	250
Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe		255
	260	265
Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu		270
	275	280
Leu Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys		285
	290	295
Thr His Arg Leu Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu		300
305	310	315
Tyr Trp Glu Leu Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro		320
	325	330
Tyr Leu Leu Asp Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg		335
	340	345
Asn Phe Val Pro Ile Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu		350
	355	360
Gly Thr Ser Glu Thr Pro Ser Ser Leu Pro Arg Pro Ile Val Pro Gly		365
	370	375
Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln		380
385	390	395
Tyr Glu Glu Ala Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr		400
	405	410
Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser		415
	420	425
Ile Gly Pro Leu Tyr Ser Ser Cys Arg Leu Thr Leu Leu Arg Pro Glu		430
	435	440
Lys Asp Lys Ala Ala Thr Arg Val Asp Ala Ile Cys Thr His His Pro		445
	450	455
Asp Pro Gln Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu		460
465	470	475
Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp		480
	485	490
Arg Asp Ser Leu Tyr Val Asp Gly Phe Thr His Trp Ser Pro Ile Pro		495
	500	505
Thr Thr Ser Thr Pro Gly Thr Ser Ile Val Asn Leu Gly Thr Ser Gly		510
	515	520
Ile Pro Pro Ser Leu Pro Glu Thr Thr Ala Thr Gly Pro Leu Leu Val		525
	530	535
Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn		540
545	550	555
Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Thr Glu Ser Val Leu		560
	565	570
Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu		575
	580	585
Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Val		590

595	600	605
Ala Thr Arg Val Asp	Ala Ile Cys Thr His Arg Pro	Asp Pro Lys Ile
610	615	620
Pro Gly Leu Asp Arg	Gln Gln Leu Tyr Trp Glu Leu Ser	Gln Leu Thr
625	630	635
His Ser Ile Thr	Glu Leu Gly Pro Tyr Thr	Leu Asp Arg Asp Ser Leu
645	650	655
Tyr Val Asn Gly	Phe Thr Gln Arg Ser Ser Val	Pro Thr Thr Ser Thr
660	665	670
Pro Gly Thr	Phe Thr Val Gln Pro	Glu Thr Ser Ser
675	680	685
Leu Pro Gly	Pro Thr Ala Thr Gly	Pro Val Leu Leu Pro Phe Thr Leu
690	695	700
Asn Phe Thr Ile	Ile Asn Leu Gln Tyr Glu	Glu Asp Met His Arg Pro
705	710	715
Gly Ser Arg Lys	Phe Asn Thr Thr Glu Arg	Val Leu Gln Gly Leu Leu
725	730	735
Met Pro Leu Phe	Lys Asn Thr Ser Val Ser	Ser Ser Leu Tyr Ser Gly Cys
740	745	750
Arg Leu Thr	Leu Leu Arg Pro Glu Lys	Asp Gly Ala Ala Thr Arg Val
755	760	765
Asp Ala Val Cys	Thr His Arg Pro Asp	Pro Lys Ser Pro Gly Leu Asp
770	775	780
Arg Glu Arg Leu	Tyr Trp Lys Leu Ser Gln	Leu Thr His Gly Ile Thr
785	790	795
Glu Leu Gly	Pro Tyr Thr Leu Asp Arg	His Ser Leu Tyr Val Asn Gly
805	810	815
Phe Thr His	Gln Ser Ser Met Thr Thr	Thr Arg Thr Pro Asp Thr Ser
820	825	830
Thr Met His	Leu Ala Thr Ser Arg	Thr Pro Ala Ser Leu Ser Gly Pro
835	840	845
Thr Thr Ala	Ser Pro Leu Leu Val Leu	Phe Thr Ile Asn Phe Thr Ile
850	855	860
Thr Asn Leu	Arg Tyr Glu Asn Met His	His Pro Gly Ser Arg Lys
865	870	875
Phe Asn Thr	Thr Glu Arg Val Leu Gln	Gly Leu Leu Arg Pro Val Phe
885	890	895
Lys Asn Thr	Ser Val Gly Pro Leu Tyr	Ser Gly Cys Arg Leu Thr Leu
900	905	910
Leu Arg Pro	Lys Lys Asp Gly Ala Ala	Thr Lys Val Asp Ala Ile Cys
915	920	925
Thr Tyr Arg	Pro Asp Pro Lys Ser	Pro Gly Leu Asp Arg Glu Gln Leu
930	935	940
Tyr Trp Glu	Leu Ser Gln Leu Thr His	Ser Ile Thr Glu Leu Gly Pro
945	950	955
Tyr Thr Leu	Asp Arg Asp Ser Leu Tyr	Val Asn Gly Phe Thr Gln Arg
965	970	975
Ser Ser Val	Pro Thr Thr Ser Ile	Pro Gly Thr Pro Thr Val Asp Leu
980	985	990
Gly Thr Ser	Gly Thr Pro Val Ser Lys	Pro Gly Pro Ser Ala Ala Ser
995	1000	1005
Pro Leu Leu	Val Leu Phe Thr Leu Asn	Phe Thr Ile Thr Asn Leu Arg
1010	1015	1020
Tyr Glu Glu	Asn Met Gln His Pro Gly	Ser Arg Lys Phe Asn Thr Thr
1025	1030	1035
Glu Arg Val	Leu Gln Gly Leu Leu Arg	Ser Leu Phe Lys Ser Thr Ser
1045	1050	1055
Val Gly Pro	Leu Tyr Ser Gly Cys Arg	Leu Thr Leu Leu Arg Pro Glu





224

				1525					1530					1535	
Gln	Gln	Leu	Tyr	Trp	Glu	Leu	Ser	Gln	Leu	Thr	His	Gly	Val	Thr	Gln
			1540					1545					1550		
Leu	Gly	Phe	Tyr	Val	Leu	Asp	Arg	Asp	Ser	Leu	Phe	Ile	Asn	Gly	Tyr
		1555					1560					1565			
Ala	Pro	Gln	Asn	Leu	Ser	Ile	Arg	Gly	Glu	Tyr	Gln	Ile	Asn	Phe	His
		1570				1575					1580				
Ile	Val	Asn	Trp	Asn	Leu	Ser	Asn	Pro	Asp	Pro	Thr	Ser	Ser	Glu	Tyr
1585				1590					1595					1600	
Ile	Thr	Leu	Leu	Arg	Asp	Ile	Gln	Asp	Lys	Val	Thr	Thr	Leu	Tyr	Lys
			1605					1610					1615		
Gly	Ser	Gln	Leu	His	Asp	Thr	Phe	Arg	Phe	Cys	Leu	Val	Thr	Asn	Leu
		1620					1625				1630				
Thr	Met	Asp	Ser	Val	Leu	Val	Thr	Val	Lys	Ala	Leu	Phe	Ser	Ser	Asn
	1635				1640				1645						
Leu	Asp	Pro	Ser	Leu	Val	Glu	Gln	Val	Phe	Leu	Asp	Lys	Thr	Leu	Asn
	1650			1655				1660							
Ala	Ser	Phe	His	Trp	Leu	Gly	Ser	Thr	Tyr	Gln	Leu	Val	Asp	Ile	His
1665			1670					1675					1680		
Val	Thr	Glu	Met	Glu	Ser	Ser	Val	Tyr	Gln	Pro	Thr	Ser	Ser	Ser	Ser
		1685					1690						1695		
Thr	Gln	His	Phe	Tyr	Xaa	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Pro	Tyr	Ser
	1700					1705					1710				
Gln	Asp	Lys	Ala	Gln	Pro	Gly	Thr	Thr	Asn	Tyr	Gln	Arg	Asn	Lys	Arg
	1715				1720				1725						
Asn	Ile	Glu	Asp	Ala	Val	Arg	Arg	Gly	Cys	Ser	Thr	Asn	Ser	Ser	Glu
	1730			1735				1740							
Thr	Ala	Ala	Ser	Arg	Val	Ile	Phe	Leu	Thr	Val	Lys	Phe	Gln	His	Ser
1745			1750					1755					1760		
Gly	Leu	Ser	Pro	Thr	Gly	Thr	Thr	Pro	Gly	Trp	Thr	Pro	Cys	Val	Thr
		1765					1770					1775			
Ser	Arg	His	Trp	Leu	Gly	Glu									
		1780													

&lt;210&gt; 215

&lt;211&gt; 5797

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 215

```

cgcggttgatc ccacgagacc tggactggac agagagcggc tatactggga gctgagccag 60
ctgaccaaca gcatcacaga gctgggaccc tacaccctgg atagggacag tctctatgtc 120
aatggcttca acccttgagg ctctgtgcca accaccagca ctccctgggac ctccacagt 180
cacctggcaa cctctgggac tccatcctcc ctgcctggcc acacagcccc tgccctctc 240
ttgataccat tcaccctcaa ctttaccatc accaacctgc attatgaaga aaacatgcaa 300
caccctgggt ccaggaagtt caacaccacg gagagggttc tgcagggtct gctcaagccc 360
ttgttcaaga gcaccagcgt tggccctctg tactctggct gcagactgac cttgctcaga 420
cctgagaaac atggggcagc cactggagtg gacgccatct gcaccctccg ccttgatccc 480
actggtcctg gactggacag agagcggcta tactgggagc tgagccagct gaccaacagc 540
gttacagagc tggggcccta caccctggac agggacagtc tctatgtcaa tggcttcacc 600
catcggagct ctgtgccaac caccagtatt cctgggacct ctgcagtgca cctggaaacc 660
tctgggactc cagcctccct ccctggccac acagcccctg gccctctcct ggtgccattc 720
accctcaact tcactatcac caacctgcag tatgaggagg acatgcgtca ccctggttcc 780
aggaagtcca acaccacgga gagagtctcg cagggtctgc tcaagccctt gttcaagagc 840
accagtgttg gccctctgta ctctggctgc agactgacct tgctcaggcc tgaaaaacgt 900
ggggcagcca ccggcgtgga caccatctgc actcaccgcc ttgaccctct aaacctgga 960
ctggacagag agcagctata ctgggagctg agcaaaactga cccgtggcat catcgagctg 1020

```

ggccccacc	tccctggacag	aggcagtcctc	tatgtcaatg	gtttcaccca	tcggaacttt	1080
gtgcccac	ccagcactcc	tgggacctcc	acagtacacc	taggaacctc	tgaaactcca	1140
tcctccctac	ctagacccat	agtgcctggc	cctctcctgg	tgccattcac	cctcaacttc	1200
accatcacca	acttgacagta	tgaggaggcc	atgcgacacc	ctggctccag	gaagttcaat	1260
accacggaga	gggtcctaca	gggtctgctc	aggcccttgt	tcaagaatac	cagtatcggc	1320
cctctgtact	ccagctgcag	actgaccttg	ctcaggccag	agaaggacaa	ggcagccacc	1380
agagtggatg	ccatctgtac	ccaccacctc	gacctcmeta	gccctggact	gaacagagag	1440
cagctgtact	gggagctgag	ccagctgacc	cacggcatca	ctgagctggg	cccctacacc	1500
ctggacaggg	acagtctcta	tgtcgatggg	ttcactcatt	ggagccccat	accaaccacc	1560
agcactcctg	ggacctccat	agtgaacctg	ggaacctctg	ggatcccacc	ttccctccct	1620
gaaactacag	ccaccggccc	tctcctgggt	ccattcacac	tcaacttcac	catcactaac	1680
ctacagtatg	aggagaacat	gggtcaccct	ggctccagga	agttcaacat	cacggagagt	1740
gttctgcagg	gtctgtctaa	gcccttggtc	aagagcacca	gtgttgggcc	tctgtattct	1800
ggctgcagac	tgaccttgct	caggcctgag	aaggacggag	tagccaccag	agtggacgcc	1860
atctgcaccc	accgccctga	ccccaaaatc	cctgggctag	acagacagca	gctatactgg	1920
gagctgagcc	agctgaccca	cagcatcact	gagctgggac	cctacaccct	ggatagggac	1980
agtctctatg	tcaatggttt	caccacagcg	agctctgtgc	ccaccaccag	cactcctggg	2040
actttcacag	tacagccgga	aacctctgag	actccatcat	ccctccctgg	ccccacagcc	2100
actggccctg	tcctgtctgc	attcacccct	aattttacca	tcattaacct	gcagtatgag	2160
gaggacatgc	atcgccctgg	ctccaggaag	ttcaacacca	cggagagggt	ccttcagggt	2220
ctgcttatgc	ccttggttcaa	gaacaccagt	gtcagctctc	tgtactctgg	ttgcagactg	2280
accttgctca	ggcctgagaa	ggatggggca	gccaccagag	tggatgctgt	ctgcacccat	2340
cgtcctgacc	ccaaaagccc	tggactggac	agagagcggc	tgtactggaa	gctgagccag	2400
ctgacccacg	gcatacctga	gctgggcccc	tacaccctgg	acaggcacag	tctctatgtc	2460
aatggtttca	cccatcagag	ctctatgacg	accaccagaa	ctcctgatac	ctccacaatg	2520
cacctggcaa	cctcgagaa	tccagcctcc	ctgtctygac	ctacgaccgc	cagccctctc	2580
ctggtgctat	tcacaattaa	cttcaccatc	actaacctgc	ggtatgagga	gaacatgcat	2640
cacctggctg	ctagaaagtt	taacaccacg	gagagagtcc	ttcagggtct	gctcaggect	2700
gtgtttcaaga	acaccagtgt	tggccctctg	tactctggct	gcagactgac	cttgctcagg	2760
cccaagaagg	atggggcagc	caccaaagtg	gatgccatct	gcacctaccg	ccctgatccc	2820
aaaagccctg	gactggacag	agagcagcta	tactgggagc	tgagccagct	aaccacagc	2880
atcactgagc	tgggccccta	cacctgggac	agggacagtc	tctatgtcaa	tggtttcaca	2940
cagcggagct	ctgtgcccac	cactagcatt	cctgggaccc	ccacagtgga	cctgggaaca	3000
tctgggactc	cagttttctaa	acctggtccc	tcggctgcca	gccctctcct	ggtgctattc	3060
actctcaact	tcaccatcac	caacctgcgg	tatgaggaga	acatgcagca	ccctggctcc	3120
aggaagtcca	acaccacgga	gagggtcctt	cagggcctgc	tcagggtccct	gttcaagagc	3180
accagtgttg	gccctctgta	ctctggctgc	agactgactt	tgtcagggcc	tgaaaaggat	3240
gggacagcca	ctggagtggg	tgccatctgc	accacaccac	ctgaccccaa	aagccctagg	3300
ctggacagag	agcagctgta	ttgggagctg	agccagctga	cccacaatat	cactgagctg	3360
ggccccctatg	ccctggacaa	cgacagcctc	tttgtcaatg	gtttcactca	tcggagctct	3420
gtgtccacca	ccagcactcc	tgggaccccc	acagtgtatc	tgggagcatc	taagactcca	3480
gcctcgatat	ttggcccttc	agctgccagc	catctcctga	tactattcac	cctcaacttc	3540
accatcacta	acctgcggta	tgaggagaac	atgtggcctg	gctccaggaa	gttcaacact	3600
acagagaggg	tccttcaggg	cctgctaagg	cccttggtta	agaacaccag	tgttggccct	3660
ctgtactctg	gctgcaggct	gaccttgctc	aggccagaga	aagatgggga	agccaccgga	3720
gtggatgcca	tctgcaccca	ccgccctgac	cccacaggcc	ctgggctgga	cagagagcag	3780
ctgtatttgg	agctgagcca	gctgaccac	agctgacctg	agctggggcc	ctacacactg	3840
gacagggaca	gtctctatgt	caatggtttc	accatcgga	gctctgtacc	caccaccagc	3900
accgggggtg	tcagcgagga	gccattcaca	ctgaacttca	ccatcaacaa	cctgcgctac	3960
atggcggaca	tgggccaacc	cggctccctc	aagttcaaca	tcacagacaa	cgtcatgcag	4020
cacctgctca	gtcctttgtt	ccagaggagc	agcctgggtg	cacggtacac	aggctgcagg	4080
gtcatcgcac	taaggtctgt	gaagaacggt	gctgagacac	gggtggacct	cctctgcacc	4140
tacctgcagc	ccctcagcgg	cccaggtctg	cctatcaagc	aggtgttcca	tgagctgagc	4200
cagcagaccc	atggcatcac	ccggctgggc	ccctactctc	tggacaaaga	cagcctctac	4260
cttaacgggt	acaatgaacc	tggccagat	gagcctccta	caactcccaa	gccagccacc	4320
acattcctgc	ctcctctgtc	agaagccaca	acagccatgg	ggtaccacct	gaagaccctc	4380
acactcaact	tcaccatctc	caatctccag	tattcaccag	atatgggcaa	gggctcagct	4440
acattcaact	ccaccgaggg	ggtccttcag	cacctgctca	gaccttggtt	ccagaagagc	4500

```

agcatggggc ccttctaactt ggggttgccaa ctgatctccc tcaggcctga gaaggatggg 4560
gcagccactg gtgtggacac cacctgcacc taccaccctg accctgtggg ccccgggctg 4620
gacatacagc agctttactg ggagctgagt cagctgaccc atggtgtcac ccaactgggc 4680
ttctatgtcc tggacaggga tagcctcttc atcaatggct atgcaccca gaatttatca 4740
atccggggcg agtaccagat aaatttccac attgtcaact ggaacctcag taatccagac 4800
cccacatcct cagagtacat caccctgctg agggacatcc aggacaaggt caccacactc 4860
tacaaaggca gtcaactaca tgacacattc cgcttctgcc tggtcaccaa cttgacgatg 4920
gactccgtgt tggctactgt caaggcattg ttctcctcca atttggaccc cagcctgggtg 4980
gagcaagtct ttctagataa gaccctgaat gcctcattcc attggctggg ctccacctac 5040
cagttggtgg acatccatgt gacagaaatg gagtcatcag ttatcaacc aacaagcagc 5100
tccagcaccg agcacttcta cccgaatttc accatcacca acctaccata ttcccaggac 5160
aaagcccagc caggcaccac caattaccag aggaacaaaa ggaatattga ggatgcgctc 5220
aaccaactct tccgaaacag cagcatcaag agttattttt ctgactgtca agtttcaaca 5280
ttcaggtctg tccccaacag gcaccacacc ggggtggact ccctgtgtaa cttctcgcca 5340
ctggctcgga gagtagacag agttgccatc tatgaggaat ttctgcggtg gacccggaat 5400
ggtacccagc tgcagaactt caccctggac aggagcagtg tccttgtgga tgggtattct 5460
cccaacagaa atgagccctt aactgggaat tctgacctc ccttctgggc tgtcatcctc 5520
atcggtctgg caggactcct gggactcatc acatgcctga tctgcggtgt cctggtgacc 5580
accgcccggc ggaagaagga aggaataac aacgtccagc aacagtgcc aggctactac 5640
cagtcacacc tagacctgga ggaatctgcaa tgactggaac ttgcccgtgc ctggggtgcc 5700
tttccccag ccagggtcca aagaagcttg gctggggcag aaataaacca tattggtcgg 5760
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 5797

```

&lt;210&gt; 216

&lt;211&gt; 1148

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 216

```

Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys
 1          5          10          15
Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val
 20          25          30
Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp
 35          40          45
Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr
 50          55          60
Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn Gly
 65          70          75          80
Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser
 85          90          95
Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro
 100          105          110
Thr Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile
 115          120          125
Thr Asn Leu Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg Lys
 130          135          140
Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe
 145          150          155          160
Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
 165          170          175
Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys
 180          185          190
Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu
 195          200          205
Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro
 210          215          220
Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg

```

225					230					235					240
Ser	Ser	Val	Pro	Thr	Thr	Ser	Ile	Pro	Gly	Thr	Pro	Thr	Val	Asp	Leu
				245					250					255	
Gly	Thr	Ser	Gly	Thr	Pro	Val	Ser	Lys	Pro	Gly	Pro	Ser	Ala	Ala	Ser
			260					265					270		
Pro	Leu	Leu	Val	Leu	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Arg
			275					280					285		
Tyr	Glu	Glu	Asn	Met	Gln	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr
			290					295				300			
Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Arg	Ser	Leu	Phe	Lys	Ser	Thr	Ser
305					310						315				320
Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu
				325							330			335	
Lys	Asp	Gly	Thr	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	His	His	Pro
			340						345				350		
Asp	Pro	Lys	Ser	Pro	Arg	Leu	Asp	Arg	Glu	Gln	Leu	Tyr	Trp	Glu	Leu
			355					360					365		
Ser	Gln	Leu	Thr	His	Asn	Ile	Thr	Glu	Leu	Gly	His	Tyr	Ala	Leu	Asp
			370				375					380			
Asn	Asp	Ser	Leu	Phe	Val	Asn	Gly	Phe	Thr	His	Arg	Ser	Ser	Val	Ser
385					390						395				400
Thr	Thr	Ser	Thr	Pro	Gly	Thr	Pro	Thr	Val	Tyr	Leu	Gly	Ala	Ser	Lys
				405						410				415	
Thr	Pro	Ala	Ser	Ile	Phe	Gly	Pro	Ser	Ala	Ala	Ser	His	Leu	Leu	Ile
			420						425				430		
Leu	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Arg	Tyr	Glu	Glu	Asn
			435					440					445		
Met	Trp	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln
			450				455					460			
Gly	Leu	Leu	Arg	Pro	Leu	Phe	Lys	Asn	Thr	Ser	Val	Gly	Pro	Leu	Tyr
465					470						475				480
Ser	Gly	Ser	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	Asp	Gly	Glu	Ala
				485						490				495	
Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	His	Arg	Pro	Asp	Pro	Thr	Gly	Pro
			500						505					510	
Gly	Leu	Asp	Arg	Glu	Gln	Leu	Tyr	Leu	Glu	Leu	Ser	Gln	Leu	Thr	His
			515				520						525		
Ser	Ile	Thr	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg	Asp	Ser	Leu	Tyr
			530				535					540			
Val	Asn	Gly	Phe	Thr	His	Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Thr	Gly
545					550						555				560
Val	Val	Ser	Glu	Glu	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Asn	Asn	Leu
				565							570				575
Arg	Tyr	Met	Ala	Asp	Met	Gly	Gln	Pro	Gly	Ser	Leu	Lys	Phe	Asn	Ile
			580												

690		695		700
Ser Glu Ala Thr Thr	Ala Met Gly Tyr His	Leu Lys Thr Leu Thr	Leu	
705	710	715	720	
Asn Phe Thr Ile Ser	Asn Leu Gln Tyr Ser	Pro Asp Met Gly Lys Gly		
	725	730	735	
Ser Ala Thr Phe Asn	Ser Thr Glu Gly Val	Leu Gln His Leu Leu Arg		
	740	745	750	
Pro Leu Phe Gln Lys	Ser Ser Met Gly Pro	Phe Tyr Leu Gly Cys Gln		
	755	760	765	
Leu Ile Ser Leu Arg	Pro Glu Lys Asp Gly	Ala Ala Thr Gly Val Asp		
	770	775	780	
Thr Thr Cys Thr Tyr	His Pro Asp Pro	Val Gly Pro Gly Leu Asp	Ile	
785	790	795	800	
Gln Gln Leu Tyr Trp	Glu Leu Ser Gln	Leu Thr His Gly Val Thr	Gln	
	805	810	815	
Leu Gly Phe Tyr Val	Leu Asp Arg Asp	Ser Leu Phe Ile Asn Gly Tyr		
	820	825	830	
Ala Pro Gln Asn Leu	Ser Ile Arg Gly Glu	Tyr Gln Ile Asn Phe His		
	835	840	845	
Ile Val Asn Trp Asn	Leu Ser Asn Pro	Asp Pro Thr Ser Ser Glu Tyr		
	850	855	860	
Ile Thr Leu Leu Arg	Asp Ile Gln Asp	Lys Val Thr Thr Leu Tyr Lys		
865	870	875	880	
Gly Ser Gln Leu His	Asp Thr Phe Arg	Phe Cys Leu Val Thr Asn Leu		
	885	890	895	
Thr Met Asp Ser Val	Leu Val Thr Val	Lys Ala Leu Phe Ser Ser Asn		
	900	905	910	
Leu Asp Pro Ser Leu	Val Glu Gln Val	Phe Leu Asp Lys Thr Leu Asn		
	915	920	925	
Ala Ser Phe His Trp	Leu Gly Ser Thr	Tyr Gln Leu Val Asp Ile His		
	930	935	940	
Val Thr Glu Met Glu	Ser Ser Val Tyr	Gln Pro Thr Ser Ser Ser Ser		
945	950	955	960	
Thr Gln His Phe Tyr	Pro Asn Phe Thr	Ile Thr Asn Leu Pro Tyr Ser		
	965	970	975	
Gln Asp Lys Ala Gln	Pro Gly Thr Thr	Asn Tyr Gln Arg Asn Lys Arg		
	980	985	990	
Asn Ile Glu Asp Ala	Leu Asn Gln Leu	Phe Arg Asn Ser Ser Ile Lys		
	995	1000	1005	
Ser Tyr Phe Ser Asp	Cys Gln Val Ser	Thr Phe Arg Ser Val Pro Asn		
	1010	1015	1020	
Arg His His Thr Gly	Val Asp Ser Leu	Cys Asn Phe Ser Pro Leu Ala		
1025	1030	1035	1040	
Arg Arg Val Asp Arg	Val Ala Ile Tyr	Glu Phe Leu Arg Met Thr		
	1045	1050	1055	
Arg Asn Gly Thr Gln	Leu Gln Asn Phe	Thr Leu Asp Arg Ser Ser Val		
	1060	1065	1070	
Leu Val Asp Gly Tyr	Ser Pro Asn Arg	Asn Glu Pro Leu Thr Gly Asn		
	1075	1080	1085	
Ser Asp Leu Pro Phe	Trp Ala Val Ile	Phe Ile Gly Leu Ala Gly Leu		
	1090	1095	1100	
Leu Gly Leu Ile Thr	Cys Leu Ile Cys	Gly Val Leu Val Thr Thr Arg		
1105	1110	1115	1120	
Arg Arg Lys Lys Glu	Gly Glu Tyr Asn	Val Gln Gln Gln Cys Pro Gly		
	1125	1130	1135	
Tyr Tyr Gln Ser His	Leu Asp Leu Glu	Asp Leu Gln		
	1140	1145		

<210> 217  
 <211> 1890  
 <212> PRT  
 <213> Homo sapiens

<400> 217

Arg	Val	Asp	Pro	Ile	Gly	Pro	Gly	Leu	Asp	Arg	Glu	Arg	Leu	Tyr	Trp
1				5				10						15	
Glu	Leu	Ser	Gln	Leu	Thr	Asn	Ser	Ile	Thr	Glu	Leu	Gly	Pro	Tyr	Thr
			20					25					30		
Leu	Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Asn	Pro	Trp	Ser	Ser
		35					40					45			
Val	Pro	Thr	Thr	Ser	Thr	Pro	Gly	Thr	Ser	Thr	Val	His	Leu	Ala	Thr
	50					55					60				
Ser	Gly	Thr	Pro	Ser	Ser	Leu	Pro	Gly	His	Thr	Ala	Pro	Val	Pro	Leu
65				70						75					80
Leu	Ile	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	His	Tyr	Glu
				85					90					95	
Glu	Asn	Met	Gln	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg
			100					105					110		
Val	Leu	Gln	Gly	Leu	Leu	Lys	Pro	Leu	Phe	Lys	Ser	Thr	Ser	Val	Gly
		115					120					125			
Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	His
	130					135					140				
Gly	Ala	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	Leu	Arg	Leu	Asp	Pro
145					150					155					160
Thr	Gly	Pro	Gly	Leu	Asp	Arg	Glu	Arg	Leu	Tyr	Trp	Glu	Leu	Ser	Gln
				165					170					175	
Leu	Thr	Asn	Ser	Val	Thr	Glu	Leu	Gly	Pro	Tyr	Thr	Leu	Asp	Arg	Asp
			180					185					190		
Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	His	Arg	Ser	Ser	Val	Pro	Thr	Thr
	195						200					205			
Ser	Ile	Pro	Gly	Thr	Ser	Ala	Val	His	Leu	Glu	Thr	Ser	Gly	Thr	Pro
	210					215						220			
Ala	Ser	Leu	Pro	Gly	His	Thr	Ala	Pro	Gly	Pro	Leu	Leu	Val	Pro	Phe
225					230					235					240
Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Gln	Tyr	Glu	Glu	Asp	Met	Arg
				245					250					255	
His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly
			260					265					270		
Leu	Leu	Lys	Pro	Leu	Phe	Lys	Ser	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser
		275					280					285			
Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	Arg	Gly	Ala	Ala	Thr
		290					295					300			
Gly	Val	Asp	Thr	Ile	Cys	Thr	His	Arg	Leu	Asp	Pro	Leu	Asn	Pro	Gly
305					310					315					320
Leu	Asp	Arg	Glu	Gln	Leu	Tyr	Trp	Glu	Leu	Ser	Lys	Leu	Thr	Arg	Gly
				325						330				335	
Ile	Ile	Glu	Leu	Gly	Pro	Tyr	Leu	Leu	Asp	Arg	Gly	Ser	Leu	Tyr	Val
			340						345					350	
Asn	Gly	Phe	Thr	His	Arg	Asn	Phe	Val	Pro	Ile	Thr	Ser	Thr	Pro	Gly
		355					360					365			
Thr	Ser	Thr	Val	His	Leu	Gly	Thr	Ser	Glu	Thr	Pro	Ser	Ser	Leu	Pro
	370					375						380			
Arg	Pro	Ile	Val	Pro	Gly	Pro	Leu	Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe
385					390					395					400
Thr	Ile	Thr	Asn	Leu	Gln	Tyr	Glu	Glu	Ala	Met	Arg	His	Pro	Gly	Ser





865		870		875		880
His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly						
	885			890		895
Leu Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser						
	900			905		910
Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr						
	915			920		925
Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly						
	930			935		940
Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser						
945		950			955	960
Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val						
	965			970		975
Asn Gly Phe Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly						
	980			985		990
Thr Pro Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Val Ser Lys Pro						
	995			1000		1005
Gly Pro Ser Ala Ala Ser Pro Leu Leu Val Leu Phe Thr Leu Asn Phe						
	1010			1015		1020
Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met Gln His Pro Gly Ser						
1025		1030			1035	1040
Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Ser						
	1045			1050		1055
Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu						
	1060			1065		1070
Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala						
	1075			1080		1085
Ile Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu						
	1090			1095		1100
Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu						
1105		1110			1115	1120
Gly Pro Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly Phe Thr						
	1125			1130		1135
His Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Val						
	1140			1145		1150
Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala						
	1155			1160		1165
Ala Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn						
	1170			1175		1180
Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn Thr						
1185		1190			1195	1200
Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr						
	1205			1210		1215
Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro						
	1220			1225		1230
Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg						
	1235			1240		1245
Pro Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu						
	1250			1255		1260
Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu						
1265		1270			1275	1280
Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val						
	1285			1290		1295
Pro Thr Thr Ser Thr Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn						
	1300			1305		1310
Phe Thr Ile Asn Asn Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly						
	1315			1320		1325
Ser Leu Lys Phe Asn Ile Thr Asp Asn Val Met Gln His Leu Leu Ser						

1330	1335	1340
Pro Leu Phe Gln Arg Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg		
1345	1350	1355
Val Ile Ala Leu Arg Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp		1360
	1365	1370
Leu Leu Cys Thr Tyr Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile		1375
	1380	1385
Lys Gln Val Phe His Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg		1390
	1395	1400
Leu Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr		1405
	1410	1415
Asn Glu Pro Gly Pro Asp Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr		1420
1425	1430	1435
Thr Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His		1440
	1445	1450
Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser		1455
	1460	1465
Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu Gly Val		1470
	1475	1480
Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro		1485
	1490	1495
Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly		1500
1505	1510	1515
Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val		1520
	1525	1530
Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu		1535
	1540	1545
Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser		1550
	1555	1560
Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu		1565
	1570	1575
Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp		1580
1585	1590	1595
Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys		1600
	1605	1610
Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe		1615
	1620	1625
Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val Lys		1630
	1635	1640
Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln Val Phe		1645
	1650	1655
Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly Ser Thr Tyr		1660
1665	1670	1675
Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser Ser Val Tyr Gln		1680
	1685	1690
Pro Thr Ser Ser Ser Thr Gln His Phe Tyr Pro Asn Phe Thr Ile		1695
	1700	1705
Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn		1710
	1715	1720
Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe		1725
	1730	1735
Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr		1740
1745	1750	1755
Phe Arg Ser Val Pro Asn Arg His His Thr Gly Val Asp Ser Leu Cys		1760
	1765	1770
Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu		1775
	1780	1785
Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr		1790

1795	1800	1805
Leu Asp Arg Ser Ser Val	Leu Val Asp Gly Tyr	Ser Pro Asn Arg Asn
1810	1815	1820
Glu Pro Leu Thr Gly Asn Ser Asp	Leu Pro Phe Trp Ala Val Ile Leu	
1825	1830	1835
Ile Gly Leu Ala Gly Leu Leu Gly	Leu Ile Thr Cys Leu Ile Cys Gly	1840
	1845	1850
Val Leu Val Thr Thr Arg Arg Arg	Lys Lys Glu Gly Glu Tyr Asn Val	1855
	1860	1865
Gln Gln Gln Cys Pro Gly Tyr Tyr	Gln Ser His Leu Asp Leu Glu Asp	1870
	1875	1880
Leu Gln		1885
1890		

<210> 218  
 <211> 4939  
 <212> DNA  
 <213> Homo sapiens

<400> 218

ttctctctcc	tccttgcaat	tttcttttct	gtctgggagc	acgccaagat	gtcccttgtg	60
actgtccctt	tctaccagaa	gagacatagg	cacttcgacc	agtcctaccg	taatattcaa	120
acacggtacc	tgctggacga	atatgcgtca	aaaaagcgag	cttccaccca	ggcatcttcc	180
cagaagtcct	tgagtcagcg	gtcgtcttca	cagagagcct	ccagccagac	gtccctggga	240
ggaaccatct	gcaggggtctg	tgcaagcgca	gtgagcacgc	aggaagatga	ggagcaggag	300
aacagaagca	ggtaccagtc	cctggtggcc	gcctatgggtg	aggccaagcg	acacggcttc	360
ctcagcgagc	tggcccactt	ggaggaggat	gtccacctgg	cacgctccca	ggcccgcgac	420
aagctggaca	aatacgccat	tcagcagatg	atggaggaca	agctggcctg	ggagagacac	480
acatttgaag	agcggataag	cagggctcct	gagatcctgg	tgcggtcgcg	atccacacac	540
gtctgggaga	ggatgtctgt	gaaactctgc	ttcacggtgc	aaggatttcc	cacgcccgtg	600
gtgcagtggt	acaaagatgg	cagtctgatt	tgccaggcgg	ctgaaccggg	aaagtacagg	660
attgagagca	actatggcgt	acacacactg	gagatcaaca	gggcagactt	tgacgacact	720
gcgacatact	cagcagtggc	caccaatgcc	cacggacaag	tgtccaccaa	cgcggcggtg	780
gtggtgagaa	ggttccgggg	agacgaggaa	ccattccggt	cggtgggact	cccgattgga	840
ttgcccctgt	catcgatgat	tccgtacacg	cacttcgacg	tccagttttt	ggagaagttt	900
ggggtcacct	tcaggaggga	aggcgagacg	gtcactctca	agtgcaccat	gctggtgacg	960
ccggacctga	agcgggtgca	gccgcgcgcc	gagtggtacc	gcgatgactt	gctgttgaaa	1020
gagtcacaag	ggacgaagat	gttcttttga	gaaggccagg	cctccctgtc	cttcagccac	1080
ctgcacaagg	acgacgaggg	cctgtacacc	ctgcgcacgc	tgtctcgggg	cggcgtcacg	1140
gaccacagcg	ccttctgtgt	tgtcagagat	gctgacccgc	tggtcacagg	ggcccccggt	1200
gcacccatgg	acttgacgtg	ccacgacgcc	aaccgggact	acgtcatcgt	gacctggaag	1260
ccgcccaca	ccaccactga	gagccccgtc	atgggctatt	ttgtggaccg	atgtgaagta	1320
ggaacgaata	attgggtgca	gtgcaatgat	gcaccgggtga	aaatctgcaa	ataccgggtc	1380
acagggcttt	ttgaagggaag	gtcttacata	ttccgagtga	gggcagtga	cagtgcgggc	1440
atcagccgac	cctccagggt	ctctgatgcg	gtggctgcac	ttgaccocct	ggacctcaga	1500
aggttacaag	ccgttcattt	ggaggagag	aaggagattg	ccatttatca	ggatgacctt	1560
gaagggtgacg	cccaggttcc	agggcctccc	accggtgtgc	acgcttccga	gatcagcaga	1620
aactatgtcg	tcctcagctg	ggagccaccc	actcccctg	gcaaggaccc	gctcatgtac	1680
ttcattgaga	agtcggtggt	ggggagcggc	acgtggcaga	gagtcaacgc	ccagacggct	1740
gtgagatccc	cgagatatgc	cgtgtttgac	ctcatggaag	ggaagtctta	tgtgttccga	1800
gtgctgtcag	caaacccgca	tgccctgagc	gaaccttcgg	agataacgtc	ccccattcag	1860
gcccaggatg	tgaccgttgt	cccttctgct	ccgggtcggg	ttcttgcttc	ccgaaacacc	1920
aagacgtcgg	tggtggtgca	gtgggaccga	cctaagcatg	aggaggacct	gctgggctac	1980
tacgtggact	gctgtgtggc	cggaaaccaac	ctctgggagc	cctgcaacca	caagcccatc	2040
ggatacaaca	ggttcgtggt	gcacggctta	accacgggag	agcagtacat	cttccgagtc	2100
aaggcgggtca	atgctgtggg	gatgagtgaa	aattcccagg	aatcagacgt	cataaaagtg	2160
caggccgcac	tcaccgtccc	gtcccacctc	tatgggatta	cgctcctcaa	ctgtgacggc	2220

```

cactccatga ccctcggctg gaaggtcccg aaattcagtg gtggctcgcc catcctgggc 2280
tactacctgg acaagcgtga agttcaccat aaaaactggc acgaggtcaa ttctcacc 2340
agcaaacgga caatcctaac ggtggacggc ttgacggaag gctcactcta cgagttcaaa 2400
atcgccgccc tcaacctggc cggcatcggg gagccctcag atcccagtg gacattcaag 2460
tgtgaggcct ggaccatgcc ggagcccggc cctgcctacg acttgacgtt ctgtgaggtc 2520
agggacacgt ccttggtcat gctgtggaag gccctgtgt actccggcag cagccctgtt 2580
tctggatatt tctggtgact cagggaggag gatgctggag agtggatcac tgtcgatcac 2640
acgacaacag ccagccgtta tttaaaggtc tctgacctgc agcaaggtaa gacctatgtc 2700
ttcagggctc gggcagtcaa tgcaaatggc gtggggaagc cctcagacac gtcggagcct 2760
gtgctggtag aggcgagacc aggcaccaag gaaatcagtg ctggtgtcga tgaacagggc 2820
aacatctatc tgggcttcga ctgccaggaa atgacagacg cgtctcagtt cactgtgtgt 2880
aaatcctacg aggagatttc agatgatgag aggtttaaaa tcgaaaccgt ggggggacac 2940
tccaagctgt acttaaagaa tccggataag gaggatttag ggacttactc cgtgtctgta 3000
agtatacag acggagtgtc ctccagtttt gttctggacc cagaagagct cgagcgtttg 3060
atggcattga gcaatgaaat aaagaacccc acaattcctc tgaaatcgga attagcttat 3120
gagatttttg ataagggcg ggttcgcttc tggctccagg ctgagcactt atcaccagat 3180
gccagctacc gatttattat taatgacaga gaagtctctg acagcgagat acacagaatt 3240
aaatgtgaca aagctactgg cattattgag atgggtgatg atcgatttag tattgaaaa 3300
gaggggacct acactgtgca gattcatgat gggaaagcca aaagtcagtc ttctctagtt 3360
cttattggag atgcattcaa gactgtgctg gaagaggctg agtttcaaa gaaagaattt 3420
ctcaggaaac aaggccctca ttttgctgag tacttgactc gggatgtcac ggaagaatgt 3480
gaagttcgac ttgtttgcaa ggttgcaaac accaagaaag aaaccgtttt caaatggctc 3540
aaggatgatg ctctgtatga aacggagaca ctgcctaacc tggagagggg aatctgtgag 3600
ctcctcatcc caaagttgtc aaagaaggac cacggtgaat acaaggcaac cttgaaagat 3660
gacagaggcc aagatgtgtc catccttgaa atagctggca aagtgtatga tgatatgatt 3720
ttggcaatga gtagagtctg tgggaaatct gcttcgccac tgaaggtact ctgcacccca 3780
gaaggataac gacttcagtg tttcatgaag tattttacag acgaaatgaa agtgaactgg 3840
tgtcacaagc atgctaagat ctcatccagt gagcatatga gaatcggggg gagtgaagag 3900
atggccttggc tgcagatatg tgagccgact gagaaggata aaggaaaata cacttttgag 3960
attttcgatg gcaaagacaa ccatcaacgc tcccttgacc tgtccggaca agcttttgat 4020
gaagcatttg cagaattcca gcaattcaaa gctgctgctt ttgcagagaa gaatcgtggc 4080
aggttgatcg gcggttgcc tgacgtggtg accatcatgg aagggaagac cttgaatctg 4140
acctgcacgg tgtttgaaa cctgacccc gaagtgtatt ggttcaagaa cgaccaggac 4200
atccagctca gcgagcactt ctcggtgaag gtggagcagg ccaagtacgt cagcatgacc 4260
atcaaaggcg tgacctccga ggactcgggc aagtacagca tcaacatcaa gaataagtat 4320
ggcggggaga agatcgacgt gacggtgagc gtgtacaaac acggggagaa gatcccggac 4380
atggcccccgc cccagcaagc caagcccaag ctcatcccc cgtctgcctc agcggcaggc 4440
cagtgaaggc gttttcctag cctggagatg ggaaaaatatg cttggcagag acaggaatgc 4500
tgtgtgcttg ttccaaatga gcagctggca tccgagtggg gtcctgtgtg ggctgatagt 4560
tgatcacaca ttgtgctttt gatttttgca tttggtgatg aatattttat acccgtctaa 4620
gggagaaagc taatgttttc cacaagactg aacaacgtgt atttacacga gggtagacgg 4680
cagatgcctg acagagagtg ggttggcaga caacacacta gcattttcac ggggtgtggc 4740
acatgggtgt ggcacctgga cgtgtgcagc atgtggcggt ctctgtgtga agccaccgtg 4800
cttctctttg gggggccgcg agatctagca tctctgaaat cctggctgtc gaggctttga 4860
agcatgtgtt acctggttaa gcttgttttc tcttgcttta ggcaataaa agtttaaaaa 4920
tcaaaaaaaa aaaaaaaaaa

```

&lt;210&gt; 219

&lt;211&gt; 1465

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 219

```

Met Ser Leu Val Thr Val Pro Phe Tyr Gln Lys Arg His Arg His Phe
 1             5             10            15
Asp Gln Ser Tyr Arg Asn Ile Gln Thr Arg Tyr Leu Leu Asp Glu Tyr
      20             25            30
Ala Ser Lys Lys Arg Ala Ser Thr Gln Ala Ser Ser Gln Lys Ser Leu

```

35					40					45					
Ser	Gln	Arg	Ser	Ser	Ser	Gln	Arg	Ala	Ser	Ser	Gln	Thr	Ser	Leu	Gly
50						55					60				
Gly	Thr	Ile	Cys	Arg	Val	Cys	Ala	Lys	Arg	Val	Ser	Thr	Gln	Glu	Asp
65					70					75					80
Glu	Glu	Gln	Glu	Asn	Arg	Ser	Arg	Tyr	Gln	Ser	Leu	Val	Ala	Ala	Tyr
				85					90					95	
Gly	Glu	Ala	Lys	Arg	His	Gly	Phe	Leu	Ser	Glu	Leu	Ala	His	Leu	Glu
			100					105					110		
Glu	Asp	Val	His	Leu	Ala	Arg	Ser	Gln	Ala	Arg	Asp	Lys	Leu	Asp	Lys
	115						120					125			
Tyr	Ala	Ile	Gln	Gln	Met	Met	Glu	Asp	Lys	Leu	Ala	Trp	Glu	Arg	His
130					135					140					
Thr	Phe	Glu	Glu	Arg	Ile	Ser	Arg	Ala	Pro	Glu	Ile	Leu	Val	Arg	Leu
145					150					155					160
Arg	Ser	His	Thr	Val	Trp	Glu	Arg	Met	Ser	Val	Lys	Leu	Cys	Phe	Thr
				165					170					175	
Val	Gln	Gly	Phe	Pro	Thr	Pro	Val	Val	Gln	Trp	Tyr	Lys	Asp	Gly	Ser
			180					185					190		
Leu	Ile	Cys	Gln	Ala	Ala	Glu	Pro	Gly	Lys	Tyr	Arg	Ile	Glu	Ser	Asn
	195						200					205			
Tyr	Gly	Val	His	Thr	Leu	Glu	Ile	Asn	Arg	Ala	Asp	Phe	Asp	Asp	Thr
210					215						220				
Ala	Thr	Tyr	Ser	Ala	Val	Ala	Thr	Asn	Ala	His	Gly	Gln	Val	Ser	Thr
225					230					235					240
Asn	Ala	Ala	Val	Val	Val	Arg	Arg	Phe	Arg	Gly	Asp	Glu	Glu	Pro	Phe
				245					250					255	
Arg	Ser	Val	Gly	Leu	Pro	Ile	Gly	Leu	Pro	Leu	Ser	Ser	Met	Ile	Pro
			260					265					270		
Tyr	Thr	His	Phe	Asp	Val	Gln	Phe	Leu	Glu	Lys	Phe	Gly	Val	Thr	Phe
	275						280					285			
Arg	Arg	Glu	Gly	Glu	Thr	Val	Thr	Leu	Lys	Cys	Thr	Met	Leu	Val	Thr
290					295						300				
Pro	Asp	Leu	Lys	Arg	Val	Gln	Pro	Arg	Ala	Glu	Trp	Tyr	Arg	Asp	Asp
305					310					315					320
Leu	Leu	Leu	Lys	Glu	Ser	Lys	Trp	Thr	Lys	Met	Phe	Phe	Gly	Glu	Gly
				325					330					335	
Gln	Ala	Ser	Leu	Ser	Phe	Ser	His	Leu	His	Lys	Asp	Asp	Glu	Gly	Leu
			340					345					350		
Tyr	Thr	Leu	Arg	Ile	Val	Ser	Arg	Gly	Gly	Val	Thr	Asp	His	Ser	Ala
	355						360					365			
Phe	Leu	Phe	Val	Arg	Asp	Ala	Asp	Pro	Leu	Val	Thr	Gly	Ala	Pro	Gly
370					375						380				
Ala	Pro	Met	Asp	Leu	Gln	Cys	His	Asp	Ala	Asn	Arg	Asp	Tyr	Val	Ile
385					390					395					400
Val	Thr	Trp	Lys	Pro	Pro	Asn	Thr	Thr	Thr	Glu	Ser	Pro	Val	Met	Gly
				405					410					415	
Tyr	Phe	Val	Asp	Arg	Cys	Glu	Val	Gly	Thr	Asn	Asn	Trp	Val	Gln	Cys
			420					425					430		
Asn	Asp	Ala	Pro	Val	Lys	Ile	Cys	Lys	Tyr	Pro	Val	Thr	Gly	Leu	Phe
	435						440					445			
Glu	Gly	Arg	Ser	Tyr	Ile	Phe	Arg	Val	Arg	Ala	Val	Asn	Ser	Ala	Gly
450					455					460					
Ile	Ser	Arg	Pro	Ser	Arg	Val	Ser	Asp	Ala	Val	Ala	Ala	Leu	Asp	Pro
465					470					475					480
Leu	Asp	Leu	Arg	Arg	Leu	Gln	Ala	Val	His	Leu	Glu	Gly	Glu	Lys	Glu
				485					490					495	
Ile	Ala	Ile	Tyr	Gln	Asp	Asp	Leu	Glu	Gly	Asp	Ala	Gln	Val	Pro	Gly





238

1425                      1430                      1435                      1440  
 Lys Ile Pro Asp Met Ala Pro Pro Gln Gln Ala Lys Pro Lys Leu Ile  
                                  1445                      1450                      1455  
 Pro Ala Ser Ala Ser Ala Ala Gly Gln  
                                  1460                      1465

&lt;210&gt; 220

&lt;211&gt; 4135

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 220

```

ctcacagccc agcacctgcg gagggagcgc tgaccatggc tccctggcct gaattgggag 60
atgccagccc caaccccgat aagtacctcg aaggggcccgc aggtcagcag cccactgccc 120
ctgataaaag caaagagacc aacaaaaata acactgaggc acctgtaacc aagattgaac 180
ttctgccgtc ctactccacg gctacactga tagatgagcc cactgagggtg gatgaccctc 240
ggaacctacc cactcttcag gactcgggga tcaagtggtc agagagagac accaaaggga 300
agattctctg tttcttccaa gggattggga gattgatttt acttctcggg tttctctact 360
ttttcgtgtg tcccttggtg attcttagta gcgccttcca gctgggtgga ggaaaaatgg 420
caggacagtt cttcagcaac agctctatta tgtccaaccc tttgttgggg ctggtgatcg 480
gggtgctggt gaccgtcttg gtgcagagct ccagcacctc aacgtccatc gttgtcagca 540
tgggtgctct ttcatgtctc actgttcggg ctgccatccc cattatcatg ggggccaaaca 600
ttggaacgtc aatcaccâac actattgttg cgctcatgca ggtgggagat cggagtgaagt 660
tcagaagagc ttttgcaagg gccactgtcc atgacttctt caactggctg tccctgttgg 720
tgctcttgcc cgtggagggtg gccacccatt acctcgagat cataacccag cttatagtgg 780
agagcttcca cttcaagaat ggagaagatg ccccgagatct tctgaaagtc atcactaagc 840
ccttcacaaa gctcattgtc cagctggata aaaaagtatt cagccaaatt gcaatgaacg 900
atgaaaaagc gaaaaacaa agtcttgtca agatttgggtg caaaaactttt accaacaaga 960
ccagatttaa cgtcactgtt ccctcgactg ctaactgcac ctccccttcc ctctgttggg 1020
cggatggcat ccaaaactgg accatgaaga atgtgacctc caaggagaac atcgccaaat 1080
gccagcatat ctttgtgaat ttccacctcc cggatcttgc tgtgggcacc atcttgtctc 1140
tactctocct gctggtcctc tgtgggttgc tgatcatgat tgtcaagatc ctgggctctg 1200
tgctcaaggg gcaggtcgcc actgtcatca agaagaccat caacactgat ttccccttcc 1260
cctttgcatg gttgactggc tacctggcca tccctgctcg ggcaggcatg accttcatcg 1320
tacagagcag ctctgtgttc acgtcggcct tgacccccct gattggaatc ggcgtgataa 1380
ccattgagag ggcttatcca ctcaacgctg gctccaacat cggcaccacc accaccgcca 1440
tcctggccgc cttagccagc cctggcaatg cattgaggag ttcaactccag atcgccctgt 1500
gccacttttt cttcaacatc tccggcatct tgcgtgtggt cccgatcccg ttcaactgcc 1560
tgcccatccg catggccaag gggctgggca acatctctgc caagtatcgc tggttcgccg 1620
tcttctacct gatcatcttc ttcttctga tcccgctgac ggtgttgggc ctctcgctgg 1680
ccggtggcgc ggtgctggtt ggtgtcgggg ttcccgctgt cttcatcatc atcctggtac 1740
tgtgcctccg actcctgcag tctcgctgcc cagcgtcctt gccgaagaaa ctccagaact 1800
ggaacttctt gccgctgtgg atgcgctcgc tgaagccctg ggtgcccgtc gtctccaagt 1860
tcaccggctg cttccagatg cgctgctgct gctgctgccg cgtgtgctgc cgcgctgct 1920
gcttgctgtg tggctgcccc aagtgtgctc gctgcagcaa gtgctgcgag gacttggagg 1980
aggcgcagga ggggcaggat gtccctgtca aggtccctga gaccttgat aacataacca 2040
ttagcagaga ggctcagggt gaggtccctg cctcggactc aaagaccgaa tgcacggcct 2100
tgtaggggac gcccagatt gtcagggatg gggggatggt ccttgagttt tgcattgctc 2160
cctccctccc acttctgcac cctttcacca cctcgaggag atttgctccc cattagcgaa 2220
tgaaattgat gcagtcctac ctaactcgat tccctttggc ttggtgggta ggcctgcagg 2280
gcaactttat tccaaccctt ggtaactcag taatctttta ctccaggaa gacacaggat 2340
gtacctaaag agaattagag aatgaacctg gcgggacgga tgtctaatac tgcacctagc 2400
tgggttggtc agtagaacct attttcagac tcaaaaacca tcttcagaaa gaaaaggccc 2460
agggaaggaa tgtatgagag gctctcccag ataggaagt gtactctcta tgactatcaa 2520
gtcaggcct ctcccttttt ttaaaccaaa gtctggcaac caagagcagc agtccatgg 2580
cctccttgcc ccagatcagc ctgggtcagg ggacatagtg tcattgtttg gaaactgcag 2640
accacaaggt gtgggtctat cccacttctt agtgcctccc acattcccca tcagggtctc 2700

```



```

ctcacgtgga caggtgtgct agtccaggca gttcacttgc agtttccttg tcctcatgct 2760
tcggggatgg gagccacgcc tgaactagag ttcaggctgg atacatgtgc tcacctgctg 2820
ctcttgtctt cctaagagac agagagtggg gcagatggag gagaagaaag tgaggaatga 2880
gtagcatagc attctgccaa aagggcccca gattcttaat ttagcaaaact aagaagccca 2940
attcaaaagc attgtggcta aagtctaacg ctctctctct ggtagataa caaaagccct 3000
ccctgttgga tcttttgaaa taaaacgtgc aagttatcca ggctcgtagc ctgcatgctg 3060
ccaccttgaa tcccaggagg tatctgcacc tgggaatagct ctccaccctt ctctgcctcc 3120
ttactttctg tgcaagatga tttcctgggt taacttcctt ctttccatcc acccaccac 3180
tggaatctct ttccaaacat ttttccattt tcccacagat gggctttgat tagctgtcct 3240
ctctccatgc ctgcaaagct ccagattttt ggggaaagct gtaccaact ggactgcca 3300
gtgaactggg atcattgagt acagtcgagc acacgtgtgt gcatgggtca aaggggtgtg 3360
ttccttctca tcttagatgc cttctctgtg ccttccacag cctcctgcct gattacacca 3420
ctgccccgcg cccaccctca gccatcccaa ttcttctctg ccagtgcgtc ccagccttat 3480
ctaggaaagg aggagtgggt gtagccgtgc agcaagattg gggcctcccc catcccagct 3540
tctccaccat cccagcaagt caggatatca gacagtcctc ccctgaccct ccccttgta 3600
gatatcaatt cccaaacaga gccaaatact ctatatctat agtcacagcc ctgtacagca 3660
tttttcataa gttatatagt aaatggtctg catgatttgt gcttctagtg ctctcatttg 3720
gaaatgaggc aggtctcttc tatgaaatgt aaagaaagaa accactttgt atattttgta 3780
ataccacctc tgtggccatg cctgccccgc ccactctgta tataatgtaag ttaaaccgg 3840
gcaggggctg tggcgtctct tgtactctgg tgatttttaa aaattgaatc tttgtacttg 3900
cattgattgt ataataattt tgagaccagg tctcgtgtgt ttgctcaggc tggctctcaa 3960
ctcctgagat caagcaatcc gccacctca gcctcccaa gtgctgagat cacaggcgtg 4020
agccaccacc aggcctgatt gtaatttttt tttttttttt tactggttat gggaaggagg 4080
aaataaaatc atcaaacccc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 4135

```

&lt;210&gt; 221

&lt;211&gt; 689

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 221

```

Met Ala Pro Trp Pro Glu Leu Gly Asp Ala Gln Pro Asn Pro Asp Lys
1          5          10          15
Tyr Leu Glu Gly Ala Ala Gly Gln Gln Pro Thr Ala Pro Asp Lys Ser
20          25          30
Lys Glu Thr Asn Lys Asn Asn Thr Glu Ala Pro Val Thr Lys Ile Glu
35          40          45
Leu Leu Pro Ser Tyr Ser Thr Ala Thr Leu Ile Asp Glu Pro Thr Glu
50          55          60
Val Asp Asp Pro Trp Asn Leu Pro Thr Leu Gln Asp Ser Gly Ile Lys
65          70          75          80
Trp Ser Glu Arg Asp Thr Lys Gly Lys Ile Leu Cys Phe Phe Gln Gly
85          90          95
Ile Gly Arg Leu Ile Leu Leu Leu Gly Phe Leu Tyr Phe Phe Val Cys
100          105          110
Ser Leu Asp Ile Leu Ser Ser Ala Phe Gln Leu Val Gly Gly Lys Met
115          120          125
Ala Gly Gln Phe Phe Ser Asn Ser Ser Ile Met Ser Asn Pro Leu Leu
130          135          140
Gly Leu Val Ile Gly Val Leu Val Thr Val Leu Val Gln Ser Ser Ser
145          150          155          160
Thr Ser Thr Ser Ile Val Val Ser Met Val Ser Ser Ser Leu Leu Thr
165          170          175
Val Arg Ala Ala Ile Pro Ile Ile Met Gly Ala Asn Ile Gly Thr Ser
180          185          190
Ile Thr Asn Thr Ile Val Ala Leu Met Gln Val Gly Asp Arg Ser Glu
195          200          205
Phe Arg Arg Ala Phe Ala Gly Ala Thr Val His Asp Phe Phe Asn Trp

```

240

210	215	220
Leu Ser Leu Leu Val	Leu Leu Pro Val Glu	Val Ala Thr His Tyr Leu
225	230	235
Glu Ile Ile Thr Gln	Leu Ile Val Glu Ser Phe	His Phe Lys Asn Gly
245	250	255
Glu Asp Ala Pro Asp	Leu Leu Lys Val Ile Thr	Lys Pro Phe Thr Lys
260	265	270
Leu Ile Val Gln Leu	Asp Lys Lys Val Ile Ser	Gln Ile Ala Met Asn
275	280	285
Asp Glu Lys Ala Lys	Asn Lys Ser Leu Val Lys	Ile Trp Cys Lys Thr
290	295	300
Phe Thr Asn Lys Thr	Gln Ile Asn Val Thr	Val Pro Ser Thr Ala Asn
305	310	315
Cys Thr Ser Pro Ser	Leu Cys Trp Thr Asp	Gly Ile Gln Asn Trp Thr
325	330	335
Met Lys Asn Val Thr	Tyr Lys Glu Asn Ile Ala	Lys Cys Gln His Ile
340	345	350
Phe Val Asn Phe His	Ileu Pro Asp Leu Ala	Val Gly Thr Ile Leu Leu
355	360	365
Ile Leu Ser Leu Leu	Val Leu Cys Gly Cys	Leu Ile Met Ile Val Lys
370	375	380
Ile Leu Gly Ser Val	Leu Lys Gly Gln Val	Ala Thr Val Ile Lys Lys
385	390	395
Thr Ile Asn Thr Asp	Phe Pro Phe Pro Phe	Ala Trp Leu Thr Gly Tyr
405	410	415
Leu Ala Ile Leu Val	Gly Ala Gly Met Thr	Phe Ile Val Gln Ser Ser
420	425	430
Ser Val Phe Thr Ser	Ala Leu Thr Pro Leu	Ile Gly Ile Gly Val Ile
435	440	445
Thr Ile Glu Arg Ala	Tyr Pro Leu Thr Leu	Gly Ser Asn Ile Gly Thr
450	455	460
Thr Thr Thr Ala Ile	Leu Ala Ala Leu Ala	Ser Pro Gly Asn Ala Leu
465	470	475
Arg Ser Ser Leu Gln	Ile Ala Leu Cys His	Phe Phe Phe Asn Ile Ser
485	490	495
Gly Ile Leu Leu Trp	Tyr Pro Ile Pro Phe	Thr Arg Leu Pro Ile Arg
500	505	510
Met Ala Lys Gly Leu	Gly Asn Ile Ser Ala	Lys Tyr Arg Trp Phe Ala
515	520	525
Val Phe Tyr Leu Ile	Ile Phe Phe Phe Leu	Ile Pro Leu Thr Val Phe
530	535	540
Gly Leu Ser Leu Ala	Gly Trp Arg Val Leu	Val Gly Val Gly Val Pro
545	550	555
Val Val Phe Ile Ile	Ile Leu Val Leu Cys	Leu Arg Leu Leu Gln Ser
565	570	575
Arg Cys Pro Arg Val	Leu Pro Lys Lys	Leu Gln Asn Trp Asn Phe Leu
580	585	590
Pro Leu Trp Met Arg	Ser Leu Lys Pro Trp	Asp Ala Val Val Ser Lys
595	600	605
Phe Thr Gly Cys Phe	Gln Met Arg Cys Cys	Cys Cys Cys Arg Val Cys
610	615	620
Cys Arg Ala Cys Cys	Leu Leu Cys Gly Cys	Pro Lys Cys Cys Arg Cys
625	630	635
Ser Lys Cys Cys Glu	Asp Leu Glu Glu Ala	Gln Glu Gly Gln Asp Val
645	650	655
Pro Val Lys Ala Pro	Glu Thr Phe Asp Asn	Ile Thr Ile Ser Arg Glu
660	665	670
Ala Gln Gly Glu Val	Pro Ala Ser Asp	Ser Lys Thr Glu Cys Thr Ala

241

675                      680                      685  
 Leu

<210> 222  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 222  
 gccgctgagc cataatggag atatcaatgc ctccacctca gatatatgta gaaaaaactc 60  
 tggccattat caaaccagat attgttgaca aagaggaggà gatacaagat attattctta 120  
 gatccggatt caccattgtt cagagaagaa aactacgcct cagccctgag caatgtagta 180  
 acttttatgt ggaaaagtat ggaaaaatgt ttttcccaa cttacagct tacatgagtt 240  
 ctggaccact tgcgcgatg atattagcta gacataaagc catctcttat tggttagaac 300  
 ttttgggacc aaataatagc ttagtagcga aggagacaca tccagacagt ctgagggcaa 360  
 tttatggcac agatgaccta aggaatgcac ttcatgggag taatgacttt gctgctgcgg 420  
 aaagagaaat acgttttatg tticctgaag tgattgttga gccattcca attggacaag 480  
 ctgctaagga ctatttaaatt ttacatataa tgccaactct gcttgaagga ctcacagagc 540  
 tttgtaagca aaaaccagca gaccttttga tttggctagc tgattggctg ctgaaaaata 600  
 atcctaacaa acccaaactt tgtcaccatc caattgtaga agaaccttat taaaaaaaaa 660  
 atcctcgaaa gaacaaatca tgaactatct tattataaaa ggctgtactt ctactgtttg 720  
 agaaaattat ttctagggtt taagtaacta ccagtaaaat aaatttattt c 771

<210> 223  
 <211> 212  
 <212> PRT  
 <213> Homo sapiens

<400> 223  
 Met Glu Ile Ser Met Pro Pro Pro Gln Ile Tyr Val Glu Lys Thr Leu  
 1                      5                      10                      15  
 Ala Ile Ile Lys Pro Asp Ile Val Asp Lys Glu Glu Glu Ile Gln Asp  
 20                      25                      30  
 Ile Ile Leu Arg Ser Gly Phe Thr Ile Val Gln Arg Arg Lys Leu Arg  
 35                      40                      45  
 Leu Ser Pro Glu Gln Cys Ser Asn Phe Tyr Val Glu Lys Tyr Gly Lys  
 50                      55                      60  
 Met Phe Phe Pro Asn Leu Thr Ala Tyr Met Ser Ser Gly Pro Leu Val  
 65                      70                      75                      80  
 Ala Met Ile Leu Ala Arg His Lys Ala Ile Ser Tyr Trp Leu Glu Leu  
 85                      90                      95  
 Leu Gly Pro Asn Asn Ser Leu Val Ala Lys Glu Thr His Pro Asp Ser  
 100                      105                      110  
 Leu Arg Ala Ile Tyr Gly Thr Asp Asp Leu Arg Asn Ala Leu His Gly  
 115                      120                      125  
 Ser Asn Asp Phe Ala Ala Ala Glu Arg Glu Ile Arg Phe Met Phe Pro  
 130                      135                      140  
 Glu Val Ile Val Glu Pro Ile Pro Ile Gly Gln Ala Ala Lys Asp Tyr  
 145                      150                      155                      160  
 Leu Asn Leu His Ile Met Pro Thr Leu Leu Glu Gly Leu Thr Glu Leu  
 165                      170                      175  
 Cys Lys Gln Lys Pro Ala Asp Pro Leu Ile Trp Leu Ala Asp Trp Leu  
 180                      185                      190  
 Leu Lys Asn Asn Pro Asn Lys Pro Lys Leu Cys His His Pro Ile Val  
 195                      200                      205  
 Glu Glu Pro Tyr

210

<210> 224  
 <211> 3463  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 224

```

atggctgagc cgactagtga ttctgagact cctatcggtt ggcattgcgtc tcccagactg 60
actcccaagt tagggcccct gagcgacact gcccgcgcgc gggacaggtg gatgttctgg 120
gcaatgtctg cgccaccgcc accaccactt acgtcctcgc ttcccgcagc cgggtcaaag 180
ccttcctctg agtcgcagcc ccccatggag gccagtcctc tcccgggggc tccgcccccc 240
ttcgacgccc agattcttcc cggggcgcaa ccccccttcg acgcccagtc tccccttgat 300
tctcagcctc aaccagcgg ccagccttg aatttccatg cttccacatc gtggtattgg 360
agacagtctt ctgatagggt tcctcgcat cagaagtcct tcaaccctgc agttaaaaaat 420
tcttattatc cacgaaagta tgatgcaaaa ttcacagact tcagcttacc tcccagtaga 480
aaacagaaaa aaaagaaaaa aaaggaacca gtttttctc ttttttgta tacctgtgat 540
cgtgggttta aaatcaaga aaagtatgac aaacacatgt ctgaacatac aaaatgccct 600
gaattagatt gctcttttac tgcacacgag aagattgtcc agttccattg gagaaatatg 660
catgtccttg gcatgaagaa gatcaagtta gacactccag aggaaattgc acggtggagg 720
gaagaaagaa ggaaaaacta tccaactctg gccaatattg aaaggaagaa gaagttaaaa 780
cttgaaaagg agaagagagg agcagtattg acaacaacac aatatggcaa gatgaagggg 840
atgtccagac attcacaat ggcaagatc agaagtcctg gcaagaatca caaatggaaa 900
aacgacaatt ctagacagag agcagtcact ggatcaggca gtcacttggt tgatttgaag 960
ctagaaggtc caccggaggc aaatgcagat cctcttggtg ttttgataaa cagtgttct 1020
gagtctgata agaggagaa accacaacat tctgtgatac ccaaggaagt gacaccagcc 1080
ctatgccac taatgagtag ctatggcagt ctttcagggt cagagagtga gccagaagaa 1140
actcccatca agactgaagc agacgttttg gcagaaaacc aggttcttga tagcagtgtc 1200
cctaagagtc caagtcaaga tgtaaagca actgttagaa atttttcaga agccaagagt 1260
gagaaccgaa agaaaagctt tgaaaaaca aaccctaaga ggaaaaaaga ttatcacaac 1320
tatcaaacgt tattcgaacc aagaacacac catccatctc tcttggaat gcttctagct 1380
ccggacattc gacatgaaag aaatgtgatt ttgcagtgtg ttcggtacat cattaaaaaa 1440
gacttttttg gactggatac taattctgcg aaaagtaaag atgtataggc atctggtgtt 1500
tcagcatata taactgaagc atgtgaaaca gtatcatcct cgttagtaga ggaaaacca 1560
aacctttttt tccgtcaaaa ttggatttgt aattaaattg taagcctcgt aggatgtatg 1620
ttggaatttt aagtctttcc tttggttcta tgcaaataaa aaaataactg attttttaag 1680
actgtgtctg tattgtttgg attgaatcta gtatttgcgt ggagaatttt ttctttgtat 1740
ttattttaat gtattgttct catgtaagaa tgactgatgt tgtgttagtt aagaattgaa 1800
gataggttta gcagtaaaga agaaagcttt taaaaggatt gattcagcta agcaaagttg 1860
ggcagagaaa tacagccatt ttgtttttaa tgcagaaaag gaagatgttc ttagcaagg 1920
gggaatattt taaaaataaa ccagatcaaa ttaatacaat cagaaggttt cgaaatgtaa 1980
atattcctta ttaagacat gttaaattc acctactagc acgacttaca tagctcaaat 2040
attgaatggt taaaatatta atacagatgg gccctcttta tgtttagata aaattgaagt 2100
acttaattga agctttttta aaattgtaaa gtaaatgaaa gctattgaga tctttttgtc 2160
tcctataata ccagggaatt tgagcttggt ttctagtcac tgtactagct gtagctattg 2220
gtctgtcctt ttgacatata gctaaaaggg actaaatttg taaaaaatta gtttgttata 2280
gttgaagatt aacttttctt aacattgtga ttattgaagt tcatgaatct tgctgtcaag 2340
gaagaaaggt aagaaagctg atagctcctc catgttggtg aaatcctctc cagaatcttg 2400
gaacacctgg catgtgacct tagtgacgtc acagacctga gatgaagatt catgttttag 2460
cagtgttttc cagccttgta cccaccatac agatctgttt attctgtttc accctactcc 2520
tccagtgagc cccatatttt gggaaattat ctgccttata cattaactaa ttcaattcat 2580
gtaacactgt tgagtgttta ctctttgtac ctctattgtg cctatattaa aggtatacaa 2640
ataaataagg ccatgtctga cttcaaggaa ctcagtttaa ttttgatata ttcaaagatg 2700
tgattcccaa ccaactcagg atgaagtaac tagtgttaca actgagttga tattctaaaa 2760
tataaccag tttgtacttt tattactagt tagcatcac attttatggc ttatgggtta 2820
ataaatgaat tcatggactc ctggactact ttcattgatg accatatctc cagggatgtt 2880
gttgatcccc aactgcctt aaggtatatt atagaaacag ttttattttc catttttctt 2940

```

```

gtttcctgat aataaatgta tttaggactg aaaatactcc tgagtactcc cctggctgta 3000
tgtctgacag tctttagcta tggtgactat tgtttatatt taatgggtat ttcagattcc 3060
aagtgtatatt aaaatttcta aggagatata atatagcctg tatggtttct actttatgga 3120
attatatggt caatatttgt aaatatttcta tgagttttgg gtgggtagag ggggtgctttg 3180
cctgttttgg gtacagggtt ttttggattt agcttgttaa ttgttcaaac tttctgcctt 3240
ctacattcct atcttattgt tcgtttaatc agtttctgaa atgtaagcat tacatgacta 3300
ttggtgagtt gtgcctttta taactgaaat actttacttt ttctcatatc ctctataatt 3360
gacttctatt ttccttaatc aaaccagctc tgggaaattt aatacattta tattaattga 3420
gattattaaa acatttggac tattaaaaaa aaaaaaaaaa aaa 3463

```

&lt;210&gt; 225

&lt;211&gt; 495

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 225

```

Met Ala Glu Pro Thr Ser Asp Phe Glu Thr Pro Ile Gly Trp His Ala
1      5      10      15
Ser Pro Glu Leu Thr Pro Thr Leu Gly Pro Leu Ser Asp Thr Ala Pro
20     25     30
Pro Arg Asp Arg Trp Met Phe Trp Ala Met Leu Pro Pro Pro Pro Pro
35     40     45
Pro Leu Thr Ser Ser Leu Pro Ala Ala Gly Ser Lys Pro Ser Ser Glu
50     55     60
Ser Gln Pro Pro Met Glu Ala Gln Ser Leu Pro Gly Ala Pro Pro Pro
65     70     75     80
Phe Asp Ala Gln Ile Leu Pro Gly Ala Gln Pro Pro Phe Asp Ala Gln
85     90     95
Ser Pro Leu Asp Ser Gln Pro Gln Pro Ser Gly Gln Pro Trp Asn Phe
100    105    110
His Ala Ser Thr Ser Trp Tyr Trp Arg Gln Ser Ser Asp Arg Phe Pro
115    120    125
Arg His Gln Lys Ser Phe Asn Pro Ala Val Lys Asn Ser Tyr Tyr Pro
130    135    140
Arg Lys Tyr Asp Ala Lys Phe Thr Asp Phe Ser Leu Pro Pro Ser Arg
145    150    155    160
Lys Gln Lys Lys Lys Lys Arg Lys Glu Pro Val Phe His Phe Phe Cys
165    170    175
Asp Thr Cys Asp Arg Gly Phe Lys Asn Gln Glu Lys Tyr Asp Lys His
180    185    190
Met Ser Glu His Thr Lys Cys Pro Glu Leu Asp Cys Ser Phe Thr Ala
195    200    205
His Glu Lys Ile Val Gln Phe His Trp Arg Asn Met His Ala Pro Gly
210    215    220
Met Lys Lys Ile Lys Leu Asp Thr Pro Glu Glu Ile Ala Arg Trp Arg
225    230    235    240
Glu Glu Arg Arg Lys Asn Tyr Pro Thr Leu Ala Asn Ile Glu Arg Lys
245    250    255
Lys Lys Leu Lys Leu Glu Lys Glu Lys Arg Gly Ala Val Leu Thr Thr
260    265    270
Thr Gln Tyr Gly Lys Met Lys Gly Met Ser Arg His Ser Gln Met Ala
275    280    285
Lys Ile Arg Ser Pro Gly Lys Asn His Lys Trp Lys Asn Asp Asn Ser
290    295    300
Arg Gln Arg Ala Val Thr Gly Ser Gly Ser His Leu Cys Asp Leu Lys
305    310    315    320
Leu Glu Gly Pro Pro Glu Ala Asn Ala Asp Pro Leu Gly Val Leu Ile
325    330    335

```

244

```

Asn Ser Asp Ser Glu Ser Asp Lys Glu Glu Lys Pro Gln His Ser Val
      340                      345                      350
Ile Pro Lys Glu Val Thr Pro Ala Leu Cys Ser Leu Met Ser Ser Tyr
      355                      360                      365
Gly Ser Leu Ser Gly Ser Glu Ser Glu Pro Glu Glu Thr Pro Ile Lys
      370                      375                      380
Thr Glu Ala Asp Val Leu Ala Glu Asn Gln Val Leu Asp Ser Ser Ala
      385                      390                      395                      400
Pro Lys Ser Pro Ser Gln Asp Val Lys Ala Thr Val Arg Asn Phe Ser
      405                      410                      415
Glu Ala Lys Ser Glu Asn Arg Lys Lys Ser Phe Glu Lys Thr Asn Pro
      420                      425                      430
Lys Arg Lys Lys Asp Tyr His Asn Tyr Gln Thr Leu Phe Glu Pro Arg
      435                      440                      445
Thr His His Pro Tyr Leu Leu Glu Met Leu Leu Ala Pro Asp Ile Arg
      450                      455                      460
His Glu Arg Asn Val Ile Leu Gln Cys Val Arg Tyr Ile Ile Lys Lys
      465                      470                      475                      480
Asp Phe Phe Gly Leu Asp Thr Asn Ser Ala Lys Ser Lys Asp Val
      485                      490                      495

```

<210> 226  
 <211> 942  
 <212> DNA  
 <213> Homo sapiens

```

<400> 226
atgagaattg cagtgatttg cttttgcctc ctaggcatca cctgtgccat accagttaaa 60
caggctgatt ctggaagttc tgaggaaaag cagctttaca acaaataccc agatgctgtg 120
gccacatggc taaaccctga cccatctcag aagcagaatc tcctagcccc acagaatgct 180
gtgtcctctg aagaaaccaa tgactttaaa caagagaccc ttccaagtaa gtccaacgaa 240
agccatgacc acatggatga tatggatgat gaagatgatg atgacatgtg ggacagccag 300
gactccattg actcgaacga ctctgatgat gtagatgaca ctgatgattc tcaccagtct 360
gatgagtctc accattctga tgaatctgat gaactggtca ctgattttcc caccggacctg 420
ccagcaaccg aagttttcac tccagttgtc cccacagtag acacatatga tggccgaggt 480
gatagtgtgg tttatggact gaggtcaaaa tctaagaagt ttgcgagacc tgacatccag 540
taccctgatg ctacagacga gcacatcacc tcacacatgg aaagcgagga gttgaatggt 600
gcatacaagg ccatccccgt tgcccaggac ctgaacgcgc cttctgattg ggacagccgt 660
gggaaggaca gttatgaaac gagtcagctg gatgaccaga gtgctgaagc ccacagccac 720
aagcagtcca gattatataa gcgaaagct aatgatgaga gcaatgagca ttccgatgtg 780
attgatagtc aggaactttc caaagtcagc cgtgaattcc acagccatga atttcacagc 840
catgaagata tgctgggttg agaccccaaa agtaaggaag aagataaaca cctgaaattt 900
cgtattttctc atgaattaga tagtgcattc tctgaggtca at 942

```

<210> 227  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

```

<400> 227
Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
  1           5           10           15
Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu
      20           25           30
Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro
      35           40           45
Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Asn Ala Val Ser Ser Glu

```

245

50		55		60
Glu Thr Asn Asp Phe Lys Gln Glu Thr Leu Pro Ser Lys Ser Asn Glu				
65		70		80
Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp Asp His				
	85		90	95
Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp Val Asp				
	100		105	110
Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser Asp Glu				
	115		120	125
Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala Thr Glu				
	130		135	140
Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly Arg Gly				
	145		150	155
Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe Arg Arg				
	165		170	175
Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu His Ile Thr Ser His				
	180		185	190
Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro Val Ala				
	195		200	205
Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys Asp Ser				
	210		215	220
Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Ala His Ser His				
	225		230	235
Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser Asn Glu				
	245		250	255
His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser Arg Glu				
	260		265	270
Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val Val Asp				
	275		280	285
Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile Ser His				
	290		295	300
Glu Leu Asp Ser Ala Ser Ser Glu Val Asn				
305		310		

&lt;210&gt; 228

&lt;211&gt; 1524

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 228

```

gcagagcaca gcatcgtcgg gaccagactc gtctcaggcc agttgcagcc ttctcagcca 60
aacgccgacc aaggaaaact cactaccatg agaattgcag tgatttgctt ttgcctccta 120
ggcatcacct gtgccatacc agttaaacag gctgattctg gaagttctga ggaaaagcag 180
ctttacaaca aatacccaga tgctgtggcc acatggctaa accctgaccc atctcagaag 240
cagaatctcc tagcccacaca gacccttcca agtaagtcca acgaaagcca tgaccacatg 300
gatgatatgg atgatgaaga tgatgatgac catgtggaca gccaggactc cattgactcg 360
aacgactctg atgatgtaga tgacactgat gattctcacc agtctgatga gtctcaccat 420
tctgatgaat ctgatgaact ggtcactgat tttcccacgg acctgccagc aaccgaagtt 480
ttcactccag ttgtcccccac agtagacaca tatgatggcc gaggtgatag tgtggtttat 540
ggactgaggt caaaatctaa gaagtttcgc agacctgaca tccagtaccc tgatgctaca 600
gacgaggaca tcacctcaca catggaaage gaggagtga atggtgcata caaggccatc 660
cccgttgccc aggacctgaa cgcgcttct gattgggaca gccgtgggaa ggacagttat 720
gaaacgagtc agctggatga ccagagtgtt gaaaccaca gccacaagca gtccagatta 780
tataagcgga aagccaatga tgagagcaat gagcattccg atgtgattga tagtcaggaa 840
ctttcaaag tcagccgtga attccacagc catgaatttc acagccatga agatatgctg 900
gttgtagacc ccaaaagtaa ggaagaagat aaacacctga aatttcgtat ttctcatgaa 960
ttagatagtg catcttctga ggtcaattaa aaggagaaaa aatacaattt ctacttttgc 1020

```

```

atttagtcaa aagaaaaaat gctttatagc aaaatgaaag agaacatgaa atgcttcctt 1080
ctcagtttat tgggtgaaatg tgtatctatt tgagtctgga aataactaat gtgtttgata 1140
attagtttag tttgtggctt catggaaact ccctgtaaac taaaagcttc agggttatgt 1200
ctatgttcat tctatagaag aaatgcaaac tatcactgta ttttaataatt tgttattctc 1260
tcatgaatag aaatttatgt agaagcaaac aaaatacttt taccactta aaaagagaat 1320
ataacatttt atgtcactat aatcttttgt tttttaagtt agtgtatatt ttgttgtgat 1380
tatctttttg tgggtggaat aaatctttta tcttgaatgt aataagaatt tgggtggtgc 1440
aattgcttat ttgttttccc acggttggtcc agcaattaat aaaacataac cttttttact 1500
gcctaaaaaa aaaaaaaaaa aaaa                                     1524

```

&lt;210&gt; 229

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 229

```

Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
 1          5          10          15
Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu
 20          25          30
Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro
 35          40          45
Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser
 50          55          60
Asn Glu Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp
 65          70          75          80
Asp His Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp
 85          90          95
Val Asp Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser
100          105          110
Asp Glu Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala
115          120          125
Thr Glu Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly
130          135          140
Arg Gly Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe
145          150          155          160
Arg Arg Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr
165          170          175
Ser His Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro
180          185          190
Val Ala Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys
195          200          205
Asp Ser Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His
210          215          220
Ser His Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser
225          230          235          240
Asn Glu His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser
245          250          255
Arg Glu Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val
260          265          270
Val Asp Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile
275          280          285
Ser His Glu Leu Asp Ser Ala Ser Ser Glu Val Asn
290          295          300

```

&lt;210&gt; 230

&lt;211&gt; 861



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 230

```

atgagaattg cagtgatttg cttttgcctc ctaggcatca cctgtgccat accagttaaa 60
caggctgatt ctggaagttc tgaggaaaag cagaatgctg tgtcctctga agaaaccaat 120
gacttttaaac aagagaccct tccaagtaag tccaacgaaa gccatgacca catggatgat 180
atggatgatg aagatgatga tgaccatgtg gacagccagg actccattga ctggaacgac 240
tctgatgatg tagatgacac tgatgattct caccagtctg atgagtctca ccattctgat 300
gaatctgatg aactggtcac tgattttccc acggacctgc cagcaaccga agttttcact 360
ccagttgtcc ccacagtaga cacatatgat ggccgaggtg atagtgtggt ttatggactg 420
aggtcaaaaat ctaagaagtt tcgcagacct gacatccagt accctgatgc tacagacgag 480
cacatcacct cacacatgga aagcgaggag ttgaatggtg catacaaggc catccccgtt 540
gccagggacc tgaacgcgcc ttctgattgg gacagccgtg ggaaggacag ttatgaaacg 600
agtcagctgg atgaccagag tgctgaagcc cacagccaca agcagtcag attatataag 660
cggaaagcta atgatgagag caatgagcat tccgatgtga ttgatagtca ggaactttcc 720
aaagtcagcc gtgaattcca cagccatgaa ttccacagcc atgaagatat gctggttgta 780
gaccccaaaa gtaagggaaga agataaacac ctgaaatttc gtatttctca tgaattagat 840
agtgcattct ctgagggtcaa t                                     861

```

&lt;210&gt; 231

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 231

```

Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
 1           5           10           15
Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Asn
          20          25          30
Ala Val Ser Ser Glu Glu Thr Asn Asp Phe Lys Gln Glu Thr Leu Pro
          35          40          45
Ser Lys Ser Asn Glu Ser His Asp His Met Asp Asp Met Asp Asp Glu
          50          55          60
Asp Asp Asp Asp His Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp
65          70          75          80
Ser Asp Asp Val Asp Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser
          85          90          95
His His Ser Asp Glu Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp
          100         105         110
Leu Pro Ala Thr Glu Val Phe Thr Pro Val Val Pro Thr Val Asp Thr
          115         120         125
Tyr Asp Gly Arg Gly Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser
          130         135         140
Lys Lys Phe Arg Arg Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu
145         150         155         160
His Ile Thr Ser His Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys
          165         170         175
Ala Ile Pro Val Ala Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser
          180         185         190
Arg Gly Lys Asp Ser Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala
          195         200         205
Glu Ala His Ser His Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn
          210         215         220
Asp Glu Ser Asn Glu His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser
225         230         235         240
Lys Val Ser Arg Glu Phe His Ser His Glu Phe His Ser His Glu Asp
          245         250         255

```

248

Met Leu Val Val Asp Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys  
                   260                  265                  270  
 Phe Arg Ile Ser His Glu Leu Asp Ser Ala Ser Ser Glu Val Asn  
                   275                  280                  285

<210> 232  
 <211> 838  
 <212> DNA  
 <213> Homo sapiens

<400> 232  
 ctgagagcca cccacagccg cagccatgct gtgcctcctg ctcaccctgg gcgtggccct 60  
 ggtctgtggt gtcccggcca tggacatccc ccagaccaag caggacctgg agctcccaa 120  
 gttggcaggg acctggcact ccatggccat ggcgaccaac aacatctccc tcatggcgac 180  
 actgaaggcc cctctgaggg tccacatcac ctactgttg cccacccccg aggacaacct 240  
 ggagatcggt ctgcacagat gggagaacaa cagctgtggt gagaagaagg tccttgagga 300  
 gaagactgag aatccaaaga agttcaagat caactatacg gtggcgaacg aggccacgct 360  
 gctcgatact gactacgaca atttcctggt tctctgccta caggacacca ccacccccat 420  
 ccagagcatg atgtgccagt acctggccag agtcctggtg gaggacgatg agatcatgca 480  
 gggattcatc agggctttca ggcccctgcc caggcaccta tggacttgc tggacttgaa 540  
 acagatggaa gagccgtgcc gtttctaggt gagctcctgc ctggtcctgc ctcctggctc 600  
 acctccgcct ccaggaagac cagactccca cccttcaca cctccagagc agtgggactt 660  
 cctcctgccc tttcaaagaa taaccacagc tcagaagacg atgacgtggt catctgtgtc 720  
 gccatccccct tctgtgtgca cacctgcacc acggccatgg ggaggctgct ccctgggggc 780  
 agagtctctg gcagagggtta ttaataaacc cttggagcat gaaaaaaaaa aaaaaaaa 838

<210> 233  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

<400> 233  
 Met Leu Cys Leu Leu Thr Leu Gly Val Ala Leu Val Cys Gly Val  
   1                  5                  10                  15  
 Pro Ala Met Asp Ile Pro Gln Thr Lys Gln Asp Leu Glu Leu Pro Lys  
                   20                  25                  30  
 Leu Ala Gly Thr Trp His Ser Met Ala Met Ala Thr Asn Asn Ile Ser  
                   35                  40                  45  
 Leu Met Ala Thr Leu Lys Ala Pro Leu Arg Val His Ile Thr Ser Leu  
                   50                  55                  60  
 Leu Pro Thr Pro Glu Asp Asn Leu Glu Ile Val Leu His Arg Trp Glu  
   65                  70                  75                  80  
 Asn Asn Ser Cys Val Glu Lys Lys Val Leu Gly Glu Lys Thr Glu Asn  
                   85                  90                  95  
 Pro Lys Lys Phe Lys Ile Asn Tyr Thr Val Ala Asn Glu Ala Thr Leu  
                   100                  105                  110  
 Leu Asp Thr Asp Tyr Asp Asn Phe Leu Phe Leu Cys Leu Gln Asp Thr  
                   115                  120                  125  
 Thr Thr Pro Ile Gln Ser Met Met Cys Gln Tyr Leu Ala Arg Val Leu  
                   130                  135                  140  
 Val Glu Asp Asp Glu Ile Met Gln Gly Phe Ile Arg Ala Phe Arg Pro  
   145                  150                  155                  160  
 Leu Pro Arg His Leu Trp Tyr Leu Leu Asp Leu Lys Gln Met Glu Glu  
                   165                  170                  175  
 Pro Cys Arg Phe  
                   180

<210> 234  
 <211> 851  
 <212> DNA  
 <213> Homo sapiens

<400> 234  
 ggctccagag ctccagagcca cccacagccc cagccatgct gtgcctcctg ctcaccctgg 60  
 gcgtggccct ggtctgtggt gtcccggcca tggacatccc ccagaccaag caggacctgg 120  
 agctcccaaa gttggcaggg acctggcact ccatggccat ggcgaccaac aacatctccc 180  
 tcatggcgac actgaaggcc cctctgaggg tccacatcac ctccactgtt cccacccccg 240  
 aggacaacct ggagatcggt ctgcacagat gggagaacaa cagctgtgtt gagaagaagg 300  
 tccttgagga gaagactgag aatccaaaga agttcaagat caactatacg gtggcgaacg 360  
 aggccacgct gctcgatact gactacgaca atttcctggt tctctgccta caggacacca 420  
 ccacccccat ccagagcatg atgtgccagt acctggccag agtcctggtg gaggacgatg 480  
 agatcatgca gggattcatc agygctttca ggcccctgcc caggcaccta tggtaacttg 540  
 tggacttgaa acagatggaa gagccgtgcc gtttctaggt gagctcctgc ctggtcctgc 600  
 ctctgggtg acctgtaaac ccaacagctc acctccgct ccaggaagac cagactccca 660  
 cccttcaca cctccagagc agtgggactt cctcctgccc tttcaaagaa taaccacagc 720  
 tcagaagacg atgacgtggt catctgtgtc gccatcccct tcctgtgca cacctgcacc 780  
 acggccatgg ggaggctgct ccctgggggc agagtctctg gcagagggtta ttaataaacc 840  
 cttggagcat g 851

<210> 235  
 <211> 811  
 <212> DNA  
 <213> Homo sapiens

<400> 235  
 catccctctg gctccagagc tcagagccac ccacagccgc agccatgctg tgcctcctgc 60  
 tcaccctggg cgtggccctg gtctgtggtg tcccggccat ggacatcccc cagaccaagc 120  
 aggacctgga gctcccaaag ttggcagggc cctggcactc catggccatg gcgaccaaca 180  
 acatctccct catggcgaca ctgaaggccc ctctgagggt ccacatcacc tccactgttg 240  
 ccacccccga ggacaacctg gagatcggtc tgcacagatg ggagaacaac agctgtgttg 300  
 agaagaaggt ccttgagag agactggga atccaaagaa gttcaagatc aactatacgg 360  
 tggcgaacga ggccacgctg ctcgatactg actacgacaa tttcctgttt ctctgcctac 420  
 aggacaccac ccccccatc cagagcatga tgtgccagta cctggccaga gtccctggtg 480  
 aggacgatga gatcatgcag ggattcatca gggctttcag gccctgccc aggcacctat 540  
 ggtacttgct ggacttgaaa cagatggaag agccgtgccg tttctagctc acctccgct 600  
 ccaggaagac cagactccca cccttcaca cctccagagc agtgggactt cctcctgccc 660  
 tttcaaagaa taaccacagc tcagaagacg atgacgtggt catctgtgtc gccatcccct 720  
 tcctgtgca cacctgcacc attgccatgg ggaggctgct ccctgggggc agagtctctg 780  
 gcagagggtta ttaataaacc cttggagcat g 811

<210> 236  
 <211> 850  
 <212> DNA  
 <213> Homo sapiens

<400> 236  
 catccctctg gctccagagc tcagagccac ccacagccgc agccatgctg tgcctcctgc 60  
 tcaccctggg cgtggccctg gtctgtggtg tcccggccat ggacatcccc cagaccaagc 120  
 aggacctgga gctcccaaag ttggcagggc cctggcactc catggccatg gcgaccaaca 180  
 acatctccct catggcgaca ctgaaggccc ctctgagggt ccacatcacc tccactgttg 240  
 ccacccccga ggacaacctg gagatcggtc tgcacagatg ggagaacaac agctgtgttg 300  
 agaagaaggt ccttgagag aagactgrga atccaaagaa gttcaagatc aactatacgg 360  
 tggcgaacga ggccacgctg ctcgatactg actacgacaa tttcctgttt ctctgcctac 420  
 aggacaccac ccccccatc cagagcatga tgtgccagta cctggccaga gtccctggtg 480

250

```

aggacgatga gatcatgcag ggattcatca gggctttcag gcccctgccc aggcacctat 540
ggtacttgct ggacttgaaa cagatggaag agccgtgccg tttctagtga cctgtaaacc 600
caacagctca cctccgcctc caggaagacc agactccac ccttccacac ctccagagca 660
gtgggacttc ctctgacctt ttcaaagaat aaccacagct cagaagacga tgacgtggtc 720
atctgtgtcg ccatcccttt cctgctgcac acctgcacca cggccatggg gaggtgtctc 780
cctgggggca gagtctctgg cagaggttat taataaacc ttggagcatg aaaaaaaaaa 840
aaaaaaaaa                                     850

```

&lt;210&gt; 237

&lt;211&gt; 598

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 237

```

catccctctg gctccagagc tcagagccac ccacagccgc agccatgctg tgcctcctgc 60
tcaccctggg cgtggccctg gtctgtggtg tcccggccat ggacatcccc cagaccaagc 120
aggacctgga gctcccaaag gacaccacca ccccatccca gagcatgatg tgccagtacc 180
tgccagagat cctggtggag gacgatgaga tcatgcaggg attcatcagg gctttcaggc 240
ccctgcccag gcacctatgg tacttgctgg acttgaaca gatggaagag ccgtgccgtt 300
tctaggtgag ctctgcctg gtctgcctc ctgggtgacc tgtaaaccac acagctcacc 360
tccgctcca ggaagaccag actcccaccc ttccacacct ccagagcagt gggacttctc 420
cctgcccttt caaagaataa ccacagctca gaagacgatg acgtggtcat ctgtgtcgcc 480
atccctctcc tgctgcacac ctgcaccacg gccatgggga ggctgctccc tgggggcaga 540
gtctctggca gaggttatta ataaaccctt ggagcatgaa aaaaaaaaaa aaaaaaaa 598

```

&lt;210&gt; 238

&lt;211&gt; 86

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 238

```

Met Leu Cys Leu Leu Leu Thr Leu Gly Val Ala Leu Val Cys Gly Val
 1             5             10            15
Pro Ala Met Asp Ile Pro Gln Thr Lys Gln Asp Leu Glu Leu Pro Lys
      20             25            30
Asp Thr Thr Thr Pro Ile Gln Ser Met Met Cys Gln Tyr Leu Ala Arg
      35             40            45
Val Leu Val Glu Asp Asp Glu Ile Met Gln Gly Phe Ile Arg Ala Phe
      50             55            60
Arg Pro Leu Pro Arg His Leu Trp Tyr Leu Leu Asp Leu Lys Gln Met
      65             70            75            80
Glu Glu Pro Cys Arg Phe
                        85

```

&lt;210&gt; 239

&lt;211&gt; 814

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 239

```

catccctctg gctccagagc tcagagccac ccacagccgc agccatgctg tgcctcctgc 60
tcaccctggg cgtggccctg gtctgtggtg tcccggccat ggacatcccc cagaccaagc 120
aggacctgga gacactgaag gcccctctga gggccacat cacctcactg ttgccacccc 180
ccgaggacaa cctggagatc gttctgcaca gatgggagaa caacagctgt gttgagaaga 240
aggtccttg agagaagact grgaatccaa agaagttcaa gatcaactat acggtggcga 300
acgaggccac gctgctcgat actgactacg acaatttct gtttctctgc ctacaggaca 360
ccaccacccc catccagagc atgatgtgcc agtacctggc cagagtcctg gtggaggacg 420

```

251

```

atgagatcat gcagggattc atcagggcct tcaggcccct gccaggcac ctatgg tact 480
tgctggactt gaaacagatg gaagagccgt gccgtttcta ggtgagctcc tgcctgg tcc 540
tgcctcctgg gtgacctgta aaccaacag ctcacctccg cctccaggaa gaccagactc 600
ccacccttcc acacctccag agcagtggga cttcctcctg ccctttcaaa gaataaccac 660
agctcagaag acgatgacgt ggtcatctgt gtcgccatcc ccttcctgct gcacacctgc 720
accacggcca tggggaggct gtcacctggg ggcagagtct ctggcagagg ttattaataa 780
acccttgagg catgaaaaaa aaaaaaaaaa aaaa 814

```

&lt;210&gt; 240

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 240

```

Met Leu Cys Leu Leu Leu Thr Leu Gly Val Ala Leu Val Cys Gly Val
1      5      10      15
Pro Ala Met Asp Ile Pro Gln Thr Lys Gln Asp Leu Glu Leu Pro Lys
20     25     30
Ala Pro Leu Arg Val His Ile Thr Ser Leu Leu Pro Thr Pro Glu Asp
35     40     45
Asn Leu Glu Ile Val Leu His Arg Trp Glu Asn Asn Ser Cys Val Glu
50     55     60
Lys Lys Val Leu Gly Glu Lys Thr Glu Asn Pro Lys Lys Phe Lys Ile
65     70     75     80
Asn Tyr Thr Val Ala Asn Glu Ala Thr Leu Leu Asp Thr Asp Tyr Asp
85     90     95
Asn Phe Leu Phe Leu Cys Leu Gln Asp Thr Thr Thr Pro Ile Gln Ser
100    105    110
Met Met Cys Gln Tyr Leu Ala Arg Val Leu Val Glu Asp Asp Glu Ile
115    120    125
Met Gln Gly Phe Ile Arg Ala Phe Arg Pro Leu Pro Arg His Leu Trp
130    135    140
Tyr Leu Leu Asp Leu Lys Gln Met Glu Glu Pro Cys Arg Phe
145    150    155

```

&lt;210&gt; 241

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 241

```

Met Leu Cys Leu Leu Leu Thr Leu Gly Val Ala Leu Val Cys Gly Val
1      5      10      15
Pro Ala Met Asp Ile Pro Gln Thr Lys Gln Asp Leu Glu Thr Leu Lys
20     25     30
Ala Pro Leu Arg Val His Ile Thr Ser Leu Leu Pro Thr Pro Glu Asp
35     40     45
Asn Leu Glu Ile Val Leu His Arg Trp Glu Asn Asn Ser Cys Val Glu
50     55     60
Lys Lys Val Leu Gly Glu Lys Thr Glu Asn Pro Lys Lys Phe Lys Ile
65     70     75     80
Asn Tyr Thr Val Ala Asn Glu Ala Thr Leu Leu Asp Thr Asp Tyr Asp
85     90     95
Asn Phe Leu Phe Leu Cys Leu Gln Asp Thr Thr Thr Pro Ile Gln Ser
100    105    110
Met Met Cys Gln Tyr Leu Ala Arg Val Leu Val Glu Asp Asp Glu Ile
115    120    125

```

Met Gln Gly Phe Ile Arg Ala Phe Arg Pro Leu Pro Arg His Leu Trp  
 130 135 140  
 Tyr Leu Leu Asp Leu Lys Gln Met Glu Glu Pro Cys Arg Phe  
 145 150 155

<210> 242  
 <211> 2707  
 <212> DNA  
 <213> Homo sapiens

<400> 242  
 ggacagaggc ttcagaagga ggagagacac cgggcccagg gcaccctcgc gggcggaccc 60  
 aagcagttag ggctgcagc cggccggcca gggcagcgcc aggcgcggcc cggacctacg 120  
 ggaggaagcc ccgagccctc ggcggtgtgc gagcgactcc ccggcgatgc ctcaaacctc 180  
 catcagatct ggccatggag ggctgaacca gctgggaggg gcctttgtga atggcagacc 240  
 tctgccggaa gtgtccgcc agcgcatcgt agacctggcc caccaggggtg taaggccctg 300  
 cgacatctct cgccagctcc gcgtcagcca tggctgcgtc agcaagatcc ttggcaggta 360  
 ctacgagact ggagcatcc ggcttgaggt gatagggggc tccaagccca aggtggccac 420  
 ccccaagggtg gtggagaaga ttggggacta caaacgccag aaccctacca tgtttgcctg 480  
 ggagatccga gaccggctcc tggctgaggg cgtctgtgac aatgacactg tgcccagtg 540  
 cagctccatt aatagaatca tccggaccaaa agtgcagcaa ccattcaacc tccctatgga 600  
 cagctgcgtg gccaccaagt ccctgagtc cggacacacg ctgatcccca gctcagctgt 660  
 aactcccccg gactcaccac agtcggattc cctgggctcc acctactcca tcaatgggct 720  
 cctgggcatc gctcagcctg gcagcgacaa gaggaaaatg gatgacagt atcaggatag 780  
 ctgccgacta agcattgact cacagagcag cagcagcgga ccccgaaagc accttcgcac 840  
 ggatgccttc agccagcacc acctcgagcc gctcgagtg ccatttgagc ggcagcacta 900  
 cccagtgccc tatgcctccc ccagccacac caaaggcgag cagggcctct acccgctgcc 960  
 cttgctcaac agcaccctgg acgacgggaa gggcaccctg accccttcca acacgccact 1020  
 ggggcgcaac ctctcgactc accagaccta ccccggtgtg gcagatcctc actcaccctc 1080  
 cgccataaag caggaaaccc ccgaggtgtc cagttctagc tccaccctt cctctttatc 1140  
 tagctccgcc tttttggatc tgcagcaagt cggctccggg gtcccgcctt tcaatgcctt 1200  
 tccccatgct gcctccgtgt acgggcagtt cacgggccag gccctcctct cagggcgaga 1260  
 gatggtgggg cccacgctgc ccgatacccc accccacatc cccaccagcg gacagggcag 1320  
 ctatgcctcc tctgccatcg caggcatggt ggcaggaagt gaatactctg gcaatgccta 1380  
 tggccacacc cctactcct cctacagcga ggctggcgcc tcccccaact ccagcttgct 1440  
 gagttcccca tattattaca gttccacatc aaggccgagt gcaccgccc cactggccac 1500  
 ggctttgac catctgtagt tgccatgggg acagtgggag cgactgagca acaggaggac 1560  
 tcagcctggg acaggcccca gagagtcaca caaaggaaatc tttatttatt acatgaaaaa 1620  
 taaccacaag tccagcattg cggcacactc cctgtgtggt taatttaagt aaccatgaaa 1680  
 gacaggatga ccttggaaca ggccaaactg tctccaaga ctcttaatg aggggcagga 1740  
 gtcccaggga aagagaacca tgccatgctg aaaaagacaa aattgaagaa gaaatgtagc 1800  
 ccccagccgg taccaccaa aggagagaag aagcaatagc cgaggaaactt ggggggatgg 1860  
 cgaatggttc ctgcccgggc ccaaggggtg cacagggcac ctccatggct ccattattaa 1920  
 cacaactcta gcaattatgg accataagca ctccctcca gcccaagc cagagcctgg 1980  
 tgccgaggct ctctcacca gccaccagg gactcacctc cctcagcctc ccgctgccc 2040  
 cacacggagg ctctggctgt cctctttctc cactccattt gcttggctct ttctacacct 2100  
 ccctcttggg catgggctga gggctggagc gactccctca gaaattccac caggctgtca 2160  
 gctgacctct tttgcctgct gctgtgaagg tatagcacca cccaggtcc tctgcagtg 2220  
 cggcatcccc ttggcagctg ccgtcagcca ggccagcccc agggagctta aaacagacat 2280  
 tccacagggc ctgggcccct gggaggtgag gtgtggtgtg cggcttcacc cagggcagaa 2340  
 caaggcagaa tgcaggaaa cccgcttccc ctccctgaca gtcctgccca agccaaatgt 2400  
 gcttctgca gctcagccc accagctact gaagggaccc aaggcacccc ctgaagccag 2460  
 cgatagaggg tccctctctg ctcccagca gctcctgccc ccaaggcctg actgtatata 2520  
 ctgtcaatga aactttgttt gggtaagct tcttctttc taccocccag actttggcct 2580  
 ctgagtgaat tctctctctt tgccctgtgg ggctctctc cttgatgctt ctttctttt 2640  
 ttaaagacaa cctgccatta ccacatgact caataaacca ttgctcttca aaaaaaaaaa 2700  
 aaaaaaa 2707

<210> 243  
 <211> 450  
 <212> PRT  
 <213> Homo sapiens

<400> 243

```

Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu
 1           5           10           15
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln
          20           25           30
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser
          35           40           45
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg
          50           55           60
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys
65          70          75          80
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys
          85          90          95
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu
          100         105         110
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile
          115         120         125
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met
          130         135         140
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile
145         150         155         160
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu
          165         170         175
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly
          180         185         190
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu
          195         200         205
Ser Ile Asp Ser Gln Ser Ser Ser Gly Pro Arg Lys His Leu Arg
          210         215         220
Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe
225         230         235         240
Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys
          245         250         255
Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp
          260         265         270
Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn
          275         280         285
Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Asp Pro His Ser Pro
          290         295         300
Phe Ala Ile Lys Gln Glu Thr Pro Glu Val Ser Ser Ser Ser Thr
305         310         315         320
Pro Ser Ser Leu Ser Ser Ser Ala Phe Leu Asp Leu Gln Gln Val Gly
          325         330         335
Ser Gly Val Pro Pro Phe Asn Ala Phe Pro His Ala Ala Ser Val Tyr
          340         345         350
Gly Gln Phe Thr Gly Gln Ala Leu Leu Ser Gly Arg Glu Met Val Gly
          355         360         365
Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly
          370         375         380
Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Gly Ser Glu Tyr
385         390         395         400
Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu Ala

```

254

	405		410		415
Trp Arg Phe	Pro Asn Ser Ser Leu	Leu Ser Ser	Pro Tyr Tyr Tyr Ser		
	420	425	430		
Ser Thr Ser	Arg Pro Ser Ala Pro	Pro Thr Thr	Ala Thr Ala Phe Asp		
	435	440	445		
His Leu					
450					

<210> 244  
 <211> 2381  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(2381)  
 <223> n = A,T,C or G

<400> 244

```

gaattcggcg atgcctcaca actccatcag atctggccat ggagggctga accagctggg 60
aggggccttt gtgaatggca gacctctgcc ggaagtggtc cgccagcgca tcgtagacct 120
ggcccaccag ggtgtaaggc cctgcgacat ctctcgccag ctccgcgtca gccatggttg 180
cgtcagcaag atccttggca ggtactacga gactggcagc atccggcctg gagtgatagg 240
gggctccaag cccaaggttg ccaccccaa ggtggtggag aagattgggg actacaaacg 300
ccagaaccct accatgtttg cctgggagat ccgagaccgg ctccctggctg agggcgtctg 360
tgacaatgac actgtgcccc gtgtcagctc cattaataga atcatccgga ccaaagtga 420
gcaaccattc aacctcccta tggacagctg cgtggccacc aagtccctga gtcccggaca 480
cacgctgata cccagctcag ctgtaactcc ccggagtcga cccagtcgg attccctggg 540
ctccacctac tccatcaatg ggctcctggg catcgctcag cctggcagcg acaagaggaa 600
aatggatgac agtgatcagg atagctgccg actaagcatt gactcacaga gcagcagcag 660
cggaccccca aagcaccttc gcacggatgc cttcagccag caccacctcg agccgctcga 720
gtgcccattt gagcggcagc actaccaga ggcctatgcc tccccagcc acaccaaagg 780
cgagcagggc ctctaccgcg tgcccttgct caacagcacc ctggacgacg ggaaggccac 840
cctgaccctt tccaacacgc cactggggcg caacctctcg actcaccaga cctaccccg 900
ggtggcaggg cgagagatgg tggggccccc gctgcccgga taccaccccc acatccccac 960
cagcggacag ggcagctatg cctcctctgc catcgaggc atggtggcag gaagtgaata 1020
ctctggcaat gcctatggcc acacccccta ctctcctac agcgaggcct ggggcttccc 1080
caactccagc ttgtgagtt ccccatatta ttacagttcc acatcaaggc cgagtgcacc 1140
gcccaccact gccacggcct ttgaccatct gtagttgccg tggggacagt gggagcgact 1200
gagcaacagg aggactcagc ctgggacagg cccagagag tcacacaaag gaatctttat 1260
tattacatga aaaataacca caagtccagc attgcggcac actccctgtg tggttaattt 1320
aatgaacat gaaagacagg atgaccttg acaaggccaa actgtcctcc aagactcctt 1380
aatgaggggc aggagtccca gggaaagaga accatgccat gctgaaaaag acaaaattga 1440
agaagaaatg tagccccagc cggtaaccctc caaaggagag aagaagcaat agccgaggaa 1500
cttgggggga tggcgaatgg ttcttgcccg ggcccaaggg tgcacagggc acctccatgg 1560
ctccattatt aacacaactc tagcaattat ggaccataag cacttccctc cagcccacaa 1620
gtcacagcct ggtgcccagg ctctgtcac cagccacca gggagtcacc tccctcagcc 1680
tcccgcctgc cccacacgga ggctctggct gtctctttc ctccactcca tttgcttggc 1740
tctttctaca cctccctctt ggatgggctg agggctggag cgagtccctc agaaattcca 1800
ccaggetgtc agctgacctc tttttcctgc tgctgtgaag gtatagcacc ancccaggte 1860
ctcctgcagt ggggcattccc cttggcagct gccgtcagcc agggcagccc caggagctt 1920
aaaacagaca ttccacaggg cctgggcccc tgggaggtga ggtgtggtgt gcggcttcac 1980
ccagggcaga acaaggcaga atcgcaggaa acccgnttc cccttctga cagctcctgc 2040
caagccaaat gtgcttcctg cagctcacgc ccaccangct actgaaggga cccaaggcca 2100
ccccnntgaa gccagcgata ganggggtccc tctctgntc ccagcagct cctgccccca 2160
naggcctgac tgtatatact gtaaataaaa ctttgtttgg gtcaagcttc cttctttcta 2220
accccnaga ctttggcctc tgagtgaat gtctctcttt gccctgtggg gcttctctcc 2280

```



255

```
tttgatgcttc tttctttttt taaagacaac ctgccattac cacatgactc aataaaccat 2340
tgctcttcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a                                2381
```

```
<210> 245
<211> 387
<212> PRT
<213> Homo sapiens
```

<400> 245

[illegible]

385

&lt;210&gt; 246

&lt;211&gt; 387

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 246

```

Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu
 1           5           10           15
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln
      20           25           30
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser
      35           40           45
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg
      50           55           60
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys
      65           70           75           80
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys
      85           90           95
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu
      100          105          110
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile
      115          120          125
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met
      130          135          140
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile
      145          150          155          160
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu
      165          170          175
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly
      180          185          190
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu
      195          200          205
Ser Ile Asp Ser Gln Ser Ser Ser Gly Pro Arg Lys His Leu Arg
      210          215          220
Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe
      225          230          235          240
Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys
      245          250          255
Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp
      260          265          270
Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn
      275          280          285
Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Gly Arg Glu Met Val
      290          295          300
Gly Pro Thr Leu Pro Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln
      305          310          315          320
Gly Ser Tyr Ala Ser Ser Ala Ile Ala Gly Met Val Ala Gly Ser Glu
      325          330          335
Tyr Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu
      340          345          350
Ala Trp Gly Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr Tyr Tyr
      355          360          365
Ser Ser Thr Ser Arg Pro Ser Ala Pro Pro Thr Thr Ala Thr Ala Phe
      370          375          380
Asp His Leu

```

385

<210> 247  
 <211> 2641  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(2641)  
 <223> n = A,T,C or G

<400> 247  
 ttcagaagga ggagagacac cgggcccagg gcaccctcgc gggcgggagg acccaagcag 60  
 tgagggcctg cagccggcgg gccagggcag cggcaggcgc ggcccggacc tacgggagga 120  
 agccccgagc cctcggcggg ctgcgagcga ctccccggcg atgcctcaca actccatcag 180  
 atctggccat ggagggtgta accagctggg aggggccttt gtgaatggca gacctctgcc 240  
 ggaagtggctc cgccagcgca tcgtagacct ggcccaccag ggtgtaaggc cctgcgacat 300  
 ctctcgccag ctccgcgtca gccatggctg cgtcagcaag atccttggca ggtactacga 360  
 gactggcagc atccggcctg gactgatagg gggctccaag cccaagggtg ccacccccaa 420  
 ggtggtggag aagattgggg actacaaacg ccagaaccct accatgtttg cctgggagat 480  
 ccgagaccgg ctctggctg agggcgtctg tgacaatgac actgtgcca gtgtcagctc 540  
 cattaataga atcatccgga ccaaagtgcg gcaaccattc aacctcccta tggacagctg 600  
 cgtggccacc aagtccctga gtcccggaca cacgctgac cccagctcag ctgtaactcc 660  
 cccggagtca cccagctggg attccctggg ctccacctac tccatcaatg ggctcctggg 720  
 catcgctcag cctggcagcg acaagaggaa aatggatgac agtgatcagg atagctgccg 780  
 actaagcatt gactcacaga gcagcagcag cggaccccga aagcaccttc gcacggatgc 840  
 cttcagccag caccacctcg agccgctcga gtgcccattt gagcggcagc actaccaga 900  
 ggcctatgcc tccccagcc acaccaaagg cgagcagggc ctctaccgcg tggccttgct 960  
 caacagcacc ctggacgacg ggaaggccac cctgaccctt tccaacacgc cactggggcg 1020  
 caacctctcg actcaccaga cctaccccggt ggtggcagct ccgccctttt ggatctgcag 1080  
 caagtccggt ccgggggtccc gcccttcaat gcctttcccc atgctgcctc cgtgtacggg 1140  
 cagttcacgg gccaggccct cctctcaggg cgagagatgg tggggccac gctgcccgga 1200  
 taccacccc acatcccac cagcggacag ggcagctatg cctcctctgc catcgaggc 1260  
 atggtggcag gaagtgaata ctctggcaat gcctatggc acacccccta ctctcctac 1320  
 agcgaggcct gggtcttccc caactccagc ttgctgagtt ccccatatta ttacagttcc 1380  
 acatcaaggc cgagtgcacc gccaccact gccacggcct ttgacctct gtagtggca 1440  
 tggggacagt gggagcgact gagcaacagg aggactcagc ctgggacagg cccagagag 1500  
 tcacacaaag gaatctttat tattacatga aaaataacca caagtccagc attgcggcac 1560  
 actccctgtg tgggttaattt aatgaaccat gaaagacagg atgaccttgg acaaggccaa 1620  
 actgtcctcc aagactcctt aatgaggggc aggagtccca' gggaaagaga accatgccat 1680  
 gctgaaaaag acaaaattga agaagaaatg tagccccagc cggtagccctc caaaggagag 1740  
 aagaagcaat agccgaggaa cttgggggga tggcgaatgg ttccctgccg ggccaaggg 1800  
 tgcacaggcg acctccatgg ctccattatt aacacaactc tagcaattat ggaccataag 1860  
 cacttccctc cagcccacaa gtcacagcct ggtgccgagg ctctgctcac cagccacca 1920  
 gggagtccac tccctcagcc tcccgctgc cccacacgga ggctctggct gtcctctttc 1980  
 ctccactcca tttgcttggc tctttctaca cctccctctt ggatgggctg agggctggag 2040  
 cgagtccctc agaaattcca ccaggctgtc agctgacctc tttttcctgc tgctgtgaag 2100  
 gtatagcacc ancccaggte ctctgcaggt gcggcatccc cttggcagct gccgtcagcc 2160  
 aggccagccc cagggagctt aaaacagaca ttccacaggg cctgggcccc tgggaggtga 2220  
 ggtgtggtgt gcggttcac ccagggcaga acaaggcaga atcgcaggaa acccgcnttc 2280  
 cccttctga cagctcctgc caagccaaat gtgcttctg cagctcacgc ccaccanget 2340  
 actgaaggga cccaaggcac cccnntgaa gccagcgata gangggctcc tctctgcntc 2400  
 cccagcagct cctgccccca naggcctgac tgtatatact gtaaataaaa ctttgtttgg 2460  
 gtcaagcttc cttctttcta acccccnaga ctttggcctc tgagtgaat gtctctcttt 2520  
 gcctgtggg gcttctctcc ttgatgttcc tttctttttt taaagacaac ctgccattac 2580  
 cacatgactc aataaaccat tgctcttcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2640

a

2641

&lt;210&gt; 248

&lt;211&gt; 398

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 248

```

Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu
 1           5           10           15
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln
 20           25           30
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser
 35           40           45
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg
 50           55           60
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys
 65           70           75           80
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys
 85           90           95
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu
 100          105          110
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile
 115          120          125
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met
 130          135          140
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile
 145          150          155          160
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu
 165          170          175
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly
 180          185          190
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu
 195          200          205
Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg
 210          215          220
Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe
 225          230          235          240
Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys
 245          250          255
Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp
 260          265          270
Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn
 275          280          285
Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Ala Pro Pro Phe Trp
 290          295          300
Ile Cys Ser Lys Ser Ala Pro Gly Ser Arg Pro Ser Met Pro Phe Pro
 305          310          315          320
Met Leu Pro Pro Cys Thr Gly Ser Ser Arg Ala Arg Pro Ser Ser Gln
 325          330          335
Gly Glu Arg Trp Trp Gly Pro Arg Cys Pro Asp Thr His Pro Thr Ser
 340          345          350
Pro Pro Ala Asp Arg Ala Ala Met Pro Pro Leu Pro Ser Gln Ala Trp
 355          360          365
Trp Gln Glu Val Asn Thr Leu Ala Met Pro Met Ala Thr Pro Pro Thr
 370          375          380
Pro Pro Thr Ala Arg Pro Gly Ala Ser Pro Thr Pro Ala Cys
 385          390          395

```

<210> 249  
<211> 2410  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(2410)  
<223> n = A,T,C or G

<400> 249  
ttcagaagga ggagagacac cgggcccagg gcaccctcgc gggcggggcg acccaagcag 60  
tgagggcctg cagccggccg gccagggcag cggcaggcgc ggcccggacc tacgggagga 120  
agccccgagc cctcggcggg ctgcgagcga ctccccggcg atgcctcaca actccatcag 180  
atctggccat ggagggctga accagctggg aggggccttt gtgaatggca gacctctgcc 240  
ggaagtggc cgccagcgca tcgtagacct ggcccaccag ggtgtaaggc cctgcgacat 300  
ctctcgccag ctccgcgtca gccatggctg cgtcagcaag atccttggca ggtactacga 360  
gactggcagc atccggcctg gagtgatagg gggctccaag cccaagggtg ccaccccaa 420  
ggtggtggag aagattgggg actacaaacg ccagaaccct accatgtttg cctgggagat 480  
ccgagaccgg ctcttgctg agggcgtctg tgacaatgac actgtgcca gtgtcagctc 540  
cattaataga atcatccgga ccaaagtga gcaaccattc aacctcccta tggacagctg 600  
cgtggccacc aagtcctga gtcccggaca cacgctgac cccagctcag ctgtaactcc 660  
cccggagtca cccagtcgg attccctggg ctccacctac tccatcaatg ggctcctggg 720  
catcgctcag cctggcagcg acaagaggaa aatggatgac agtgatcagg atagctgccg 780  
actaagcatt gactcacaga gcagcagcag cggacccga aagcaccttc gcacggatgc 840  
cttcagccag caccacctcg agccgctcga gtgcccattt gagcggcagc actaccaga 900  
ggcctatgcc tccccagcc acaccaaagg cgagcagggc gagagatggt ggggcccacg 960  
ctgcccggat acccaccoca catccccacc agcggacagg gcagctatgc ctctctgcc 1020  
atcgcaggca tgggtggcagg aagtgaatac tctggcaatg cctatggcca caccacctac 1080  
tcctcctaca gcgaggcctg gggcttcccc aactccagct tgctgagttc cccatattat 1140  
tacagttcca catcaaggcc gagtgcaccg cccaccactg ccacggcctt tgaccatctg 1200  
tagttgccat ggggacagtg ggagcgactg agcaacagga ggactcagcc tgggacaggc 1260  
cccagagagt cacacaaagg aatctttatt attacatgaa aaataaccac aagtccagca 1320  
ttgcggcaca ctccctgtgt ggttaattta atgaaccatg aaagacagga tgaccttga 1380  
caaggccaaa ctgtcctcca agactcctta atgaggggca ggagtcccag ggaaagagaa 1440  
ccatgccatg ctgaaaaaga caaaattgaa gaagaaatgt agccccagcc ggtaccctcc 1500  
aaaggagaga agaagcaata gccgaggaac ttggggggat ggcgaatggt tcctgcccgg 1560  
gcccagggt gcacaggga cctccatggc tccattatta acacaactct agcaattatg 1620  
gaccataagc acttccctcc agcccacaag tcacagcctg gtgcccaggc tctgtcacc 1680  
agccaccag ggagtcacct cctcagcct cccgcctgcc ccacacggag gctctggctg 1740  
tcctctttcc tccactccat ttgcttggt ctttctacac ctccctcttg gatgggtga 1800  
gggctggagc gagtccctca gaaattccac caggctgtca gctgacctct ttttctgct 1860  
gctgtgaagg tatagacca nccaggtcc tctgcagtg cggcatcccc ttggcagctg 1920  
ccgtcagcca ggccagcccc agggagctta aaacagacat tccacagggc ctggggccct 1980  
gggagggtgag gtgtggtgtg cggttcacc cagggcagaa caaggcagaa tcgcaggaaa 2040  
ccgcnttcc ccttctgac agtcctgcc aagccaaatg tgcttctgc agctcacgcc 2100  
caccangcta ctgaaggga ccaaggcacc cccnntgaag ccagcgatag angggtccct 2160  
ctctgcntcc ccagcagctc ctgccccan aggcctgact gtatatactg taaatgaaac 2220  
tttgtttggg tcaagcttcc ttctttctaa ccccnagac tttggcctct gagtgaatg 2280  
tctctctttg ccctgtgggg cttctctcct tgatgcttct ttcttttttt aaagacaacc 2340  
tgccattacc acatgactca ataaaccatt gctcttcaaa aaaaaaaaaa aaaaaaaaaa 2400  
aaaaaaaaaa 2410

<210> 250  
<211> 321  
<212> PRT

260

&lt;213&gt; Homo sapiens

&lt;400&gt; 250

```

Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu
 1          5          10          15
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln
          20          25          30
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser
          35          40          45
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg
          50          55          60
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys
65          70          75          80
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys
          85          90          95
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu
          100          105          110
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile
          115          120          125
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met
          130          135          140
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile
145          150          155          160
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu
          165          170          175
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly
          180          185          190
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu
          195          200          205
Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg
          210          215          220
Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe
225          230          235          240
Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys
          245          250          255
Gly Glu Gln Gly Glu Arg Trp Trp Gly Pro Arg Cys Pro Asp Thr His
          260          265          270
Pro Thr Ser Pro Pro Ala Asp Arg Ala Ala Met Pro Pro Leu Pro Ser
          275          280          285
Gln Ala Trp Trp Gln Glu Val Asn Thr Leu Ala Met Pro Met Ala Thr
          290          295          300
Pro Pro Thr Pro Pro Thr Ala Arg Pro Gly Ala Ser Pro Thr Pro Ala
305          310          315          320
Cys

```

&lt;210&gt; 251

&lt;211&gt; 2308

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(2308)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 251

261

```

ttcagaagga ggagagacac cgggcccagg gcaccctcgc gggcgggcgg acccaagcag 60
tgagggcctg cagccggccg gccagggcag cggcaggcgc ggcccggacc tacgggagga 120
agccccgagc cctcgggcgg ctgcgagcga ctccccggcg atgcctcaca actccatcag 180
atctggccat ggagggctga accagctggg aggggccttt gtgaatggca gacctctgcc 240
ggaagtggtc cgccagcgca tcgtagacct ggcccaccag ggtgtaaggc cctgcgacat 300
ctctcgccag ctccgcgtca gccatggctg cgtcagcaag atccttggca ggtactacga 360
gactggcagc atccggcctg gagtgatagg gggctccaag cccaaggtgg ccacccccaa 420
ggtggtggag aagattgggg actacaaacg ccagaaccct accatgtttg cctgggagat 480
ccgagaccgg ctctggctg agggcgtctg tgacaatgac actgtgcca gtgtcagctc 540
cattaataga atcatccgga ccaaagtga gcaaccattc aacctcccta tggacagctg 600
cgtggccacc aagtcctga gtcccggaca cacgctgac ccagctcag ctgtaactcc 660
cccggagtca cccagtcgg attccctggg ctccacctac tccatcaatg ggctcctggg 720
catcgctcag cctggcagcg acaagaggaa aatggatgac agtgatcagg atagctgccg 780
actaagcatt gactcacaga gcagcagcag cggaccccgga aagcaccttc gcacggatgc 840
cttcagccag caccacctcg agccgctcga gtgcccattt gagcggcagc actaccaga 900
ggcctatgcc tccccagcc acaccaaagg cgrcaggaa gtgaatactc tggcaatgcc 960
tatggccaca cccctactc ctctacagc gaggcctggg gcttcccaa ctccagcttg 1020
ctgagttccc catattatta cagttccaca tcaaggccga gtgcaccgcc caccactgcc 1080
acggcctttg accatctgta gttgccatga ggacagtggg agcgactgag caacaggagg 1140
actcagcctg ggacaggcc cagagagtca cacaaggaa tctttattat tacatgaaaa 1200
ataaccacaa gtccagcatt gcggcacact cctgtgtgg ttaatttaat gaacctgaa 1260
agacaggatg accttggaca aggccaaact gtcctccaag actccttaat gaggggcagg 1320
agtcccaggg aaagagaacc atgccatgct gaaaaagaca aaattgaaga agaaatgtag 1380
ccccagccgg taccctcaa aggagagaag aagcaatagc cgaggaaactt ggggggatgg 1440
cgaatggttc ctgcccgggc ccaagggtgc acagggcacc tccatggctc cattattaac 1500
acaactctag caattatgga ccataagcac ttcctccag cccacaagtc acagcctgg 1560
gccgaggtc tgctcaccag ccacccaggg agtcacctcc ctgagcctcc cgcctgcccc 1620
acacggaggc tctggtgtc ctcttctc cactccattt gcttggctct ttctacacct 1680
ccctcttgga tgggtgagg gctggagcga gtccctcaga aattccacca ggctgtcagc 1740
tgacctctt ttctgtgtc tgtgaaggta tagcaccanc ccaggtcctc ctgcagtgcg 1800
gcatccccctt ggcagctgcc gtcagccagg ccagcccgag ggagcttaaa acagacattc 1860
cacaggcctt gggcccctgg gaggtgaggt gtggtgtgcg gcttcaccca gggcagaaca 1920
aggcagaatc gcaggaaacc cgenttcccc ttcttgacag ctctgcca gccaatgtg 1980
cttctgtcag ctacgccc caangctact gaagggaccc aaggcacccc cnntgaagcc 2040
agcgatagan gggctcctct ctgntcccc agcagctcct gccccanag gcctgactgt 2100
atatactgta aatgaaactt tgtttgggtc aagcttcctt ctttctaacc ccnagactt 2160
tggcctctga gtgaaatgtc tctctttgcc atgtggggt tctctccttg atgttcttt 2220
ctttttttta agacaacctg ccattaccac atgactcaat aaaccattgc tcttcaaaaa 2280
aaaaaaaaaa aaaaaaaaaa aaaaaaaa 2308

```

&lt;210&gt; 252

&lt;211&gt; 287

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 252

```

Met Pro His Asn Ser Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu
 1             5             10             15
Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln
                20             25             30
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser
                35             40             45
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg
                50             55             60
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys
65             70             75             80
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys
                85             90             95

```

262

Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu  
                   100                  105                  110  
 Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile  
                   115                  120                  125  
 Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met  
                   130                  135                  140  
 Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile  
                   145                  150                  155                  160  
 Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu  
                   165                  170                  175  
 Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly  
                   180                  185                  190  
 Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu  
                   195                  200                  205  
 Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg  
                   210                  215                  220  
 Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe  
                   225                  230                  235                  240  
 Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys  
                   245                  250                  255  
 Gly Glu Gln Glu Val Asn Thr Leu Ala Met Pro Met Ala Thr Pro Pro  
                   260                  265                  270  
 Thr Pro Pro Thr Ala Arg Pro Gly Ala Ser Pro Thr Pro Ala Cys  
                   275                  280                  285

&lt;210&gt; 253

&lt;211&gt; .2148

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 253

gcttcagggt acagctcccc cgcagccaga agccggggcct gcagcccctc agcaccgctc 60  
 cgggacaccc caccgcttc ccaggcgtga cctgtcaaca gcaacttcgc ggtgtggtga 120  
 actctctgag gaaaaacat tttgattatt actctcagac gtgcgtggca acaagtgact 180  
 gagacctaga aatccaagcg ttggaggtcc tgaggccagc ctaagtcgct tcaaaatgga 240  
 acgaaggcgt ttgtggggtt ccattcagag ccgatacatc agcatgagtg tgtggacaag 300  
 cccacggaga cttgtggagc tggcagggca gagcctgctg aaggatgagg ccctggccat 360  
 tgccgccttg gaggttgctc ccagggagct cttcccgcca ctcttcatgg cagcctttga 420  
 cgggagacac agccagaccc tgaaggcaat ggtgcaggcc tggcccttca cctgcctccc 480  
 tctgggagtg ctgatgaagg gacaacatct tcacctggag accttcaaag ctgtgcttga 540  
 tggacttgat gtgtccttg cccaggaggt tcgccccagg aggtggaaac ttcaagtgtc 600  
 ggatttacgg aagaactctc atcaggactt ctggactgta tggctctgga acagggccag 660  
 tctgtactca tttccagagc cagaagcagc tcagcccctg acaaagaagc gaaaagtaga 720  
 tggtttgagc acagaggcag agcagccctt cattccagta gaggtgctcg tagacctgtt 780  
 cctcaaggaa ggtgcctgtg atgaattgtt ctcctacctc attgagaaag tgaagcgaag 840  
 gaaaaatgta ctacgcctgt gctgtaagaa gctgaagatt tttgcaatgc ccatgcagga 900  
 tatcaagatg atcctgaaaa tgggtgcagct ggactctatt gaagatttgg aagtgacttg 960  
 tacctggaag ctacccacct tggcgaaatt ttctccttac ctgggccaga tgattaatct 1020  
 gcgtagactc ctctctctcc acatccatgc atcttcctac atttccccgg agaaggaaga 1080  
 gcagtatatc gccagttca cctctcagtt cctcagtcgt cagtgcctgc aggtctcta 1140  
 tgtggactct ttatttttcc ttagaggccg cctggatcag ttgctcaggc acgtgatgaa 1200  
 ccccttgga accctctcaa taactaactg ccggctttcg gaaggggatg tgatgcatct 1260  
 gtocccagag cccagcgtca gtcagctaag tgtcctgagt ctaagtgggg tcatgctgac 1320  
 cgatgtaagt cccgagcccc tccaagctct gctggagaga gcctctgcca ccctccagga 1380  
 cctggtcttt gatgagtgtg ggatcacgga tgatcagctc cttgccctcc tgccttcctc 1440  
 gagccactgc tcccagctta caaccttaag cttctacggg aattccatct ccatactctc 1500  
 cttgcagagt ctctgcagc acctcatcgg gctgagcaat ctgacccacg tgctgtatcc 1560



```

.tgtccccctg gagagttatg aggacatcca tggtagccctc cacctggaga ggcttgcccta 1620
tctgcatgcc aggctcaggg agttgctgtg tgagttgggg cggcccagca tggctctggct 1680
tagtgccaac ccctgtcctc actgtgggga cagaaccttc tatgaccggg agcccatcct 1740
gtgcccctgt ttcatgccta actagctggg tgcacatata aaatgcttca ttctgcatac 1800
ttggacacta aagccaggat gtgcatgcat cttgaagcaa caaagcagcc acagtttcag 1860
acaaatgttc agtgtgagtg aggaaaacat gttcagttag gaaaaaacat tcagacaaat 1920
gttcagttag gaaaaaaagg ggaagttggg gataggcaga tgttgacttg aggagttaat 1980
gtgatctttg gggagataca tcttatagag ttagaaatag aatctgaatt tctaaaggga 2040
gattctggct tgggaagtac atgtaggagt taatccctgt gtagactgtt gtaaagaaac 2100
tgttgaaaat aaagagaagc aatgtgaagc aaaaaaaaaa aaaaaaaa 2148

```

&lt;210&gt; 254

&lt;211&gt; 509

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 254

```

Met Glu Arg Arg Leu Trp Gly Ser Ile Gln Ser Arg Tyr Ile Ser
 1           5           10           15
Met Ser Val Trp Thr Ser Pro Arg Arg Leu Val Glu Leu Ala Gly Gln
          20           25           30
Ser Leu Leu Lys Asp Glu Ala Leu Ala Ile Ala Ala Leu Glu Leu Leu
          35           40           45
Pro Arg Glu Leu Phe Pro Pro Leu Phe Met Ala Ala Phe Asp Gly Arg
          50           55           60
His Ser Gln Thr Leu Lys Ala Met Val Gln Ala Trp Pro Phe Thr Cys
          65           70           75           80
Leu Pro Leu Gly Val Leu Met Lys Gly Gln His Leu His Leu Glu Thr
          85           90           95
Phe Lys Ala Val Leu Asp Gly Leu Asp Val Leu Leu Ala Gln Glu Val
          100          105          110
Arg Pro Arg Arg Trp Lys Leu Gln Val Leu Asp Leu Arg Lys Asn Ser
          115          120          125
His Gln Asp Phe Trp Thr Val Trp Ser Gly Asn Arg Ala Ser Leu Tyr
          130          135          140
Ser Phe Pro Glu Pro Glu Ala Ala Gln Pro Met Thr Lys Lys Arg Lys
          145          150          155          160
Val Asp Gly Leu Ser Thr Glu Ala Glu Gln Pro Phe Ile Pro Val Glu
          165          170          175
Val Leu Val Asp Leu Phe Leu Lys Glu Gly Ala Cys Asp Glu Leu Phe
          180          185          190
Ser Tyr Leu Ile Glu Lys Val Lys Arg Lys Lys Asn Val Leu Arg Leu
          195          200          205
Cys Cys Lys Lys Leu Lys Ile Phe Ala Met Pro Met Gln Asp Ile Lys
          210          215          220
Met Ile Leu Lys Met Val Gln Leu Asp Ser Ile Glu Asp Leu Glu Val
          225          230          235          240
Thr Cys Thr Trp Lys Leu Pro Thr Leu Ala Lys Phe Ser Pro Tyr Leu
          245          250          255
Gly Gln Met Ile Asn Leu Arg Arg Leu Leu Leu Ser His Ile His Ala
          260          265          270
Ser Ser Tyr Ile Ser Pro Glu Lys Glu Glu Gln Tyr Ile Ala Gln Phe
          275          280          285
Thr Ser Gln Phe Leu Ser Leu Gln Cys Leu Gln Ala Leu Tyr Val Asp
          290          295          300
Ser Leu Phe Phe Leu Arg Gly Arg Leu Asp Gln Leu Leu Arg His Val
          305          310          315          320
Met Asn Pro Leu Glu Thr Leu Ser Ile Thr Asn Cys Arg Leu Ser Glu

```

264

				325						330					335
Gly	Asp	Val	Met	His	Leu	Ser	Gln	Ser	Pro	Ser	Val	Ser	Gln	Leu	Ser
			340					345					350		
Val	Leu	Ser	Leu	Ser	Gly	Val	Met	Leu	Thr	Asp	Val	Ser	Pro	Glu	Pro
		355					360					365			
Leu	Gln	Ala	Leu	Leu	Glu	Arg	Ala	Ser	Ala	Thr	Leu	Gln	Asp	Leu	Val
	370					375					380				
Phe	Asp	Glu	Cys	Gly	Ile	Thr	Asp	Asp	Gln	Leu	Leu	Ala	Leu	Leu	Pro
385					390				395						400
Ser	Leu	Ser	His	Cys	Ser	Gln	Leu	Thr	Thr	Leu	Ser	Phe	Tyr	Gly	Asn
			405						410					415	
Ser	Ile	Ser	Ile	Ser	Ala	Leu	Gln	Ser	Leu	Leu	Gln	His	Leu	Ile	Gly
	420							425					430		
Leu	Ser	Asn	Leu	Thr	His	Val	Leu	Tyr	Pro	Val	Pro	Leu	Glu	Ser	Tyr
	435					440					445				
Glu	Asp	Ile	His	Gly	Thr	Leu	His	Leu	Glu	Arg	Leu	Ala	Tyr	Leu	His
	450				455						460				
Ala	Arg	Leu	Arg	Glu	Leu	Leu	Cys	Glu	Leu	Gly	Arg	Pro	Ser	Met	Val
465					470				475						480
Trp	Leu	Ser	Ala	Asn	Pro	Cys	Pro	His	Cys	Gly	Asp	Arg	Thr	Phe	Tyr
			485						490					495	
Asp	Pro	Glu	Pro	Ile	Leu	Cys	Pro	Cys	Phe	Met	Pro	Asn			
			500					505							

&lt;210&gt; 255

&lt;211&gt; 2261

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 255

```

ccgcgggttcc ggcgtgctccg ggcaggcgac ccttgggtcgc gcgctgcggg cgaggtgggc 60
aggtaggtgg gcggacggcc gcggttctcc ggcaagcgca ggcgcgagg tccccacgg 120
cgcccgaagc gcccccgca ccccggcct ccagcgttga ggcggggag tgaggagatg 180
ccgacccaga gggacagcag caccatgtcc cacacggtcg caggcgggcg cagcggggac 240
cattcccacc aggtccgggt gaaagcctac taccgcgggg atatcatgat aacacatttt 300
gaaccttcca tctcctttga gggcctttgc aatgaggttc gagacatgtg ttcttttgac 360
aacgaacagc tcttcacat gaaatggata gatgaggaag gagaccgtg tacagtatca 420
tctcagttgg agttagaaga agcctttaga ctttatgagc taaacaagga ttctgaactc 480
ttgattcatg tgttcccttg tgtaccagaa cgtcctggga tgccttgtcc aggagaagat 540
aaatccatct accgtagagg tgcacgccgc tggagaaagc tttattgtgc caatggccac 600
actttccaag ccaagcggtt caacaggcgt gctcactgtg ccatctgcac agaccgaata 660
tggggacttg gacgccaagg atataagtgc atcaactgca aactcttggg tcataagaag 720
tgccataaac tcgtcacaat tgaatgtggg cggcattcct tgccacagga accagtgtg 780
cccatggatc agtcatccat gcattctgac catgcacaga cagtaattcc atataatcct 840
tcaagtcatg agagtttgga tcaagttggt gaagaaaaag aggcaatgaa caccagggaa 900
agtggcaaat cttcatccag tctaggtctt caggattttg atttgctccg ggtaatatga 960
agaggaagtt atgccaaagt actgttggtt cgattaaaaa aaacagatcg tatttatgca 1020
atgaaagttg tgaaaaaaga gcttgtaaat gatgatgagg atattgattg ggtacagaca 1080
gagaagcatg tgtttgagca ggcattccat catcctttcc ttgttgggct gcattcttgc 1140
tttcagacag aaagcagatt gttctttgtt atagagtatg taaatggagg agacctaatg 1200
tttcatatgc agcgacaaag aaaacttctt gaagaacatg ccagatttta ctctgcagaa 1260
atcagtctag cattaaatta tcttcatgag cgagggataa tttatagaga tttgaaactg 1320
gacaatgtat tactggactc tgaaggccac attaaactca ctgactacgg catgtgtaag 1380
gaaggattac ggccaggaga tacaaccagc actttctgtg gtactcctaa ttacattgct 1440
cctgaaattt taagaggaga agattatggt ttcagtgttg actggtgggc tcttggagtg 1500
ctcatgtttg agatgatgc aggaaggtct ccatttgata ttgttgggag ctccgataac 1560
cctgaccaga acacagagga ttatctcttc caagttattt tggaaaaaca aattcgcata 1620

```

```

ccacgttctc tgtctgtaaa agctgcaagt gttctgaaga gttttcttaa taaggaccct 1680
aaggaacgat tgggttgtca tctcaaaca ggatttgctg atattcaggg acaccggtc 1740
ttccgaaatg ttgattgga tatgatggag caaaaacagg tggtaacctcc ctttaaacca 1800
aatatttctg gggaatttg tttggacaac tttgattctc agtttactaa tgaacctgtc 1860
cagctcactc cagatgacga tgacattgtg aggaagattg atcagtctga atttgaaggt 1920
tttgagtata tcaatcctct tttgatgtct gcagaagaat gtgtctgatc ctcatttttc 1980
aaccatgtat tctactcatg ttgccattta atgcatggat aaacttgctg caagcctgga 2040
tacaattaac cattttatat ttgccaccta caaaaaaaca cccaatatct tctcttgtag 2100
actatatgaa tcaattatta catctgtttt actatgaaaa aaaaattaat actactagct 2160
tccagacaat catgtcaaaa tttagttgaa ctgggttttc agtttttaaa aggcctacag 2220
atgagtaatg aagttacctt ttttgtttaa aaaaaaaaaa g 2261

```

&lt;210&gt; 256

&lt;211&gt; 587

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 256

```

Met Ser His Thr Val Ala Gly Gly Gly Ser Gly Asp His Ser His Gln
 1          5          10          15
Val Arg Val Lys Ala Tyr Tyr Arg Gly Asp Ile Met Ile Thr His Phe
 20          25          30
Glu Pro Ser Ile Ser Phe Glu Gly Leu Cys Asn Glu Val Arg Asp Met
 35          40          45
Cys Ser Phe Asp Asn Glu Gln Leu Phe Thr Met Lys Trp Ile Asp Glu
 50          55          60
Glu Gly Asp Pro Cys Thr Val Ser Ser Gln Leu Glu Leu Glu Glu Ala
 65          70          75          80
Phe Arg Leu Tyr Glu Leu Asn Lys Asp Ser Glu Leu Leu Ile His Val
 85          90          95
Phe Pro Cys Val Pro Glu Arg Pro Gly Met Pro Cys Pro Gly Glu Asp
100          105          110
Lys Ser Ile Tyr Arg Arg Gly Ala Arg Arg Trp Arg Lys Leu Tyr Cys
115          120          125
Ala Asn Gly His Thr Phe Gln Ala Lys Arg Phe Asn Arg Arg Ala His
130          135          140
Cys Ala Ile Cys Thr Asp Arg Ile Trp Gly Leu Gly Arg Gln Gly Tyr
145          150          155          160
Lys Cys Ile Asn Cys Lys Leu Leu Val His Lys Lys Cys His Lys Leu
165          170          175
Val Thr Ile Glu Cys Gly Arg His Ser Leu Pro Gln Glu Pro Val Met
180          185          190
Pro Met Asp Gln Ser Ser Met His Ser Asp His Ala Gln Thr Val Ile
195          200          205
Pro Tyr Asn Pro Ser Ser His Glu Ser Leu Asp Gln Val Gly Glu Glu
210          215          220
Lys Glu Ala Met Asn Thr Arg Glu Ser Gly Lys Ala Ser Ser Ser Leu
225          230          235          240
Gly Leu Gln Asp Phe Asp Leu Leu Arg Val Ile Gly Arg Gly Ser Tyr
245          250          255
Ala Lys Val Leu Leu Val Arg Leu Lys Lys Thr Asp Arg Ile Tyr Ala
260          265          270
Met Lys Val Val Lys Lys Glu Leu Val Asn Asp Asp Glu Asp Ile Asp
275          280          285
Trp Val Gln Thr Glu Lys His Val Phe Glu Gln Ala Ser Asn His Pro
290          295          300
Phe Leu Val Gly Leu His Ser Cys Phe Gln Thr Glu Ser Arg Leu Phe
305          310          315          320

```

266

Phe Val Ile Glu Tyr Val Asn Gly Gly Asp Leu Met Phe His Met Gln  
 325 330 335  
 Arg Gln Arg Lys Leu Pro Glu Glu His Ala Arg Phe Tyr Ser Ala Glu  
 340 345 350  
 Ile Ser Leu Ala Leu Asn Tyr Leu His Glu Arg Gly Ile Ile Tyr Arg  
 355 360 365  
 Asp Leu Lys Leu Asp Asn Val Leu Leu Asp Ser Glu Gly His Ile Lys  
 370 375 380  
 Leu Thr Asp Tyr Gly Met Cys Lys Glu Gly Leu Arg Pro Gly Asp Thr  
 385 390 395 400  
 Thr Ser Thr Phe Cys Gly Thr Pro Asn Tyr Ile Ala Pro Glu Ile Leu  
 405 410 415  
 Arg Gly Glu Asp Tyr Gly Phe Ser Val Asp Trp Trp Ala Leu Gly Val  
 420 425 430  
 Leu Met Phe Glu Met Met Ala Gly Arg Ser Pro Phe Asp Ile Val Gly  
 435 440 445  
 Ser Ser Asp Asn Pro Asp Gln Asn Thr Glu Asp Tyr Leu Phe Gln Val  
 450 455 460  
 Ile Leu Glu Lys Gln Ile Arg Ile Pro Arg Ser Leu Ser Val Lys Ala  
 465 470 475 480  
 Ala Ser Val Leu Lys Ser Phe Leu Asn Lys Asp Pro Lys Glu Arg Leu  
 485 490 495  
 Gly Cys His Pro Gln Thr Gly Phe Ala Asp Ile Gln Gly His Pro Phe  
 500 505 510  
 Phe Arg Asn Val Asp Trp Asp Met Met Glu Gln Lys Gln Val Val Pro  
 515 520 525  
 Pro Phe Lys Pro Asn Ile Ser Gly Glu Phe Gly Leu Asp Asn Phe Asp  
 530 535 540  
 Ser Gln Phe Thr Asn Glu Pro Val Gln Leu Thr Pro Asp Asp Asp Asp  
 545 550 555 560  
 Ile Val Arg Lys Ile Asp Gln Ser Glu Phe Glu Gly Phe Glu Tyr Ile  
 565 570 575  
 Asn Pro Leu Leu Met Ser Ala Glu Glu Cys Val  
 580 585

&lt;210&gt; 257

&lt;211&gt; 6742

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 257

gtcgaccccg cgtccggcgc ggcagctctt ttctttcttc ctccacttcc cctaccctcc 60  
 accgtccggg agccgccgcc accgccgccg aggagtcagg aagttcaaga tggccgccgc 120  
 ggagaccag tcgtacggg agcagccaga gatggaagat gctaattctg aaaagagtat 180  
 aaatgaagaa aatggagaag tatcagaaga ccagtctcaa aataagcaca gtcgtcacia 240  
 aaaaaagaag cataaacaca gaagtaaaca taagaaacat aaacattcct cagaagaaga 300  
 caaggataaa aaacataaac ataagcataa acataagaaa cacaaaagaa aagagggttat 360  
 tgatgcttct gataaagagg gtatgtctcc agcaaaaaga actaaacttg atgatttagc 420  
 tttgctagaa gacttggaag aacagagagc cttgattaag gccgaacttg ataatgagtt 480  
 aatggaagga aaggtccagt ctggtatggg gctcattttg caaggttatg agtctggctc 540  
 tgaagaagag ggggaaattc atgaaaaggc aagaaatgga aataggtcta gtactagatc 600  
 ttcaagtaca aaggggaaac ttgaacttgt ggacaataaa attactacaa agaaacgaag 660  
 taaaagcaga tccaaagaac ggactagaca taggtctgat aaaaagaaaa gtaagggggg 720  
 tattgaaatc gttaaagaga aaacaactag gagcaagtca aaggagagga aaaaatctaa 780  
 aagcccatcc aaaagaagta agtctcaaga tcaagcaagg aaatcaaaat cccctaccct 840  
 tagaaggcga tctcaagaga aaattggtta ggccagatct cctactgatg ataagggttaa 900  
 aattgaagat aaaagtaaat caaaagatag gaaaaaatcc ccaattataa atgaaagtag 960

aagtcgcat	cgaggtaaaa	aatccagatc	cccagttgat	ttaagaggt	aatccaaaga	1020
cagaaggtca	cggtccaaag	agagaaaatc	aaaacggtct	gaaactgata	aagaaaagaa	1080
gccaattaaa	tctccctcta	aagatgcttc	atctgggaaa	gaaaataggt	caccacagcag	1140
aagacctggt	cgtagtctta	aaagaagaag	tttgtctcca	aaaccacgtg	ataaatcaag	1200
aagaagcagg	tctccacttt	tgaatgatag	aagatctaag	cagagcaaat	ccccctcgcg	1260
gacactgtct	cctgggagaa	gagccaagag	ccgatcctta	gaaagaaaac	gacgagaacc	1320
agagaggaga	cgactttctt	ctccaagaac	acgacctoga	gatgatatacc	tcagtagacg	1380
tgaagatca	aaagatgcca	gccccatcaa	tagatggtct	ccaacccgaa	gaagaagtag	1440
atctcccat	agaaggaggt	ctcgttcccc	actcagacgt	agcaggtctc	caagaagaag	1500
aagcagatct	cctcggagaa	gggacagagg	tcggaggagc	agatcacgct	tgcaaggcg	1560
gtctcgatca	cgcggtggtc	gtagacgaag	gagcagaagc	aaagtaaagg	aagataaatt	1620
taaaggaagt	gttctgaag	gaatgaaagt	tgagcaggaa	tcttcgtctg	atgataacct	1680
tgaagacttt	gatgtagagg	aagaagatga	agaagcccta	atagaacaga	gaagaatcca	1740
aaggcaggca	attgttcaga	aatataaata	ccttgctgaa	gatagcaaca	tgtctgtgcc	1800
atctgaacca	agcagcccc	agagcagtac	gagaacacga	tcaccatctc	cagatgacat	1860
tctggagcga	gtagctgctg	atgttaaaga	gtatgaacgg	gaaaatgttg	atacatttga	1920
ggcctcagtg	aaagccaagc	ataatctaata	gacagttgaa	cagaataatg	gttcatctca	1980
gaagaagttg	ttggcacctg	atatgtttac	agaatctgat	gatatgtttg	ctgcgtattt	2040
tgatagtgtc	cgtcttcggg	ccgctggcat	tggaagagat	ttcaaagaga	atcccaacct	2100
cagagataac	tggaccgatg	cagaaggcta	ttatcgtgtg	aacataggtg	aagtcctaga	2160
taaacgttac	aatgtgtatg	gctacactgg	gcaagggtga	ttcagtaatg	ttgtacgagc	2220
cagagataat	gcaagagcca	accaagaagt	ggctgtaaag	atcatcagaa	acaatgagct	2280
catgcaaaag	actggtttta	aagaattaga	gttcttgaaa	aaacttaatg	atgctgatcc	2340
tgatgacaaa	tttcattgtc	tgagactctt	caggcacttc	tatcacaagc	agcatctttg	2400
tctggtattc	gagcctctca	gcatgaactt	acgagaggtg	ttaaaaaat	atggtaaaga	2460
tgttggtctt	catattaaag	ctgtaagatc	ctatagtcag	cagttgtttc	tggcattgaa	2520
actccttaaa	agatgcaata	tcctacatgc	agatatcaag	ccagacaata	tcctggttaa	2580
tgaatccaaa	actattttta	agctttgcga	ttttgggtcg	gcttcacatg	ttgcggataa	2640
tgacataaca	ccttatcttg	tcagtagatt	ttatcgtgct	cctgaaatca	ttataggtaa	2700
aagctatgac	tatggtatag	atatgtggtc	tgtaggttgc	accttatacg	aactctatac	2760
tggaaaaatt	ttattccctg	gcaaaaccaa	taaccatatg	ctgaagcttg	caatggatct	2820
caaaggaaaag	atgccaaata	agatgattcg	aaaagggtgtg	ttcaaagatc	agcattttga	2880
tcaaaatctc	aacttcattg	acatagaagt	tgataaagta	acagagaggg	agaaaagtac	2940
tgttatgagc	accattaatc	caactaaaga	cctgttggtc	gacttgattg	ggtgccagag	3000
acttcctgaa	gaccaacgta	agaaagtaca	ccagctaaag	gacttgtttg	accagattct	3060
gatgttgagc	ccagctaaac	gaattagcat	caaccaggcc	ctacagcacg	ccttcatcca	3120
ggaaaaaatt	taacaagat	gaagaaactc	caagggtttg	agtaaataca	aagactgaag	3180
aaatttcaca	gcagtttatt	aatgtatata	aacttataaa	tatttctcca	gcaaatttga	3240
ggaagcatga	tatatattga	ttaacaccaa	gggtgatatt	tcttttagag	atgttagtta	3300
atctgttttg	tgtcttacgt	gaaatttcac	tgtagactgt	tttaaattgc	caagactgca	3360
caaaattaca	gtgctaattg	atatggttgc	agttcacata	aagacaaaag	catctgttat	3420
gaaatgagta	gtaaatattg	gtggttgatt	tgttcttagc	agacttggtc	tcattttggt	3480
cttgagataa	aatggccagc	ataaatgctg	tttatattca	cgttttccta	ggtgtgtgtg	3540
tgcaggccac	agcagcatgc	ccttggtgta	gtcagtgccg	aaaggggtct	gttccttctt	3600
gagcctgcct	gcagggatgg	tctcctttta	aagcaggttg	tgtgcagcat	tcagtacact	3660
gaaggtaaagc	taaaccatca	acatctctgg	tgtttttaaga	tgttatttta	ttggaacaac	3720
tgacaaatga	gggatgttag	ccttggtgca	gaattccctg	catgtgtgat	aactgatctt	3780
gttttatttt	ttggcattgc	aactgtggca	tagttacaat	ttctgtttgt	tcacacatt	3840
taaaattgga	agagaacgcg	cttgatggat	agagcgctt	cagtgtactg	tttcttatta	3900
actttacttt	ttttaaatca	acttgctata	gactttatat	acattttgtt	aaatatagtt	3960
cctagtgaca	tagaaacgat	gcgtagtttt	catttactaa	ttacaaatgt	tgaggcctaa	4020
ttctgaaagt	cctcatattt	aaaggctaga	caacgtaatg	aaatttttaa	ctatttgtat	4080
gtcatttttg	aagtgtactg	ctttatggta	aaagtgtttt	tcatttgttc	attgttttca	4140
ttatttgtga	tcatgttgtc	tttcaataca	ggcataaacc	ttccactctt	gaacaaagca	4200
gctgcttttt	taagcgggta	attgcttctt	taccttttat	ttcttttgta	aatgaagctt	4260
ttctttaaga	atgtgacttt	aaagtgttgt	ctattgcata	aaacagttga	cactcactta	4320
ttgtaaaagt	aagattgttc	tactgcatgt	gaagtggacc	atgcagattt	ctgtatgttc	4380
tcagtatgca	tcactagata	ataaagtctt	ttgtgaacaa	ggcatttgta	gccattttta	4440

```

aaagtttttg tcttcagtcg tggtaagtca ggtaaaccat aaatagttaa aagcaacctt 4500
ttgttttttt cctgaaagtt ttttaattgaa agtattatta gttaaagatg taaacctagc 4560
caaaattacc agtttattaa taattaggat cctaattatt tcaaaaaatc ctacaaatat 4620
tgtcagcttt cagtgtagt agattattcc tgtagggtat ggggtataat tcaggattta 4680
actaatgttt ctgctatttt ctcacttttc cttttgatgg tgcggaaaga gaaaaaggaa 4740
aacggggcac aggccattcg acgccttctc caaggggtct gatttgctga gacaccagct 4800
tcaccttctt aacaaggtgc agctcagtg aagatgatga caaccagaag acatgagcta 4860
aggtttctgt cctataaaag atttattaaa aaacaatcct tcatttattt tttgtctaatt 4920
tttttagttt tcagcattat gatttgggtt ttattgggtt ttggtattta gaattagtgc 4980
tgttgtggag tgcgtctgta aagtgcctgt tttatcatac ttctgcctc tcccctcccc 5040
cagtttctcc tcccataaaa taaaaatagt ggccaacttt agtaataata aaggctgctg 5100
gatgctgaga ttccacataa cacatgggtg tcaaaaattg atgttaagga ttcttagaaa 5160
aacagcaacc accagaatag catatatcta aaagtagtct tcagctttag gcagatgcaa 5220
aagaatacaa actggaatat taagaatact gttcaactcc tttagtatct gttccccaac 5280
ttaccttgta gaaacctcgt tattaaccag tgttccagtc ttaaagtaga caaaatattc 5340
agagccattt tttttaaggg aaatgaaaaa gatactctgg gttttttata ctccccaatt 5400
tagcatatct agactacctt tttgaaagga accctatcaa ctgtcttatg taogttacat 5460
gattttccta cactctgtaa ttttgcctgag gtgcaatttg gaactctgca agacctacta 5520
gattgaattt atttagttaa tgctcctgaa taaatgtgca ttctctttt agagtagctg 5580
tatgcttttc aaatgctatc tgccgtgaat tttttgcttt tattatactt tatggcaaaa 5640
gtgatataca gtgattgtca gacttgaggg ctcatagaag tgttaggtac ggctctcaaa 5700
gatgttacag tttttctag gggtgggaga atagttgaga tctggaaagc atagacattt 5760
tttacactct ggatagactt tattcttgaa gatcatcaga aatgaggttg gaatttcgag 5820
gttttgagca gggggagcat cttatattca cccttaaact gttattaata catcctgttt 5880
tcttcattcc ctgatagcta tctcatttca ctctactgtc tcaaaaattt gttttaaaat 5940
aatagaaatg ttttgcattt attaatgacc actttattcc taacaaaaat aagtactcag 6000
gacttttttt tcaaaatgaa atatttatgt actgttttat ggtatgtggt agagtaagta 6060
aaatgtaatg ttctcagttt tgttccatat ttgcattcct cttatgcttt acctgtattt 6120
tatcatttgt aagcagaact ctagctatat ggggtagaaa taaaatctct gagatgaaac 6180
aaaggaatca acatgataaa atttaggcga agtagttaag aaatggccct tttgaatgtt 6240
gaagatagga aagaaagcca tatattcaaa tatgtaattt tctcatttta gttataatga 6300
catctttacc aattgggctt cataaatgtg tttctttctt aatagtatcc tagttccagc 6360
atatattcaa catgaatttt atcattctcc tctaatgga atgtcttctt tatagaaatg 6420
ttcacgacaa attcatttgt gttttttaca tgtcaataat gtatgctaaa ttaaaatgtt 6480
ttccagttat tctgatagat gtcattatgg catccttaat ttttcttctc cttctgtata 6540
tagggtaagg gactgttctg aagaaccttt ccatttagtg atcaagatat ggaagctgat 6600
ttctgaaaaat gctcagtgtg tactctaatt atttatggta ccatttgaat tgtaacttgc 6660
attttagcag tgcattgttc taattgactt actgggaaac tgaataaaat atgcctctta 6720
ttatcaaaaa aaaaaaaaaa gg

```

&lt;210&gt; 258

&lt;211&gt; 1043

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 258

```

Ser Thr Pro Arg Pro Ala Arg Gln Leu Phe Ser Phe Phe Leu His Phe
1          5          10          15
Pro Tyr Pro Pro Pro Ser Gly Ser Arg Arg His Arg Arg Arg Gly Val
20          25          30
Arg Lys Phe Lys Met Ala Ala Ala Glu Thr Gln Ser Leu Arg Glu Gln
35          40          45
Pro Glu Met Glu Asp Ala Asn Ser Glu Lys Ser Ile Asn Glu Glu Asn
50          55          60
Gly Glu Val Ser Glu Asp Gln Ser Gln Asn Lys His Ser Arg His Lys
65          70          75          80
Lys Lys Lys His Lys His Arg Ser Lys His Lys Lys His Lys His Ser
85          90          95

```

269

Ser	Glu	Glu	Asp	Lys	Asp	Lys	Lys	His	Lys	His	Lys	His	Lys	His	Lys	100	105	110
Lys	His	Lys	Arg	Lys	Glu	Val	Ile	Asp	Ala	Ser	Asp	Lys	Glu	Gly	Met	115	120	125
Ser	Pro	Ala	Lys	Arg	Thr	Lys	Leu	Asp	Asp	Leu	Ala	Leu	Leu	Glu	Asp	130	135	140
Leu	Glu	Lys	Gln	Arg	Ala	Leu	Ile	Lys	Ala	Glu	Leu	Asp	Asn	Glu	Leu	145	150	155
Met	Glu	Gly	Lys	Val	Gln	Ser	Gly	Met	Gly	Leu	Ile	Leu	Gln	Gly	Tyr	165	170	175
Glu	Ser	Gly	Ser	Glu	Glu	Glu	Gly	Glu	Ile	His	Glu	Lys	Ala	Arg	Asn	180	185	190
Gly	Asn	Arg	Ser	Ser	Thr	Arg	Ser	Ser	Ser	Thr	Lys	Gly	Lys	Leu	Glu	195	200	205
Leu	Val	Asp	Asn	Lys	Ile	Thr	Thr	Lys	Lys	Arg	Ser	Lys	Ser	Arg	Ser	210	215	220
Lys	Glu	Arg	Thr	Arg	His	Arg	Ser	Asp	Lys	Lys	Lys	Ser	Lys	Gly	Gly	225	230	235
Ile	Glu	Ile	Val	Lys	Glu	Lys	Thr	Thr	Arg	Ser	Lys	Ser	Lys	Glu	Arg	245	250	255
Lys	Lys	Ser	Lys	Ser	Pro	Ser	Lys	Arg	Ser	Lys	Ser	Gln	Asp	Gln	Ala	260	265	270
Arg	Lys	Ser	Lys	Ser	Pro	Thr	Leu	Arg	Arg	Arg	Ser	Gln	Glu	Lys	Ile	275	280	285
Gly	Lys	Ala	Arg	Ser	Pro	Thr	Asp	Asp	Lys	Val	Lys	Ile	Glu	Asp	Lys	290	295	300
Ser	Lys	Ser	Lys	Asp	Arg	Lys	Lys	Ser	Pro	Ile	Ile	Asn	Glu	Ser	Arg	305	310	315
Ser	Arg	Asp	Arg	Gly	Lys	Lys	Ser	Arg	Ser	Pro	Val	Asp	Leu	Arg	Gly	325	330	335
Lys	Ser	Lys	Asp	Arg	Arg	Ser	Arg	Ser	Lys	Glu	Arg	Lys	Ser	Lys	Arg	340	345	350
Ser	Glu	Thr	Asp	Lys	Glu	Lys	Lys	Pro	Ile	Lys	Ser	Pro	Ser	Lys	Asp	355	360	365
Ala	Ser	Ser	Gly	Lys	Glu	Asn	Arg	Ser	Pro	Ser	Arg	Arg	Pro	Gly	Arg	370	375	380
Ser	Pro	Lys	Arg	Arg	Ser	Leu	Ser	Pro	Lys	Pro	Arg	Asp	Lys	Ser	Arg	385	390	395
Arg	Ser	Arg	Ser	Pro	Leu	Leu	Asn	Asp	Arg	Arg	Ser	Lys	Gln	Ser	Lys	405	410	415
Ser	Pro	Ser	Arg	Thr	Leu	Ser	Pro	Gly	Arg	Arg	Ala	Lys	Ser	Arg	Ser	420	425	430
Leu	Glu	Arg	Lys	Arg	Arg	Glu	Pro	Glu	Arg	Arg	Arg	Leu	Ser	Ser	Pro	435	440	445
Arg	Thr	Arg	Pro	Arg	Asp	Asp	Ile	Leu	Ser	Arg	Arg	Glu	Arg	Ser	Lys	450	455	460
Asp	Ala	Ser	Pro	Ile	Asn	Arg	Trp	Ser	Pro	Thr	Arg	Arg	Arg	Ser	Arg	465	470	475
Ser	Pro	Ile	Arg	Arg	Arg	Ser	Arg	Ser	Pro	Leu	Arg	Arg	Ser	Arg	Ser	485	490	495
Pro	Arg	Arg	Arg	Ser	Arg	Ser	Pro	Arg	Arg	Arg	Asp	Arg	Gly	Arg	Arg	500	505	510
Ser	Arg	Ser	Arg	Leu	Arg	Arg	Arg	Ser	Arg	Ser	Arg	Gly	Gly	Arg	Arg	515	520	525
Arg	Arg	Ser	Arg	Ser	Lys	Val	Lys	Glu	Asp	Lys	Phe	Lys	Gly	Ser	Leu	530	535	540
Ser	Glu	Gly	Met	Lys	Val	Glu	Gln	Glu	Ser	Ser	Ser	Asp	Asp	Asn	Leu	545	550	555

Glu	Asp	Phe	Asp	Val	Glu	Glu	Glu	Asp	Glu	Glu	Ala	Leu	Ile	Glu	Gln	565	570	575
Arg	Arg	Ile	Gln	Arg	Gln	Ala	Ile	Val	Gln	Lys	Tyr	Lys	Tyr	Leu	Ala	580	585	590
Glu	Asp	Ser	Asn	Met	Ser	Val	Pro	Ser	Glu	Pro	Ser	Ser	Pro	Gln	Ser	595	600	605
Ser	Thr	Arg	Thr	Arg	Ser	Pro	Ser	Pro	Asp	Asp	Ile	Leu	Glu	Arg	Val	610	615	620
Ala	Ala	Asp	Val	Lys	Glu	Tyr	Glu	Arg	Glu	Asn	Val	Asp	Thr	Phe	Glu	625	630	635
Ala	Ser	Val	Lys	Ala	Lys	His	Asn	Leu	Met	Thr	Val	Glu	Gln	Asn	Asn	645	650	655
Gly	Ser	Ser	Gln	Lys	Lys	Leu	Leu	Ala	Pro	Asp	Met	Phe	Thr	Glu	Ser	660	665	670
Asp	Asp	Met	Phe	Ala	Ala	Tyr	Phe	Asp	Ser	Ala	Arg	Leu	Arg	Ala	Ala	675	680	685
Gly	Ile	Gly	Lys	Asp	Phe	Lys	Glu	Asn	Pro	Asn	Leu	Arg	Asp	Asn	Trp	690	695	700
Thr	Asp	Ala	Glu	Gly	Tyr	Tyr	Arg	Val	Asn	Ile	Gly	Glu	Val	Leu	Asp	705	710	715
Lys	Arg	Tyr	Asn	Val	Tyr	Gly	Tyr	Thr	Gly	Gln	Gly	Val	Phe	Ser	Asn	725	730	735
Val	Val	Arg	Ala	Arg	Asp	Asn	Ala	Arg	Ala	Asn	Gln	Glu	Val	Ala	Val	740	745	750
Lys	Ile	Ile	Arg	Asn	Asn	Glu	Leu	Met	Gln	Lys	Thr	Gly	Leu	Lys	Glu	755	760	765
Leu	Glu	Phe	Leu	Lys	Lys	Leu	Asn	Asp	Ala	Asp	Pro	Asp	Asp	Lys	Phe	770	775	780
His	Cys	Leu	Arg	Leu	Phe	Arg	His	Phe	Tyr	His	Lys	Gln	His	Leu	Cys	785	790	795
Leu	Val	Phe	Glu	Pro	Leu	Ser	Met	Asn	Leu	Arg	Glu	Val	Leu	Lys	Lys	805	810	815
Tyr	Gly	Lys	Asp	Val	Gly	Leu	His	Ile	Lys	Ala	Val	Arg	Ser	Tyr	Ser	820	825	830
Gln	Gln	Leu	Phe	Leu	Ala	Leu	Lys	Leu	Leu	Lys	Arg	Cys	Asn	Ile	Leu	835	840	845
His	Ala	Asp	Ile	Lys	Pro	Asp	Asn	Ile	Leu	Val	Asn	Glu	Ser	Lys	Thr	850	855	860
Ile	Leu	Lys	Leu	Cys	Asp	Phe	Gly	Ser	Ala	Ser	His	Val	Ala	Asp	Asn	865	870	875
Asp	Ile	Thr	Pro	Tyr	Leu	Val	Ser	Arg	Phe	Tyr	Arg	Ala	Pro	Glu	Ile	885	890	895
Ile	Ile	Gly	Lys	Ser	Tyr	Asp	Tyr	Gly	Ile	Asp	Met	Trp	Ser	Val	Gly	900	905	910
Cys	Thr	Leu	Tyr	Glu	Leu	Tyr	Thr	Gly	Lys	Ile	Leu	Phe	Pro	Gly	Lys	915	920	925
Thr	Asn	Asn	His	Met	Leu	Lys	Leu	Ala	Met	Asp	Leu	Lys	Gly	Lys	Met	930	935	940
Pro	Asn	Lys	Met	Ile	Arg	Lys	Gly	Val	Phe	Lys	Asp	Gln	His	Phe	Asp	945	950	955
Gln	Asn	Leu	Asn	Phe	Met	Tyr	Ile	Glu	Val	Asp	Lys	Val	Thr	Glu	Arg	965	970	975
Glu	Lys	Val	Thr	Val	Met	Ser	Thr	Ile	Asn	Pro	Thr	Lys	Asp	Leu	Leu	980	985	990
Ala	Asp	Leu	Ile	Gly	Cys	Gln	Arg	Leu	Pro	Glu	Asp	Gln	Arg	Lys	Lys	995	1000	1005
Val	His	Gln	Leu	Lys	Asp	Leu	Leu	Asp	Gln	Ile	Leu	Met	Leu	Asp	Pro	1010	1015	1020



Ala Lys Arg Ile Ser Ile Asn Gln Ala Leu Gln His Ala Phe Ile Gln  
 1025 1030 1035 1040  
 Glu Lys Ile

<210> 259  
 <211> 5265  
 <212> DNA  
 <213> Homo sapiens

<400> 259  
 gtcgaccccg cgtccggcgc ggcagctctt ttcccttctc ctccacttcc cctaccctcc 60  
 accgtccggg agccgccgcc accgccgccg aggagtcagg aagttcaaga tggccgccgc 120  
 ggagaccagc tcgtacccgg agcagccaga gatggaagat gctaattctg aaaagagtat 180  
 aaatgaagaa aatggagaag tatcagaaga ccagtctcaa aataagcaca gtcgtcacaa 240  
 aaaaaagaag cataaacaca gaagtaaaca taagaaacat aaacattcct cagaagaaga 300  
 caaggataaa aacataaac ataagcataa acataagaaa cacaaaagaa aagaggttat 360  
 tgaatcttct gataaagagg gtatgtctcc agcaaaaaga actaaacttg atgatttagc 420  
 tttgctagaa gacttggaag aacagagagc cttgattaaag gccgaacttg ataatgagtt 480  
 aatggaagga aaggccaggt ctggtatggg gctcattttg caaggttatg agtctggctc 540  
 tgaagaagag ggggaaattc atgaaaaggc aagaaatgga aataggtcta gtactagatc 600  
 ttcaagtaca aaggggaaac ttgaacttgt ggacaataaa attactaca agaaacgaag 660  
 taaaagcaga tccaaagaac ggactagaca taggtctgat aaaaagaaaa gtaagggggg 720  
 tattgaaatc gttaaagaga aaacaactag gagcaagtca aaggagagga aaaaatctaa 780  
 aagcccattc aaaaagaagta agtctcaaga tcaagcaagg aaatcaaaat cccctaccct 840  
 tagaaggcga tctcaagaga aaattggtta ggccagatct cctactgatg ataaggttaa 900  
 aattgaagat aaaaagtaaat caaaagatag gaaaaaatcc caattataa atgaaagtag 960  
 aagtcgcgat cgaggtaaaa aatccagatc ccagttgat ttaagaggta aatccaaaaga 1020  
 cagaagggtca cgggtccaaag agagaaaatc aaacgggtct gaaactgata aagaaaagaa 1080  
 gccaatataa tctccctcta aagatgcttc atctgggaaa gaaaataggt caccagcag 1140  
 aagacctggg cgtagtctta aaagaagaag tttgtctcca aaaccacgtg ataaatcaag 1200  
 aagaagcagg tctccacttt tgaatgatag aagatctaag cagagcaaat cccctcgcg 1260  
 gacactgtct cctgggagaa gagccaagag ccgatcctta gaaagaaaac gacgagaacc 1320  
 agagaggaga cgactttctt ctccaagaac acgacctcga gatgatatac tcagtagacg 1380  
 tgaagcatca aaagatgcca gcccatcaa tagatgggtc ccaaccgaa gaagaagtag 1440  
 atctccattt agaaggaggc ctcgttcccc actcagacgt agcaggctc caagaagaag 1500  
 aagcagatct cctcggagaa gggacagagg tcggaggagc agatcacgct tgccaaggcg 1560  
 gtctcgatca cgcggtgggc gtagacgaag gagcagaagc aaagtaaagg aagataaatt 1620  
 taaaggaagt ctttctgaag gaatgaaagt tgagcaggaa tcttcgtctg atgataacct 1680  
 tgaagacttt gatgtagagg aagaagatga agaagcccta atagaacaga gaagaatcca 1740  
 aaggcaggca attgttcaga aatataaata ccttgctgaa gatagcaaca tgtctgtgcc 1800  
 atctgaacca agcagccccc agagcagtag gagaacacga tcaccatctc cagatgacat 1860  
 tctggagcga gtagctgctg atgttaaaga gtatgaacgg gaaaatgttg atacatttga 1920  
 ggcctcagtg aaagccaagc ataactaat gagagttgaa cagaataatg gttcatctca 1980  
 gaagaagttg ttggcacctg atatgtttac agaactctgat gatatgtttg ctgctgtttt 2040  
 tgatagtgtc cgtcttcggg ccgctggcat tggaaaagat ttcaaagaga atcccaacct 2100  
 cagagataac tggaccgatg cagaaggcta ttatcgtgtg aacatagggtg aagtcctaga 2160  
 taaacgttac aatgtgtatg gctacactgg gcaagggtga ttacagtaag ttgtacgagc 2220  
 cagagataat gcaagagcca accaagaagt ggctgtaaag atcatcagaa acaatgagct 2280  
 catgcaaaag actggtttaa aagaattaga gttcttgaaa aaacttaatg atgctgatcc 2340  
 tgatgacaaa tttcattgtc tgagactctt caggcacttc tatcacaagc agcatctttg 2400  
 tctgggtatt gagcctctca gcatgaactt acgagagggtg ttaaaaaaat atggttaaaga 2460  
 tgttggctct catattaaag ctgtaagatc ctatagtcag cagttgttcc tggcattgaa 2520  
 actctctaaa agatgcaata tcctacatgc agatatcaag ccagacaata tcctggttaa 2580  
 tgaatccaaa actattttaa agctttgcga ttttgggtcg gcttcacatg ttgcggataa 2640  
 tgacataaca ccttatcttg tcagtagatt ttatcgtgct cctgaaatca ttataggtaa 2700  
 aagctatgac tatggtatag atatgtggtc tgtaggttgc accttatacg aactctatac 2760

tggaaaaaatt	ttattccctg	gcaaaaccaa	taaccatatg	ctgaagcttg	caatggatct	2820
caaaaggaaag	atgccaaata	agatgattcg	aaaagggtgtg	ttcaaagatc	agcatttttga	2880
tcaaaatctc	aacttcatgt	acatagaagt	tgataaagta	acagagaggg	agaaagttac	2940
tgttatgagc	accattaatc	caactaagga	cctgttggct	gacttgattg	ggtgccagag	3000
acttcctgaa	gaccaacgta	agaaagtaca	ccagctaaag	gacttgttgg	accagattct	3060
gatgttggac	ccagctaaac	gaattagcat	caaccaggcc	ctacagcacg	ccttcatcca	3120
ggaaaaaatt	taaacaagat	gaagaaactc	caaggggttg	agtaaataca	aagactgaag	3180
aaatttcaca	gcagtttatt	aatgtatata	aacttataaa	tatttctcca	gcaaatttga	3240
ggaagcatga	tatatttgaa	ttaacaccaa	gggtgatatt	tcttttagag	atgttagtta	3300
atctgttttg	tgtcttacgt	gaaatttcac	tgtagactgt	tttaaattgc	caagactgca	3360
caaaattaca	gtgctaattg	atatggttgc	agttcacata	aagacaaaag	catctgttat	3420
gaaatgagta	gtaatatgtg	gtgggtgatt	tgttcttagc	agacttggct	tcattttggg	3480
cctgagataa	aatggccagc	ataaatgctg	tttatattca	cgttttccta	ggtgtgtgtg	3540
tgcaggccac	agcagcatgc	ccttgggtga	gtcagtgccg	aaaggggtct	gttccttctt	3600
gagcctgcct	gcagggatgg	tctcctttta	aagcaggttg	tgtgcagcat	tcagtacact	3660
gaaggtaagc	taaaccatca	acatctctgg	tgttttaaga	tgtattttta	ttggaacaac	3720
tgacaaatga	gggatgttag	ccttgtggca	gaattccctg	catgtgtgat	aactgatctt	3780
gttttatttt	ttggcattgc	aactgtggca	tagttacaat	ttctgtttgt	tcatacatt	3840
taaaatttga	agagaacgcg	cctgatggat	agagcgctt	cagtgtactg	tttcttatta	3900
actttacttt	ttttaaatca	acttgcata	gactttatat	acattttgtt	aaatatagtt	3960
cctagtgaac	tagaaaacgat	gcgtagtttt	catttactaa	ttacaaatgt	tgaggcctaa	4020
ttctgaaagt	cctcatattt	aaaggctaga	caacgtaatg	aaatttttaa	ctatttgtat	4080
gtcattttga	aagtgtactg	ccttatggta	aaagtgtttt	tcatttgttc	attgttttca	4140
ttatttgtga	tcagttytgc	tttcaataca	ggcataaacc	ttccactctt	gaacaaagca	4200
gctgcttttt	aaaagcggta	attgcttctt	taccttttat	ttcttttgta	aatgaagctt	4260
ttctttaaga	atgtgacttt	aaagtgttgt	ctattgcata	aaacagttga	cactcactta	4320
ttgtaaagtg	aagattgttc	tactgcatgt	gaagtggacc	atgcagattt	ctgtatgttc	4380
tcagtatgca	tcactagata	ataaagtctt	ttgtgaacaa	ggcatttgta	gccattttta	4440
aaagtttttg	tcttcagtcg	tggttaagtca	ggtaaaccat	aaatagttaa	aagcaacctt	4500
ttgttttttt	cctgaaagtt	tttaattgaa	agtattatta	gttaaagatg	taaacctagc	4560
caaaattacc	agttttattaa	taattaggat	cctaattatt	tcaaaaaatc	ctacaaatat	4620
tgtcagcttt	cagtgtagtg	agattattcc	tgtaggttat	gggtataat	tcaggattta	4680
actaatgttt	ctgctatttt	ctcacttttc	cctttgatgg	tgcggaaga	gaaaaaggaa	4740
aacggggcac	aggccattcg	acgccttctc	caaggggtct	gatttgctga	gacaccagct	4800
tcaccttctt	aacaaggcac	ctaattacaa	caagcatgca	cattttgggtg	cattcaagaa	4860
tggaaaatca	gaatagcagc	attgattcct	ctgggtgggtt	ttgtccatt	taaagacatg	4920
aaatgaacta	cagccaggaa	ggtgatagat	gatataataa	gccacctctg	aacctacacc	4980
ccgtctcttc	acgggtttaga	cttactaaaa	taaatacaag	gtgcagctca	gtggaagatg	5040
atgacaacca	gaagacatga	gctaagggtg	agggactgtt	ctgaagaacc	tttccattta	5100
gtgatcaaga	tatggaagct	gattttctgaa	aatgctcagt	gtgtactcta	attattttatg	5160
gtaccatttg	aattgtaact	tgcattttag	cagtgcagt	ttctaattga	cttactggga	5220
aactgaataa	aatatgcctc	ttattatcaa	aaaaaaaaaa	aaagg		5265

&lt;210&gt; 260

&lt;211&gt; 5138

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 260

gtcgaccccg	cgtccggcgc	ggcagctctt	ttccttcttc	ctccacttcc	cctaccctcc	60
accgtccggg	agccgcgcgc	accgccgcgc	aggagtcagg	aagttcaaga	tggccgcgcg	120
ggagaccag	tcgctacggg	agcagccaga	gatggaagat	gctaattctg	aaaagagtat	180
aatgaagaa	aatggagaag	tatcagaaga	ccagtctcaa	aataagcaca	gtcgtcacia	240
aaaaaagaag	cataaacaca	gaagtaaaca	taagaaacat	aaacattcct	cagaagaaga	300
caaggataaa	aaacataaac	ataagcataa	acataagaaa	cacaaaagaa	aagaggttat	360
tgatgcttct	gataaagagg	gtatgtctcc	agcaaaaaag	actaaacttg	atgatttagc	420
tttgctagaa	gacttggaag	aacagagagc	ccttgattaag	gccgaacttg	ataatgagtt	480
aatggaagga	aaggtccagt	ctgggtatggg	gctcattttg	caaggttatg	agtctggctc	540

tgaagaagag	ggggaaattc	atgaaaaggc	aagaaatgga	aataggtcta	gtactagatc	600
ttcaagtaca	aaggggaaac	ttgaacttgt	ggacaataaa	attactacaa	agaaacgaag	660
taaaagcaga	tccaaagaac	ggactagaca	taggtctgat	aaaaagaaaa	gtaagggggg	720
tattgaaatc	gttaaagaga	aaacaactag	gagcaagtca	aaggagagga	aaaaatctaa	780
aagcccatcc	aaaagaagta	agtctcaaga	tcaagcaagg	aatcaaaat	cccctaccct	840
tagaaggcga	tctcaagaga	aaattggtta	ggccagatct	cctactgatg	ataagggtta	900
aattgaagat	aaaagtaa	caaaagatag	gaaaaaatcc	ccaattataa	atgaaagtag	960
aagtcgcgat	cgaggtaaaa	aatccagatc	cccagttgat	ttaagaggta	aatccaaaga	1020
cagaaggta	cgggtccaaag	agagaaaatc	aaaacggtct	gaaactgata	aagaaaagaa	1080
gccaattaaa	tctccctcta	aagatgcttc	atctgggaaa	gaaaataggt	caccagcag	1140
aagacctggt	cgtagtccta	aaagaagaag	tttgtctcca	aaaccacgtg	ataaatcaag	1200
aagaagcagg	tctccacttt	tgaatgatag	aagatctaag	cagagcaaat	cccctcgcg	1260
gacactgtct	cctgggagaa	gagccaagag	ccgatcctta	gaaagaaaac	gacgagaacc	1320
agagaggaga	cgactttctt	ctccaagaac	acgacctcga	gatgatattc	tcagtagacg	1380
tgaagatca	aaagatgcc	gccccatcaa	tagatggtct	ccaacccgaa	gaagaagtag	1440
atctccatt	agaaggaggt	ctcggtcccc	actcagacgt	agcaggtctc	caagaagaag	1500
aagcagatct	cctcgagaa	gggacagagg	tccggaggagc	agatcacgct	tgcaaggcg	1560
gtctcgatca	cgcggtggtc	gtagacgaag	gagcagaagc	aaagtaaagg	aagataaatt	1620
taaaggaagt	ctttctgaag	gaatgaaagt	tgagcaggaa	tcttcgtctg	atgataacct	1680
tgaagacttt	gtagtagag	aagaagccta	agaagcccta	atagaacaga	gaagaatcca	1740
aaggcaggca	attgttcaga	aatataaata	ccttgctgaa	gatagcaaca	tgtctgtgcc	1800
atctgaacca	agcagcccc	agagcagtac	gagaacacga	tcaccatctc	cagatgacat	1860
tctggagcga	gtagctgtg	atgttaaaga	gtatgaacgg	gaaaatgttg	atacatttga	1920
ggcctcagtg	aaagccaagc	ataatcta	gacagttgaa	cagaataatg	gttcattctca	1980
gaagaagttg	ttggcacctg	atatgtttac	agaatctgat	gatattgttg	ctgcgtattt	2040
tgatagtgt	cgtcttcggg	ccgctggcat	tggaaaagat	ttcaaagaga	atcccaacct	2100
cagagataac	tgagccgatg	cagaaggcta	ttatcgtgtg	aacataggtg	aagtcctaga	2160
taaagcttac	aatgtgtatg	gctacactgg	gcaaggtgta	ttcagtaatg	ttgtacgagc	2220
cagagataat	gcaagagcca	accaagaagt	ggctgtaaag	atcatcagaa	acaatgact	2280
catgcaaaag	actggtttta	aagaattaga	gttcttgaaa	aaacttaatg	atgctgatcc	2340
tgatgacaaa	tttcattgtc	tgagactctt	caggcacttc	tatcacaagc	agcatctttg	2400
tctggtatcc	gagcctctca	gcatgaactt	acgagaggtg	ttaaaaaat	atggtaaaga	2460
tggttggtctt	catattaaag	ctgtaagatc	ctatagtcag	cagttgttcc	tggcattgaa	2520
actccttaaa	agatgcaata	tctacatgc	agatatcaag	ccagacaata	tcctggttaa	2580
tgaatccaaa	actattttta	agctttgcga	ttttgggtcg	gcttcacatg	ttgcgataa	2640
tgacataaca	ccttatcttg	tcagtagatt	ttatcgtgct	cctgaaatca	ttataggtaa	2700
aagctatgac	ttgggtatag	atatgtggtc	tgtaggttgc	acctatacag	aactctatac	2760
tggaaaaatt	ttattccctg	gcaaaaccaa	taaccatag	ctgaagcttg	caatggatct	2820
caaaggaaaag	atgccaaaata	agatgattcg	aaaagggtgtg	ttcaaagatc	agcattttga	2880
tcaaaatctc	aacttcatgt	acatagaagt	tgataaagta	acagagaggg	agaaagttac	2940
tgttatgagc	accattaatc	caactaagga	cctgttggct	gacttgattg	ggtgccagag	3000
acttcctgaa	gaccaacgta	agaaagtaca	ccagctaaag	gacttgttgg	accagattct	3060
gatgttgga	ccagctaaac	gaattagcat	caaccaggcc	ctacagcacg	ccttcatcca	3120
ggaaaaaatt	taaacaagat	gaagaaatc	caagggtttg	agtaaataca	aagactgaag	3180
aaatttcaca	gcagtttatt	aatgtatata	aacttataaa	tatttctcca	gcaaatttga	3240
ggaagcatga	tatatgtgaa	ttaacaccaa	gggtgatatt	tcttttagag	atgttagtta	3300
atctgttttg	tgtcttacgt	gaaatttcac	tgtagactgt	tttaaattgc	caagactgca	3360
caaaattaca	gtgctaattg	atatggttgc	agttcacata	aagacaaaag	catctgttat	3420
gaaatgagta	gtaattattg	gtggttgatt	tgttcttagc	agacttggct	tcatttttgt	3480
cttgagataa	aatggccagc	ataaatgctg	tttatattca	cgttttccta	ggtgtgtgtg	3540
tgaggccac	agcagcatgc	ccttggtgta	gtcagtgccg	aaaggggtct	gttccttctt	3600
gagcctgcct	gcagggatgg	tctcctttta	aagcaggttg	tgtgcagcat	tcagtacact	3660
gaaggtaagc	taaacatca	acatctctgg	tgttttaaga	tgttatttta	ttggaacaac	3720
tgacaaatga	gggatgttag	ctttgtggca	gaattccctg	catgtgtgat	aactgatctt	3780
gttttatttt	ttggcatg	aactgtggca	tagttacaat	ttctgtttgt	tcacacatt	3840
taaaattgga	agagaacg	cttgatggat	agagcgctt	cagtgtactg	tttcttatta	3900
actttacttt	ttttaaatca	acttgctata	gactttatat	acattttgtt	aaatatagtt	3960
cctagtgaca	tagaaacgat	gcgtagtttt	catttactaa	ttacaaatgt	tgaggcctaa	4020

ttctgaaagt	cctcatat	aaaggctaga	caacgtaatg	aaatttttaa	ctattttgat	4080
gtcattttga	aagtgtactg	ctttatggta	aaagtgtttt	tcattttgtc	attgttttca	4140
ttattttgtga	tcattgttgc	tttcaataca	ggcataaaacc	ttccactcct	gaacaaagca	4200
gctgcttttt	aaaagcggta	attgcttctt	taccttttat	ttcttttgta	aatgaagctt	4260
ttctttaaga	atgtgacttt	aaagtgttgt	ctattgcata	aaacagttga	cactcactta	4320
ttgtaaagtg	aagattgttc	tactgcatgt	gaagtggacc	atgcagattt	ctgtatgttc	4380
tcagtatgca	tcactagata	ataaagtctt	ttgtgaacaa	ggcattttgt	gccattttta	4440
aaagtttttg	tcttcagtgc	tggtaaagtca	ggtaaaccat	aaatagttaa	aagcaacctt	4500
ttgttttttt	cctgaaagtt	tttaattgaa	agtattatta	gttaaagatg	taaacctagc	4560
caaaattacc	agttttattaa	taattagatg	cctaattatt	tcaaaaaatc	ctacaaatat	4620
tgtcagcttt	cagtgtagtg	agattattcc	tgtaggttat	gggtataat	tcaggattta	4680
actaatgttt	ctgctatttt	ctcaactttt	cttttgatgg	tgcggaaga	gaaaaaggaa	4740
aacggggcac	aggccattcg	acgccttctc	caagggtct	gatttgctga	gacaccagct	4800
tcaccttctt	aacaaggcac	ctaattacaa	caagcatgca	cattttggtg	cattcaagaa	4860
tggaaaatca	gaatagcagc	attgattctt	ctggcgagc	tcagtggag	atgatgacaa	4920
ccagaagaca	tgagctaagg	gtaagggact	gttctgaaga	acctttccat	ttagtatca	4980
agatatggaa	gctgatttct	gaaaatgctc	agtgtgtact	ctaattattt	atggtaccat	5040
ttgaattgta	acttgcattt	tagcagtgc	tgtttcta	tgacttactg	ggaaactgaa	5100
taaaatagc	ctcttattat	caaaaaaaaa	aaaaaagg			5138

&lt;210&gt; 261

&lt;211&gt; 1834

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 261

agacgggtgct	ggtgactcgt	ccacactgct	cgcttcggat	actccaggcg	tctcccgttg	60
cgcccgctcc	ctgccttaga	ggccagcctt	ggacacttgc	tgcccccttc	cagcccggat	120
tctgggatcc	ttccctctga	gccaacatct	gggtcctgcc	ttcgacacca	ccccaggct	130
tcctaccttg	cgtgcctgga	gtctgcccc	ggggcccttg	tcctggccat	ggcccagaag	240
ggggctcctgg	ggcctgggca	gctgggggct	gtggccattc	tgtctatct	tggtactct	300
cggtcgggga	caggagcgga	aggggcagaa	gctccctgcg	gtgtggcccc	ccaagcacgc	360
atcacagggtg	gcagcagtcg	agtcgcccgt	cagtggccct	ggcaggtcag	catcacctat	420
gaaggcgtcc	atgtgtgtgg	tggctctctc	gtgtctgagc	agtgggtgct	gtcagctgct	480
cactgcttcc	ccagcgagca	ccacaaggaa	gcctatgagg	tcaagctggg	ggcccaccag	540
ctagactcct	actccgagga	cgccaaggte	agcacctga	aggacatcat	ccccacccc	600
agctacctcc	aggagggtc	ccagggcgac	attgcaactc	tccaactcag	cagacccatc	660
accttctccc	gtacatccg	gcccactctg	ctccctgcag	ccaacgcctc	cttccccaac	720
ggcctccact	gcactgtcac	tggctgggg	catgtggccc	cctcagtgag	cctcctgacg	780
cccaagccac	tgcagcaact	cgagggtgct	ctgatcagtc	gtgagacgtg	taactgcctg	840
tacaacatcg	acgccaagcc	tgaggagccg	cactttgtcc	aagaggacat	ggtgtgtgct	900
ggctatgtgg	aggggggcaa	ggacgcctgc	cagggtgact	ctggggggcc	actctcctgc	960
cctgtggagg	gtctctggtg	cctgacgggc	attgtgagct	ggggagatgc	ctgtggggcc	1020
cgcaacaggc	ctggtgtgta	cactctggcc	tccagctatg	cctcctggat	ccaaagcaag	1080
gtgacagaac	tccagcctcg	tgtggtgccc	caaaccagg	agtcccagcc	cgacagcaac	1140
ctctgtggca	gccacctggc	cttcagctct	gccccagccc	agggttgct	gaggccatc	1200
cttttctctg	ctctgggcct	ggctctgggc	ctcctctccc	catggctcag	cgagcactga	1260
gctggcccta	cttcaggat	ggatgcatca	cactcaagga	caggagcctg	gtccttccct	1320
gatggccttt	ggaccaggg	cctgacttga	gccactcctt	ccttcaggac	tctgcgggag	1380
gctggggccc	catcttgatc	tttgagccca	ttcttctggg	tgtgcttttt	gggaccatca	1440
ctgagagtca	ggagttttac	tgctgtagc	aatggccaga	gcctctggcc	cctcaccac	1500
catggaccaag	ccattggcc	gagctcctgg	ggagctcctg	ggacccttgg	ctatgaaaat	1560
gagccctggc	tcccacctgt	ttctggaaga	ctgctcccgg	ccgcctgccc	cagactgatg	1620
agcacatctc	tctgccctct	ccctgtgttc	tgggctgggg	ccaccttctg	gcagcttcga	1680
ggacaggaaa	ggccccaatc	ttgcccactg	gccgtgagc	gccccgagc	cctgactcct	1740
ggactccgga	ggactgagcc	cccaccggaa	ctgggctggc	gcttgatct	ggggtgggag	1800
taacagggca	gaaatgatta	aaatgtttga	gcac			1834

275

<210> 262  
 <211> 343  
 <212> PRT  
 <213> Homo sapiens

<400> 262  
 Met Ala Gln Lys Gly Val Leu Gly Pro Gly Gln Leu Gly Ala Val Ala  
 1 5 10 15  
 Ile Leu Leu Tyr Leu Gly Leu Leu Arg Ser Gly Thr Gly Ala Glu Gly  
 20 25 30  
 Ala Glu Ala Pro Cys Gly Val Ala Pro Gln Ala Arg Ile Thr Gly Gly  
 35 40 45  
 Ser Ser Ala Val Ala Gly Gln Trp Pro Trp Gln Val Ser Ile Thr Tyr  
 50 55 60  
 Glu Gly Val His Val Cys Gly Gly Ser Leu Val Ser Glu Gln Trp Val  
 65 70 75 80  
 Leu Ser Ala Ala His Cys Phe Pro Ser Glu His His Lys Glu Ala Tyr  
 85 90 95  
 Glu Val Lys Leu Gly Ala His Gln Leu Asp Ser Tyr Ser Glu Asp Ala  
 100 105 110  
 Lys Val Ser Thr Leu Lys Asp Ile Ile Pro His Pro Ser Tyr Leu Gln  
 115 120 125  
 Glu Gly Ser Gln Gly Asp Ile Ala Leu Leu Gln Leu Ser Arg Pro Ile  
 130 135 140  
 Thr Phe Ser Arg Tyr Ile Arg Pro Ile Cys Leu Pro Ala Ala Asn Ala  
 145 150 155 160  
 Ser Phe Pro Asn Gly Leu His Cys Thr Val Thr Gly Trp Gly His Val  
 165 170 175  
 Ala Pro Ser Val Ser Leu Leu Thr Pro Lys Pro Leu Gln Gln Leu Glu  
 180 185 190  
 Val Pro Leu Ile Ser Arg Glu Thr Cys Asn Cys Leu Tyr Asn Ile Asp  
 195 200 205  
 Ala Lys Pro Glu Glu Pro His Phe Val Gln Glu Asp Met Val Cys Ala  
 210 215 220  
 Gly Tyr Val Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly  
 225 230 235 240  
 Pro Leu Ser Cys Pro Val Glu Gly Leu Trp Tyr Leu Thr Gly Ile Val  
 245 250 255  
 Ser Trp Gly Asp Ala Cys Gly Ala Arg Asn Arg Pro Gly Val Tyr Thr  
 260 265 270  
 Leu Ala Ser Ser Tyr Ala Ser Trp Ile Gln Ser Lys Val Thr Glu Leu  
 275 280 285  
 Gln Pro Arg Val Val Pro Gln Thr Gln Glu Ser Gln Pro Asp Ser Asn  
 290 295 300  
 Leu Cys Gly Ser His Leu Ala Phe Ser Ser Ala Pro Ala Gln Gly Leu  
 305 310 315 320  
 Leu Arg Pro Ile Leu Phe Leu Pro Leu Gly Leu Ala Leu Gly Leu Leu  
 325 330 335  
 Ser Pro Trp Leu Ser Glu His  
 340

<210> 263  
 <211> 2554  
 <212> DNA  
 <213> Homo sapiens

<400> 263

```

gcgccatgag ccggagtctc ttgctccggt tcttgctggt cctgctcctg ctcccgcgc 60
tccccgtcct gctcgcggac ccaggggcgc ccacgccagt gaatccctgt tgttactatc 120
catgccagca ccagggcatc tgtgtccgct tcggccttga ccgctaccag tgtgactgca 180
cccgacggg ctattccggc cccaactgca ccatccctgg cctgtggacc tggctccgga 240
attcactgcg gccagcccc tctttcacc acttctgct cactcacggg cgctggttct 300
gggagtttgt caatgccacc ttcacccgag agatgctcat gcgcctggtg ctcacagtgc 360
gctccaacct tatccccagt ccccccacct acaactcagc acatgactac atcagctggg 420
agtctttctc caacgtgagc tattacactc gtattctgcc ctctgtgcct aaagattgcc 480
ccacacccat gggaaccaa gggaagaagc agttgccaga tgcccagctc ctggcccgc 540
gcttctcgt caggaggaag ttcatacctg accccaagg caccaacctc atgtttgcct 600
tctttgcaca acacttcacc caccagttct tcaaaacttc tggcaagatg ggtcctggct 660
tcaccaaggc cttgggcat gggttagacc tcggccacat ttatggagac aatctggagc 720
gtcagtatca actgcggctc tttaaggatg ggaaactcaa gtaccaggtg ctggatggag 780
aatgtatccc gccctcggtg gaagaggcgc ctgtgttgat gcactacccc cgaggcatcc 840
cgcccagag ccagatggct gtgggcccag aggtgtttgg gctgttctc gggctcatgc 900
tgtatgccac gctctggcta cgtgagcaca accgtgtgtg tgacctgctg aaggctgagc 960
accccacctg gggcgtgag cagcttttcc agacgacccg cctcatcctc ataggggaga 1020
ccatcaagat tgtcatcgag gagtacgtgc agcagctgag tggctatttc ctgcagctga 1080
aatttgacc agagctgctg ttcggtgtcc agttccaata ccgcaaccgc attgccatgg 1140
agttcaacca tctctaccac tggcaccccc tcatgcctga ctcttcaag gtgggctccc 1200
aggagtacag ctacgagcag ttcttggtca acacctcat gttggtggac tatggggtt 1260
aggccctggt ggatgccttc tctcgccaga ttgctggccg gatcggtggg ggcaggaaca 1320
tggaccacca catcctgcat gtggctgtgg atgtcatcag ggagtctcg gagatgcggc 1380
tgcagccctt caatgagtag cgcaagaggt ttggcatgaa accctacacc tccttcagg 1440
agctcgtagg agagaaggag atggcagcag agttggagga attgtatgga gacattgatg 1500
cgttggagtt ctaccctgga ctgcttcttg aaaagtgcc tccaaactct atctttggg 1560
agagtatgat agagattggg gctccctttt cctcaaggg tctcctaggg aatcccctc 1620
gttctccgga gtactggaag ccgagcacat ttggcggcga ggtgggcttt aacattgtca 1680
agacggccac actgaagaag ctggtctgcc tcaacaccaa gacctgtccc tacgtttcct 1740
tccgtgtgcc ggatgccagt caggatgatg ggctgtgtt ggagcgacca tccacagagc 1800
tctgaggggc agaaaagcag cattctggag gggagagctt tgtgcttgtc attccagagt 1860
gctgaggcca gggctgatgg tcttaaatgc tcatcttctg gtttggcatg gtgagtgtt 1920
gggttgacat ttagaacttt aagtctcacc cattatctgg aatattgtga ttctgtttat 1980
tcttcagaa tgctgaactc cttgttagcc ctacagattg ttaggagtgg ttctcattt 2040
gtctgccaga atactgggtt cttagttagc aacctagaat gtcagatttc tggttgatt 2100
gtaacacagt cattctagga tgtggagcta ctgatgaaat ctgtagaaa gttaggggt 2160
tcttattttg cattccagaa tcttgacttt ctgattggtg attcaaagtg ttgtgttccc 2220
tggtgatga tccagaacag tggctcgtat cccaaatctg tcagcatctg gctgtctaga 2280
atgtggattt gattcatttt cctgttcagt gagatatcat agagacggag atcctaaggt 2340
ccaacaagaa tgcattccct gaatctgtgc ctgcactgag agggcaagga agtggggtgt 2400
tcttcttggg accccacta agaccctggt ctgaggatgt agagagaaca ggtgggctgt 2460
attcacgcca ttggttgga gctaccagag ctctatcccc atccaggtct tgactcatgg 2520
cagctgtttc tcatgaagct aataaaattc gccc 2554

```

&lt;210&gt; 264

&lt;211&gt; 599

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 264

```

Met Ser Arg Ser Leu Leu Leu Arg Phe Leu Leu Phe Leu Leu Leu Leu
1          5          10          15
Pro Pro Leu Pro Val Leu Leu Ala Asp Pro Gly Ala Pro Thr Pro Val
20          25          30
Asn Pro Cys Cys Tyr Tyr Pro Cys Gln His Gln Gly Ile Cys Val Arg
35          40          45
Phe Gly Leu Asp Arg Tyr Gln Cys Asp Cys Thr Arg Thr Gly Tyr Ser
50          55          60

```

Gly	Pro	Asn	Cys	Thr	Ile	Pro	Gly	Leu	Trp	Thr	Trp	Leu	Arg	Asn	Ser	65	70	75	80
Leu	Arg	Pro	Ser	Pro	Ser	Phe	Thr	His	Phe	Leu	Leu	Thr	His	Gly	Arg	85	90	95	
Trp	Phe	Trp	Glu	Phe	Val	Asn	Ala	Thr	Phe	Ile	Arg	Glu	Met	Leu	Met	100	105	110	
Arg	Leu	Val	Leu	Thr	Val	Arg	Ser	Asn	Leu	Ile	Pro	Ser	Pro	Pro	Thr	115	120	125	
Tyr	Asn	Ser	Ala	His	Asp	Tyr	Ile	Ser	Trp	Glu	Ser	Phe	Ser	Asn	Val	130	135	140	
Ser	Tyr	Tyr	Thr	Arg	Ile	Leu	Pro	Ser	Val	Pro	Lys	Asp	Cys	Pro	Thr	145	150	155	160
Pro	Met	Gly	Thr	Lys	Gly	Lys	Lys	Gln	Leu	Pro	Asp	Ala	Gln	Leu	Leu	165	170	175	
Ala	Arg	Arg	Phe	Leu	Leu	Arg	Arg	Lys	Phe	Ile	Pro	Asp	Pro	Gln	Gly	180	185	190	
Thr	Asn	Leu	Met	Phe	Ala	Phe	Phe	Ala	Gln	His	Phe	Thr	His	Gln	Phe	195	200	205	
Phe	Lys	Thr	Ser	Gly	Lys	Met	Gly	Pro	Gly	Phe	Thr	Lys	Ala	Leu	Gly	210	215	220	
His	Gly	Val	Asp	Leu	Gly	His	Ile	Tyr	Gly	Asp	Asn	Leu	Glu	Arg	Gln	225	230	235	240
Tyr	Gln	Leu	Arg	Leu	Phe	Lys	Asp	Gly	Lys	Leu	Lys	Tyr	Gln	Val	Leu	245	250	255	
Asp	Gly	Glu	Met	Tyr	Pro	Pro	Ser	Val	Glu	Glu	Ala	Pro	Val	Leu	Met	260	265	270	
His	Tyr	Pro	Arg	Gly	Ile	Pro	Pro	Gln	Ser	Gln	Met	Ala	Val	Gly	Gln	275	280	285	
Glu	Val	Phe	Gly	Leu	Leu	Pro	Gly	Leu	Met	Leu	Tyr	Ala	Thr	Leu	Trp	290	295	300	
Leu	Arg	Glu	His	Asn	Arg	Val	Cys	Asp	Leu	Leu	Lys	Ala	Glu	His	Pro	305	310	315	320
Thr	Trp	Gly	Asp	Glu	Gln	Leu	Phe	Gln	Thr	Thr	Arg	Leu	Ile	Leu	Ile	325	330	335	
Gly	Glu	Thr	Ile	Lys	Ile	Val	Ile	Glu	Glu	Tyr	Val	Gln	Gln	Leu	Ser	340	345	350	
Gly	Tyr	Phe	Leu	Gln	Leu	Lys	Phe	Asp	Pro	Glu	Leu	Leu	Phe	Gly	Val	355	360	365	
Gln	Phe	Gln	Tyr	Arg	Asn	Arg	Ile	Ala	Met	Glu	Phe	Asn	His	Leu	Tyr	370	375	380	
His	Trp	His	Pro	Leu	Met	Pro	Asp	Ser	Phe	Lys	Val	Gly	Ser	Gln	Glu	385	390	395	400
Tyr	Ser	Tyr	Glu	Gln	Phe	Leu	Phe	Asn	Thr	Ser	Met	Leu	Val	Asp	Tyr	405	410	415	
Gly	Val	Glu	Ala	Leu	Val	Asp	Ala	Phe	Ser	Arg	Gln	Ile	Ala	Gly	Arg	420	425	430	
Ile	Gly	Gly	Gly	Arg	Asn	Met	Asp	His	His	Ile	Leu	His	Val	Ala	Val	435	440	445	
Asp	Val	Ile	Arg	Glu	Ser	Arg	Glu	Met	Arg	Leu	Gln	Pro	Phe	Asn	Glu	450	455	460	
Tyr	Arg	Lys	Arg	Phe	Gly	Met	Lys	Pro	Tyr	Thr	Ser	Phe	Gln	Glu	Leu	465	470	475	480
Val	Gly	Glu	Lys	Glu	Met	Ala	Ala	Glu	Leu	Glu	Glu	Leu	Tyr	Gly	Asp	485	490	495	
Ile	Asp	Ala	Leu	Glu	Phe	Tyr	Pro	Gly	Leu	Leu	Leu	Glu	Lys	Cys	His	500	505	510	
Pro	Asn	Ser	Ile	Phe	Gly	Glu	Ser	Met	Ile	Glu	Ile	Gly	Ala	Pro	Phe	515	520	525	

278

Ser Leu Lys Gly Leu Leu Gly Asn Pro Ile Cys Ser Pro Glu Tyr Trp  
 530 535 540  
 Lys Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Asn Ile Val Lys Thr  
 545 550 555 560  
 Ala Thr Leu Lys Lys Leu Val Cys Leu Asn Thr Lys Thr Cys Pro Tyr  
 565 570 575  
 Val Ser Phe Arg Val Pro Asp Ala Ser Gln Asp Asp Gly Pro Ala Val  
 580 585 590  
 Glu Arg Pro Ser Thr Glu Leu  
 595

<210> 265  
 <211> 3000  
 <212> DNA  
 <213> Homo sapiens

<400> 265  
 ccgccggccg gggcgccctgg ctgcactcag cgccggagcc gggagctagc ggccgccgcc 60  
 atgtcccacc agaccggcat ccaagcaagt gaagatgtta aagagatctt tgccagagcc 120  
 agaaatggaa agtacagact tctgaaaata tctattgaaa atgagcaact tgtgattgga 180  
 tcatatagtc agccttcaga ttcttgggat aaggattatg attcctttgt tttacccttg 240  
 ttggaggaca aacaacctatg ctatatatta ttcagggttag attctcagaa tgcccaggga 300  
 tatgaatgga tattcattgc atggtctcca gatcattctc atgttcgtca aaaaatgttg 360  
 tatgcagcaa caagagcaac tctgaagaag gaatttggag gtggccacat taaagatgaa 420  
 gtatttggaa cagtaaagga agatgtatca ttacatggat ataaaaaata cttgctgtca 480  
 caatcttccc ctgcccact gactgcagct gaggaagaac tacgacagat taaaatcaat 540  
 gaggtacaga ctgacgtggg tgtggacact aagcatcaaa cactacaagg agtagcattt 600  
 cccatttctc gagaagcctt tcaggctttg gaaaaattga ataatagaca gctcaactat 660  
 gtgcagtttg aaatagatat aaaaaatgaa attataattt tggccaacac aacaaataca 720  
 gaactgaaag atttgccaaa gaggattccc aaggattcag ctcgttacca tttctttctg 780  
 tataaacatt cccatgaagg agactattta gagtccatag tttttattta ttcaatgcct 840  
 ggatacacat gcagtataag agagcggatg ctgtattcta gctgcaagag ccgtctgcta 900  
 gaaattgtag aaagacaact acaaatggat gtaattagaa agatcgagat agacaatggg 960  
 gatgagttga ctgcagactt cttttatgaa gaagtacatc ccaagcagca tgcacacaag 1020  
 caaagttttg caaaaccaa aggtcctgca ggaaaaagag gaattcgaag actaattagg 1080  
 ggcccagcgg aaactgaagc tactactgat taaagtcac acattaaaca ttgtaatact 1140  
 agttttttta aagtccagct tttagtacag gagaactgaa atcattccat gttgatataa 1200  
 agtagggaaa aaaattgtac tttttgaaa atagcacttt tcacttctgt gtgtttttta 1260  
 aattaatgtt atagaagact catgatttct atttttgagt taaagctaga aaagggttca 1320  
 acataatgtt taattttgtc acactgtttt catagcgttg attccacact tcaaatactt 1380  
 cttaaaattt tatacagttg ggccagttct agaaagtctg atgtctcaa gggtaaactt 1440  
 actactttct tgtgggacag aaagacctta aaatattcat attacttaat gaatatgtta 1500  
 aggaccagc tagagtattt tctaagctgg aaacttagtg tgccttgaa aagccgcaag 1560  
 ttgcttactc cgagtagctg tgctagctct gtcagactgt aggatcatgt ctgcaacttt 1620  
 tagaaatagt gctttatatt gcagcagtct tttatatttg actttttttt aatagcatta 1680  
 aaattgcaga tcagctcact ctgaaacttt aagggtacca gatattttct atactgcagg 1740  
 atttctgatg acattgaaag actttaaaca gccttagtaa attatctttc taatgctctg 1800  
 tgaggccaaa catttatgtt cagattgaaa tttaaattaa tatcattcaa aaggaaacaa 1860  
 aaaatgttga gttttaaaaa tcaggattga cttttttctc caaaaccata catttatggg 1920  
 caaattgtgt tctttatcac ttccgagcaa atactcagat ttaaaattac tttaaagtcc 1980  
 tggtaactta caggctaacg tagataaaca ccttaataat ctgagttaat actgtatttc 2040  
 aaaacacatt taactgtttt ctaatgcttt gcattatcag ttacaacct gagagatttt 2100  
 gagcctcata tttctttgat acttgaaata gagggagcta gaacacttaa tgtttaatct 2160  
 gttaaacctg ctgcaagagc cataactttg aggcattttc taaatgaact gtggggatcc 2220  
 aggatttgtg atttcttgat ctaaacttta tgctgcataa atcacttata ggaaatgcac 2280  
 atttcatagt gtgaagcact catttctaaa ccttattatc taaggtaata tatgcacctt 2340  
 tcagaaattt gtgttcgagt aagtaaagca tattagaata attgtgggtt gacagatttt 2400



taaaatagaa tttagagtat ttgggggtttt gtttgtttac aaataatcag actataatat 2460  
 ttaaaccatgc aaaataactg acaataatgt tgcacttggt tactaaagat ataagttggt 2520  
 ccatgggtgt acacgtagac agacacacat acacccaaat tattgcatta agaatcctgg 2580  
 agcagaccat agctgaagct gttattttca gtcaggaaga ctacctgtca tgaaggata 2640  
 aaataattta gaagtgaatg tttttctgta ccatctatgt gcaattatac tctaaattcc 2700  
 actacactac attaaagtaa atggacattc cagaatatag atgtgattat agtcttaaac 2760  
 taattattat taaaccaatg attgctgaaa atcagtgatg catttggtat agagtataac 2820  
 tcacgttta cagtatgttt tagttggcag tatcatacct agatggtgaa taacatattc 2880  
 ccagtaaatt tatatagcag tgaagaatta catgccttct ggtggacatt ttataagtgc 2940  
 attttatatc acaataaaaa ttttttctct ttaaaaaaaa aaaacaagaa aaaaaaaaaa 3000

<210> 266

<211> 350

<212> PRT

<213> Homo sapiens

<400> 266

Met	Ser	His	Gln	Thr	Gly	Ile	Gln	Ala	Ser	Glu	Asp	Val	Lys	Glu	Ile	1	5	10	15
Phe	Ala	Arg	Ala	Arg	Asn	Gly	Lys	Tyr	Arg	Leu	Leu	Lys	Ile	Ser	Ile	20	25	30	
Glu	Asn	Glu	Gln	Leu	Val	Ile	Gly	Ser	Tyr	Ser	Gln	Pro	Ser	Asp	Ser	35	40	45	
Trp	Asp	Lys	Asp	Tyr	Asp	Ser	Phe	Val	Leu	Pro	Leu	Leu	Glu	Asp	Lys	50	55	60	
Gln	Pro	Cys	Tyr	Ile	Leu	Phe	Arg	Leu	Asp	Ser	Gln	Asn	Ala	Gln	Gly	65	70	75	80
Tyr	Glu	Trp	Ile	Phe	Ile	Ala	Trp	Ser	Pro	Asp	His	Ser	His	Val	Arg	85	90	95	
Gln	Lys	Met	Leu	Tyr	Ala	Ala	Thr	Arg	Ala	Thr	Leu	Lys	Lys	Glu	Phe	100	105	110	
Gly	Gly	Gly	His	Ile	Lys	Asp	Glu	Val	Phe	Gly	Thr	Val	Lys	Glu	Asp	115	120	125	
Val	Ser	Leu	His	Gly	Tyr	Lys	Lys	Tyr	Leu	Leu	Ser	Gln	Ser	Ser	Pro	130	135	140	
Ala	Pro	Leu	Thr	Ala	Ala	Glu	Glu	Glu	Leu	Arg	Gln	Ile	Lys	Ile	Asn	145	150	155	160
Glu	Val	Gln	Thr	Asp	Val	Gly	Val	Asp	Thr	Lys	His	Gln	Thr	Leu	Gln	165	170	175	
Gly	Val	Ala	Phe	Pro	Ile	Ser	Arg	Glu	Ala	Phe	Gln	Ala	Leu	Glu	Lys	180	185	190	
Leu	Asn	Asn	Arg	Gln	Leu	Asn	Tyr	Val	Gln	Leu	Glu	Ile	Asp	Ile	Lys	195	200	205	
Asn	Glu	Ile	Ile	Ile	Leu	Ala	Asn	Thr	Thr	Asn	Thr	Glu	Leu	Lys	Asp	210	215	220	
Leu	Pro	Lys	Arg	Ile	Pro	Lys	Asp	Ser	Ala	Arg	Tyr	His	Phe	Phe	Leu	225	230	235	240
Tyr	Lys	His	Ser	His	Glu	Gly	Asp	Tyr	Leu	Glu	Ser	Ile	Val	Phe	Ile	245	250	255	
Tyr	Ser	Met	Pro	Gly	Tyr	Thr	Cys	Ser	Ile	Arg	Glu	Arg	Met	Leu	Tyr	260	265	270	
Ser	Ser	Cys	Lys	Ser	Arg	Leu	Leu	Glu	Ile	Val	Glu	Arg	Gln	Leu	Gln	275	280	285	
Met	Asp	Val	Ile	Arg	Lys	Ile	Glu	Ile	Asp	Asn	Gly	Asp	Glu	Leu	Thr	290	295	300	
Ala	Asp	Phe	Leu	Tyr	Glu	Glu	Val	His	Pro	Lys	Gln	His	Ala	His	Lys	305	310	315	320

Gln Ser Phe Ala Lys Pro Lys Gly Pro Ala Gly Lys Arg Gly Ile Arg  
325 330 335  
Arg Leu Ile Arg Gly Pro Ala Glu Thr Glu Ala Thr Thr Asp  
340 345 350

<400> 267

cactccggag	acggcggttg	ttttggggtg	tgggggggtg	gtggcactat	gtggcgcgtc	60
tgtgcgcgac	gggctcagaa	tgtagcccca	tgggcgggac	tcgaggctcg	gtggacgggc	120
ttgcaggagc	taccocgaac	tccacgagtg	acctcgcat	ctggcccggc	tcccgttcgt	180
cgcaacagcg	tgactacagc	gatatggcgg	gtccgggcac	tgtgcggctg	gacccccagt	240
ctctggggcca	cgcccgaggaa	cgcgcttactg	ctcgagcttt	tgggttcgcc	cggccgcgcg	300
tattacagtc	ttcccccgca	tcagaagggt	ccattgcctt	ctctttcccc	cacaatgc	358

```

<400> 268
Met Trp Arg Val Cys Ala Arg Arg Ala Gln Asn Val Ala Pro Trp Ala
 1          5          10          15
Gly Leu Glu Ala Arg Trp Thr Ala Leu Gln Glu Val Pro Gly Thr Pro
 20          25          30
Arg Val Thr Ser Arg Ser Gly Pro Ala Pro Val Arg Arg Asn Ser Val
 35          40          45
Thr Thr Gly Tyr Gly Gly Val Arg Ala Leu Cys Gly Trp Thr Pro Ser
 50          55          60
Ser Gly Ala Thr Pro Arg Asn Arg Leu Leu Leu Gln Leu Leu Gly Ser
 65          70          75          80
Pro Gly Arg Arg Tyr Tyr Ser Leu Pro Pro His Gln Lys Val Pro Leu
 85          90          95
Pro Ser Leu Ser Pro Thr Met
 100

```

<400>	269						
ggactgttga	agacaggtct	ccacacacag	ctccagcagc	cacatttgc	accttggcca	60	
tctgtccaga	acctgctccc	acctcaggcc	caggccaacc	gtgcaactgt	gcaatgggct	120	
ctgagctgga	gacggcgatg	gagaccctca	tcaacgtgtt	ccacgcccac	tcggggcaaa	180	
agggggcaaa	gtacaagctg	agcaagaagg	agctgaaaga	gctgctgcag	acggagctct	240	
ctggcttcct	ggatgcccg	aaggatgtgg	atgctgtgga	caaggtgatg	aaggagctag	300	
acgagaatgg	gacgggggag	gtggacttcc	aggagtatgt	ggtgctttgt	gctgctctca	360	
cagtggcctg	taacaatttc	ttctgggaga	acagttgagc	agacagccac	attgggcagc	420	
gcccttcctc	tccaccctcc	cagacctgcc	tcttcccctc	gcttccacct	caccccaact	480	
atccctctcc	ataaccccac	ccttgcccac	cccaccccca	ccccaccaca	gggcgcaaga	540	
ctgcggtgcc	aagcctgcaa	ctcatctttc	attaaaggct	tctctctcac	cagcaaaaaa	600	
aaaaaaa						607	

281

<210> 270  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<400> 270  
 Met Gly Ser Glu Leu Glu Thr Ala Met Glu Thr Leu Ile Asn Val Phe  
 1 5 10 15  
 His Ala His Ser Gly Lys Glu Gly Asp Lys Tyr Lys Leu Ser Lys Lys  
 20 25 30  
 Glu Leu Lys Glu Leu Leu Gln Thr Glu Leu Ser Gly Phe Leu Asp Ala  
 35 40 45  
 Gln Lys Asp Val Asp Ala Val Asp Lys Val Met Lys Glu Leu Asp Glu  
 50 55 60  
 Asn Gly Asp Gly Glu Val Asp Phe Gln Glu Tyr Val Val Leu Val Ala  
 65 70 75 80  
 Ala Leu Thr Val Ala Cys Asn Asn Phe Phe Trp Glu Asn Ser  
 85 90

<210> 271  
 <211> 595  
 <212> DNA  
 <213> Homo sapiens

<400> 271  
 gggcaaggct gggccgggaa gggcggtgggt tgaggagaggt ctccagaccc gcacgccgcg 60  
 cgcacagagc tctcagcgcc gctcccagcc acagcctccc gcgcctcgct cagctccaac 120  
 atggcaaaaa tctccagccc tacagagact gagcgggtgca tcgagtccct gattgctgtc 180  
 ttccagaagt atgctggaaa ggatggttat aactacactc tctccaagac agagttccta 240  
 agcttcatga atacagaact agctgccttc acaaagaacc agaaggaccc tgggtgcctt 300  
 gaccgcatga tgaagaaact ggacaccaac agtgatggtc agctagattt ctcagaattt 360  
 cttaatctga ttggtggcct agctatggct tgccatgact ccttcctcaa ggctgtccct 420  
 tcccagaagc ggacctgagg accccttggc cctggccttc aaacccaccc cctttccttc 480  
 cagcctttct gtcatcatct ccacagccca cccatccct gagcacacta accacctcat 540  
 gcaggcccca cctgccaata gtaataaagc aatgtcactt ttttaaaaca tgaaa 595

<210> 272  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 272  
 Met Ala Lys Ile Ser Ser Pro Thr Glu Thr Glu Arg Cys Ile Glu Ser  
 1 5 10 15  
 Leu Ile Ala Val Phe Gln Lys Tyr Ala Gly Lys Asp Gly Tyr Asn Tyr  
 20 25 30  
 Thr Leu Ser Lys Thr Glu Phe Leu Ser Phe Met Asn Thr Glu Leu Ala  
 35 40 45  
 Ala Phe Thr Lys Asn Gln Lys Asp Pro Gly Val Leu Asp Arg Met Met  
 50 55 60  
 Lys Lys Leu Asp Thr Asn Ser Asp Gly Gln Leu Asp Phe Ser Glu Phe  
 65 70 75 80  
 Leu Asn Leu Ile Gly Gly Leu Ala Met Ala Cys His Asp Ser Phe Leu  
 85 90 95  
 Lys Ala Val Pro Ser Gln Lys Arg Thr  
 100 105

<210> 273  
 <211> 428  
 <212> DNA  
 <213> Homo sapiens

<400> 273  
 ctgggtctgt ctctgccacc tggctctgcc cagatccatg atgtgcagtt ctctggagca 60  
 ggcgctggct gtgctgggtca ctaccttcca caagtactcc tgccaagagg gcgacaagtt 120  
 caagctgagt aagggggaaa tgaaggaact tctgcacaag gagctgccc gctttgtggg 180  
 ggagaaagtg gatgaggagg ggctgaagaa gctgatgggc agcctggatg agaacagtga 240  
 ccagcaggtg gacttccagg agtatgctgt ttccctggca ctcactactg tcatgtgcaa 300  
 tgacttcttc cagggctgcc cagaccgacc ctgaagcaga actcttgact tcctgccatg 360  
 gatctcttgg gcccaggact gttgatgcct ttgagttttg tattcaataa actttttttg 420  
 tctgttga 428

<210> 274  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 274  
 Met Cys Ser Ser Leu Glu Gln Ala Leu Ala Val Leu Val Thr Thr Phe  
 1 5 10 15  
 His Lys Tyr Ser Cys Gln Glu Gly Asp Lys Phe Lys Leu Ser Lys Gly  
 20 25 30  
 Glu Met Lys Glu Leu Leu His Lys Glu Leu Pro Ser Phe Val Gly Glu  
 35 40 45  
 Lys Val Asp Glu Glu Gly Leu Lys Lys Leu Met Gly Ser Leu Asp Glu  
 50 55 60  
 Asn Ser Asp Gln Gln Val Asp Phe Gln Glu Tyr Ala Val Phe Leu Ala  
 65 70 75 80  
 Leu Ile Thr Val Met Cys Asn Asp Phe Phe Gln Gly Cys Pro Asp Arg  
 85 90 95  
 Pro

<210> 275  
 <211> 470  
 <212> DNA  
 <213> Homo sapiens

<400> 275  
 gggaccgcta taaggccagt cggactgcga catagcccat cccctcgacc gctcgcgtcg 60  
 catttggccg cctccctacc gctccaagcc cagccctcag ccatggcatg cccctggat 120  
 caggccattg gcctcctcgt ggccatcttc cacaagtact ccggcaggga gggtgacaag 180  
 cacaccctga gcaagaagga gctgaaggag ctgatccaga aggagctcac cattggctcg 240  
 aagctgcagg atgctgaaat tgcaaggctg atggaagact tggaccggaa caaggaccag 300  
 gaggtgaact tccaggagta tgtcaccttc ctgggggcct tggctttgat ctacaatgaa 360  
 gcctcaagg gctgaaaata aataggggaag atggagacac ctctgggggt cctctctgag 420  
 tcaaatccag tgggtgggtaa ttgtacaata aatttttttt ggtcaaattt 470

<210> 276  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

283

&lt;400&gt; 276

Met	Ala	Cys	Pro	Leu	Asp	Gln	Ala	Ile	Gly	Leu	Leu	Val	Ala	Ile	Phe
1				5				10					15		
His	Lys	Tyr	Ser	Gly	Arg	Glu	Gly	Asp	Lys	His	Thr	Leu	Ser	Lys	Lys
			20				25					30			
Glu	Leu	Lys	Glu	Leu	Ile	Gln	Lys	Glu	Leu	Thr	Ile	Gly	Ser	Lys	Leu
		35				40					45				
Gln	Asp	Ala	Glu	Ile	Ala	Arg	Leu	Met	Glu	Asp	Leu	Asp	Arg	Asn	Lys
	50				55						60				
Asp	Gln	Glu	Val	Asn	Phe	Gln	Glu	Tyr	Val	Thr	Phe	Leu	Gly	Ala	Leu
65				70					75						80
Ala	Leu	Ile	Tyr	Asn	Glu	Ala	Leu	Lys	Gly						
			85						90						

&lt;210&gt; 277

&lt;211&gt; 3151

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 277

ccggccagcg	ggcgggctcc	ccagccaggc	cgctgcacct	gtcaggggaa	caagctggag	60
gagcaggacc	ctagacctct	gcagcccata	ccaggtctca	tggaggggaa	caagctggag	120
gagcaggact	ctagccctcc	acagtccact	ccagggctca	tgaaggggaa	caagcgtgag	180
gagcaggggc	tgggccccga	acctgcggcg	ccccagcagc	ccacggcgga	ggaggaggcc	240
ctgatcgagt	tccaccgctc	ctaccgagag	ctcttcgagt	tcttctgcaa	caacaccacc	300
atccacggcg	ccatccgcct	ggtgtgctcc	cagcacaacc	gcatgaagac	ggccttctgg	360
gcagtgtgtg	ggctctgcac	ctttggcatg	atgtactggc	aattcggcct	gcttttcgga	420
gagtacttca	gctaccccg	cagcctcaac	atcaacctca	actcggacaa	gctcgtcttc	480
cccgcagtga	ccatctgcac	cctcaatccc	tacaggtacc	cggaaattaa	agaggagctg	540
gaggagctgg	accgcatcac	agagcagacg	ctctttgacc	tgtacaaata	cagctccttc	600
accactctcg	tggccggctc	ccgcagccgt	cgcgacctgc	gggggactct	gccgcacccc	660
ttgcagcgcc	tgaggggtccc	gccccgcct	cacggggccc	gtcgagcccg	tagcgtggcc	720
tccagcttgc	gggacaacaa	ccccagggtg	gactggaagg	actggaagat	cggcttccag	780
ctgtgcaacc	agaacaaatc	ggactgtctc	taccagacat	actcatcagg	ggtggatgcg	840
gtgagggagt	gtatccgctt	ccactacatc	aacatcctgt	cgaggctgcc	agagactctg	900
ccatccctgg	aggaggacac	gctgggcaac	ttcatcttcg	cctgccgctt	caaccaggtc	960
tcctgcaacc	aggcgaatta	ctctcacttc	caccaccgga	tgtatggaaa	ctgctatact	1020
ttcaatgaca	agaacaactc	caacctctgg	atgtcttcca	tgcttggaat	caacaacggg	1080
ctgtccctga	tgtctgcgcg	agagcagaat	gacttcattc	ccctgctgtc	cacagtgact	1140
ggggcccggg	taatggtgca	cgggcaggat	gaacctgcct	ttatggatga	tgggtggctt	1200
aacttgcggc	ctggcggtga	gacctccatc	agcatgagga	aggaaaacct	ggacagactt	1260
gggggcgatt	atggcgactg	caccaagaat	ggcagtgatg	ttcctgttga	gaacctttac	1320
ccttcaaagt	acacacagca	ggtgtgtatt	cactcctgct	tccaggagag	catgatcaag	1380
gagtgtggct	gtgcctacat	cttctatccg	cggccccaga	acgtggagta	ctgtgactac	1440
agaaagcaca	gttcctgggg	gtactgctac	tataagctcc	aggttgactt	ctcctcagac	1500
cacctgggct	gtttcaccaa	gtgccggaag	ccatgcagcg	tgaccagcta	ccagctctct	1560
gctggttact	cacgatggcc	ctcggtgaca	tcccaggaat	gggtcttcca	gatgctatcg	1620
cgacagaaca	attacaccgt	caacaacaag	agaaatggag	tggccaaagt	caacatcttc	1680
ttcaaggagc	tgaactacaa	aaccaattct	gagtctccct	ctgtcacgat	ggtcacccctc	1740
ctgtccaacc	tgggcagcca	gtggagcctg	tggttcggct	cctcgggtgt	gtctgtggtg	1800
gagatggctg	agctcgtctt	tgacctgctg	gtcatcatgt	tcctcatgct	gctccgaagg	1860
ttccgaagcc	gatactggtc	tccaggccga	gggggcaggg	gtgctcagga	ggtagcctcc	1920
accctggcat	cctcccctcc	ttcccacttc	tgccccacc	ccatgtctct	gtccttgtcc	1980
cagccaggcc	ctgtccctc	tccagccttg	acagccctc	cccctgccta	tgccaccctg	2040
ggcccccgcc	catctccagg	gggtctgca	ggggccagtt	cctccacctg	tcctctgggg	2100
gggcctgag	agggaaggag	aggtttctca	caccaaggca	gatgctcctc	tgggtgggag	2160

```

gtgctggccc tggcaagatt gaaggatgtg cagggcttcc tctcagagcc gcccaaactg 2220
ccgttgatgt gtggagggga agcaagatgg gtaagggctc aggaagttgc tccaagaaca 2280
gtagctgatg aagctgcccc gaagtgcctt ggctccagcc ctgtaccctt tggtagtgc 2340
tctgaacact ctggtttccc caccctaactg cggctaagtc tctttttccc ttggatcagc 2400
caagcgaaac ttggagcttt gacaaggaac tttcctaaga aaccgctgat aaccaggaca 2460
aaacacaacc aaggggtacac gcaggcatgc acgggtttcc tgcccagcga cggcttaagc 2520
cagcccccca ctggcctggc cacactgttc tccagtagca cagatgtctg ctcctcctct 2580
tgaacttggg tgggaaaccc caccctttgt acccgggtaa gtaaaggcag acccagggt 2640
cctgactccc gagggctagg gctagagcag acccgggtaa gtaaaggcag acccagggt 2700
cctctagcct catacccggt ccctcacaga gccatgcccc ggcacctctg ccctgtgtct 2760
ttcatacctc tacatgtctg cttgagatat ttctcagcc tgaaagtttc cccaaccatc 2820
tgccagagaa ctcctatgca tcccttagaa ccctgtcag acaccattac ttttgtgaac 2880
gcttctgcca catcttgtct tccccaaat tgatcactcc gccttctcct gggctcccgt 2940
agcacactat aacatctgct ggagtgttgc tgttgacca tactttcttg tacatttgtg 3000
tctcccttcc caactagact gtaagtgcct tgcggtcagg gactgaatct tgcccgttta 3060
tgtatgtctc atgtctagcc catcatctg cttggagcaa gtaggcagga gctcaataaa 3120
tgtttgttgc atgaaaaaaaa aaaaaaaaaa a 3151

```

&lt;210&gt; 278

&lt;211&gt; 669

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 278

```

Met Glu Gly Asn Lys Leu Glu Glu Gln Asp Ser Ser Pro Pro Gln Ser
1          5          10          15
Thr Pro Gly Leu Met Lys Gly Asn Lys Arg Glu Glu Gln Gly Leu Gly
20          25          30
Pro Glu Pro Ala Ala Pro Gln Gln Pro Thr Ala Glu Glu Glu Ala Leu
35          40          45
Ile Glu Phe His Arg Ser Tyr Arg Glu Leu Phe Glu Phe Phe Cys Asn
50          55          60
Asn Thr Thr Ile His Gly Ala Ile Arg Leu Val Cys Ser Gln His Asn
65          70          75          80
Arg Met Lys Thr Ala Phe Trp Ala Val Leu Trp Leu Cys Thr Phe Gly
85          90          95
Met Met Tyr Trp Gln Phe Gly Leu Leu Phe Gly Glu Tyr Phe Ser Tyr
100         105         110
Pro Val Ser Leu Asn Ile Asn Leu Asn Ser Asp Lys Leu Val Phe Pro
115         120         125
Ala Val Thr Ile Cys Thr Leu Asn Pro Tyr Arg Tyr Pro Glu Ile Lys
130         135         140
Glu Glu Leu Glu Glu Leu Asp Arg Ile Thr Glu Gln Thr Leu Phe Asp
145         150         155         160
Leu Tyr Lys Tyr Ser Ser Phe Thr Thr Leu Val Ala Gly Ser Arg Ser
165         170         175
Arg Arg Asp Leu Arg Gly Thr Leu Pro His Pro Leu Gln Arg Leu Arg
180         185         190
Val Pro Pro Pro Pro His Gly Ala Arg Arg Ala Arg Ser Val Ala Ser
195         200         205
Ser Leu Arg Asp Asn Asn Pro Gln Val Asp Trp Lys Asp Trp Lys Ile
210         215         220
Gly Phe Gln Leu Cys Asn Gln Asn Lys Ser Asp Cys Phe Tyr Gln Thr
225         230         235         240
Tyr Ser Ser Gly Val Asp Ala Val Arg Glu Trp Tyr Arg Phe His Tyr
245         250         255
Ile Asn Ile Leu Ser Arg Leu Pro Glu Thr Leu Pro Ser Leu Glu Glu
260         265         270

```

285

```

Asp Thr Leu Gly Asn Phe Ile Phe Ala Cys Arg Phe Asn Gln Val Ser
      275                      280                      285
Cys Asn Gln Ala Asn Tyr Ser His Phe His His Pro Met Tyr Gly Asn
      290                      295                      300
Cys Tyr Thr Phe Asn Asp Lys Asn Asn Ser Asn Leu Trp Met Ser Ser
305                      310                      315                      320
Met Pro Gly Ile Asn Asn Gly Leu Ser Leu Met Leu Arg Ala Glu Gln
      325                      330                      335
Asn Asp Phe Ile Pro Leu Leu Ser Thr Val Thr Gly Ala Arg Val Met
      340                      345                      350
Val His Gly Gln Asp Glu Pro Ala Phe Met Asp Asp Gly Gly Phe Asn
      355                      360                      365
Leu Arg Pro Gly Val Glu Thr Ser Ile Ser Met Arg Lys Glu Thr Leu
      370                      375                      380
Asp Arg Leu Gly Gly Asp Tyr Gly Asp Cys Thr Lys Asn Gly Ser Asp
385                      390                      395                      400
Val Pro Val Glu Asn Leu Tyr Pro Ser Lys Tyr Thr Gln Gln Val Cys
      405                      410                      415
Ile His Ser Cys Phe Gln Glu Ser Met Ile Lys Glu Cys Gly Cys Ala
      420                      425                      430
Tyr Ile Phe Tyr Pro Arg Pro Gln Asn Val Glu Tyr Cys Asp Tyr Arg
      435                      440                      445
Lys His Ser Ser Trp Gly Tyr Cys Tyr Tyr Lys Leu Gln Val Asp Phe
      450                      455                      460
Ser Ser Asp His Leu Gly Cys Phe Thr Lys Cys Arg Lys Pro Cys Ser
465                      470                      475                      480
Val Thr Ser Tyr Gln Leu Ser Ala Gly Tyr Ser Arg Trp Pro Ser Val
      485                      490                      495
Thr Ser Gln Glu Trp Val Phe Gln Met Leu Ser Arg Gln Asn Asn Tyr
      500                      505                      510
Thr Val Asn Asn Lys Arg Asn Gly Val Ala Lys Val Asn Ile Phe Phe
      515                      520                      525
Lys Glu Leu Asn Tyr Lys Thr Asn Ser Glu Ser Pro Ser Val Thr Met
      530                      535                      540
Val Thr Leu Leu Ser Asn Leu Gly Ser Gln Trp Ser Leu Trp Phe Gly
545                      550                      555                      560
Ser Ser Val Leu Ser Val Val Glu Met Ala Glu Leu Val Phe Asp Leu
      565                      570                      575
Leu Val Ile Met Phe Leu Met Leu Leu Arg Arg Phe Arg Ser Arg Tyr
      580                      585                      590
Trp Ser Pro Gly Arg Gly Gly Arg Gly Ala Gln Glu Val Ala Ser Thr
      595                      600                      605
Leu Ala Ser Ser Pro Pro Ser His Phe Cys Pro His Pro Met Ser Leu
      610                      615                      620
Ser Leu Ser Gln Pro Gly Pro Ala Pro Ser Pro Ala Leu Thr Ala Pro
625                      630                      635                      640
Pro Pro Ala Tyr Ala Thr Leu Gly Pro Arg Pro Ser Pro Gly Gly Ser
      645                      650                      655
Ala Gly Ala Ser Ser Ser Thr Cys Pro Leu Gly Gly Pro
      660                      665

```

&lt;210&gt; 279

&lt;211&gt; 3174

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<221> misc\_feature  
 <222> (1)... (3174)  
 <223> n = A,T,C or G

<400> 279

```

ccagcgggcg ggctccccag ccaggccgct gcacctgtca ggggaacaag ctggaggagc 60
aggaccctag acctctgcag occataccag gtctcatgga ggggaacaag ctggaggagc 120
aggactctag ccctccacag tccactccag ggctcatgaa ggggaacaag cgtgaggagc 180
aggggctggg ccccgaaacct gggcgcccc agcagccac ggcggaggag gaggccctga 240
tcgagttcca ccgctcctac cgagagctct tcgagttctt ctgcaacaac accaccatcc 300
acggcgccat ccgctgggtg tgctcccagc acaaccgcat gaagacggcc ttctgggcag 360
tgctgtggct ctgcaccttt ggcatgatgt actggcaatt cggcctgctt ttcggagagt 420
acttcagcta ccccgtcagc ctcaacatca acctcaactc ggacaagctc gtcttccccg 480
cagtgaccat ctgcaccttc aatccctaca ggtaccggga aattaaagag gagctggagg 540
agctggaccg catcacagag cagacgctct ttgacctgta caaatacagc tccttcacca 600
ctctcgtggc cggctcccgc agcgtcgcg acctgcgggg gactctgcgc cacccttgc 660
agcgcttag ggctccgccc ccgctcacg gggccgctcg agcccgtagc gtggcctcca 720
gcttgcgga caacaacccc cagggtgact ggaaggactg gaagatcggc ttccagctgt 780
gcaaccagaa caaatcggac tgcttctacc agacatactc atcaggggtg gatgcggtga 840
gggagtggta ccgcttcac tacatcaaca tctgtcgag gctgcagag actctgccat 900
ccctggagga ggacacgctg ggcaacttca tcttcgcctg ccgcttcaac caggtctcct 960
gcaaccaggc gaattactct cacttccacc acccgatgta tggaaactgc tatactttca 1020
atgacaagaa caactccaac ctctggatgt cttccatgcc tggaaatcaac aacggtctgt 1080
ccctgatgct gcgcgcagag cagaatgact tcattcccct gctgtccaca gtgactgggg 1140
cccgggtaat ggtgcacggg caggatgaac ctgcctttat ggatgatggt ggctttaact 1200
tgcggcctgg cgtggagacc tccatcagca tgaggaagga aacctggac agacttgggg 1260
gcgattatgg cgactgcacc aagaatggca gtgatgttcc tgttgagaac ctttaccctt 1320
caaagtacac acagcaggtg tgtattcact cctgcttcca ggagagcatg atcaaggagt 1380
gtggctgtgc ctacatcttc tatccgcgc ccagaacgt ggagtactgt gactacagaa 1440
agcacagttc ctgggggtac tgctactata agctccaggt tgacttctcc tcagaccacc 1500
tgggctgttt caccaagtgc cggagccat gcagcgtgac cagctaccag ctctctgctg 1560
gttactcacg atggccctcg gtgacatccc aggaatgggt cttccagatg ctatcgcgac 1620
agaacaatta caccgtcaac aacaagagaa atggagtggc caaagtcaac atcttcttca 1680
aggagctgaa ctacaaaacc aattctgagt ctccctctgt cacgatggtc accctcctgt 1740
ccaacctggg cagccagtgg agcctgtggt tcggctcctc ggtgttgtct gtggtggaga 1800
tggttgagct cgtctttgac ctgctgttca tcatgttctc catgctgtct cgaaggttcc 1860
gaagccgata ctggtctcca ggccgagggg gcaggggtgc tcaggaggta gcctccacc 1920
tggcatcctc ccctccttcc cacttctgcc cccaccccat gtctctgtcc ttgtccagc 1980
caggccctgc tccctctcca gccttgacag cccctcccc tgctatgcc accctgggcc 2040
ccgcccac tcagggggc tctgcagggg ccagttctct cgctgtcct ctgggggggc 2100
cctgagaggg aaggagaggt ttctcacacc aaggcagatg ctctctggt gggaggggtg 2160
tggccctggc aagattgaag gatgtgcagg gcttctctc agagccgccc aaactgccgt 2220
tgatgtgtgg aggggaagca agatgggtaa gggctcagga agttgctcca agaacagtag 2280
ctgatgaagc tgcccagaag tgcttggct ccagccctgt accccttgg actgctctg 2340
aacactctgg ttccccacc caactgcggc taagtctctt tttcccttgg atcagccaag 2400
cgaaacttgg agctttgaca aggnaacttt cctaagaaac cgctgataac caggacaaa 2460
cacaaccaag ggtacacgca ggcatgcacg ggtttcctgc ccagcgacg ctttaagccag 2520
ccccgactn ggcttgcca cacntgctct ccagtagcac nagatgtctn gctcctcctc 2580
ttgaacttgg gtgggaaanc cccaccnaa aagccccctt tgttacttag gcaattcccc 2640
ttcctgact ncccgagggc tagggctaga gcangaccg ggtaagtaaa ggcagacca 2700
gggctcctct agcctcatac ccgtgccctc acangagcca ntgcccogn cacctctgcc 2760
ctgtgntctt tncatacctc tacatgtctg cttgagatat ttctcagcc tgaaaagttt 2820
cccaaccatc tgccagagaa ctctatgca tcccttnaga accctgctca gacaccatta 2880
cttttgtgaa cgcttctgcc acatctgtc ttccccaaaa ttgatcactc cgcttctcc 2940
ntgggctccc tagcacact ataacatctg ctggagtgtt gcntgttgca ccatacttcc 3000
ttgtacctnc gggcgcgacc gscacaackr ggagctsyaa gtgccttgcg gtcagggact 3060
gaatcttgcc cgtttatgta tgctccatgt ctagcccatc atcctgcttg gagcaagtag 3120
gcaggagctc aataaatgtt tgttgcatga annnnnnnnn nnnnnnnnnn nnnn 3174

```



<210> 280  
 <211> 669  
 <212> PRT  
 <213> Homo sapiens

<400> 280

Met	Glu	Gly	Asn	Lys	Leu	Glu	Glu	Gln	Asp	Ser	Ser	Pro	Pro	Gln	Ser
1				5					10					15	
Thr	Pro	Gly	Leu	Met	Lys	Gly	Asn	Lys	Arg	Glu	Glu	Gln	Gly	Leu	Gly
			20					25					30		
Pro	Glu	Pro	Ala	Ala	Pro	Gln	Gln	Pro	Thr	Ala	Glu	Glu	Glu	Ala	Leu
		35				40					45				
Ile	Glu	Phe	His	Arg	Ser	Tyr	Arg	Glu	Leu	Phe	Glu	Phe	Phe	Cys	Asn
	50					55				60					
Asn	Thr	Thr	Ile	His	Gly	Ala	Ile	Arg	Leu	Val	Cys	Ser	Gln	His	Asn
65				70						75				80	
Arg	Met	Lys	Thr	Ala	Phe	Trp	Ala	Val	Leu	Trp	Leu	Cys	Thr	Phe	Gly
			85						90					95	
Met	Met	Tyr	Trp	Gln	Phe	Gly	Leu	Leu	Phe	Gly	Glu	Tyr	Phe	Ser	Tyr
			100					105					110		
Pro	Val	Ser	Leu	Asn	Ile	Asn	Leu	Asn	Ser	Asp	Lys	Leu	Val	Phe	Pro
		115				120						125			
Ala	Val	Thr	Ile	Cys	Thr	Leu	Asn	Pro	Tyr	Arg	Tyr	Pro	Glu	Ile	Lys
		130				135					140				
Glu	Glu	Leu	Glu	Glu	Leu	Asp	Arg	Ile	Thr	Glu	Gln	Thr	Leu	Phe	Asp
145					150					155					160
Leu	Tyr	Lys	Tyr	Ser	Phe	Thr	Thr	Leu	Val	Ala	Gly	Ser	Arg	Ser	
			165					170					175		
Arg	Arg	Asp	Leu	Arg	Gly	Thr	Leu	Pro	His	Pro	Leu	Gln	Arg	Leu	Arg
			180					185					190		
Val	Pro	Pro	Pro	Pro	His	Gly	Ala	Arg	Arg	Ala	Arg	Ser	Val	Ala	Ser
		195				200						205			
Ser	Leu	Arg	Asp	Asn	Asn	Pro	Gln	Val	Asp	Trp	Lys	Asp	Trp	Lys	Ile
	210				215						220				
Gly	Phe	Gln	Leu	Cys	Asn	Gln	Asn	Lys	Ser	Asp	Cys	Phe	Tyr	Gln	Thr
225				230						235				240	
Tyr	Ser	Ser	Gly	Val	Asp	Ala	Val	Arg	Glu	Trp	Tyr	Arg	Phe	His	Tyr
			245						250					255	
Ile	Asn	Ile	Leu	Ser	Arg	Leu	Pro	Glu	Thr	Leu	Pro	Ser	Leu	Glu	Glu
		260						265					270		
Asp	Thr	Leu	Gly	Asn	Phe	Ile	Phe	Ala	Cys	Arg	Phe	Asn	Gln	Val	Ser
		275				280						285			
Cys	Asn	Gln	Ala	Asn	Tyr	Ser	His	Phe	His	His	Pro	Met	Tyr	Gly	Asn
	290				295						300				
Cys	Tyr	Thr	Phe	Asn	Asp	Lys	Asn	Asn	Ser	Asn	Leu	Trp	Met	Ser	Ser
305				310						315				320	
Met	Pro	Gly	Ile	Asn	Asn	Gly	Leu	Ser	Leu	Met	Leu	Arg	Ala	Glu	Gln
			325						330					335	
Asn	Asp	Phe	Ile	Pro	Leu	Leu	Ser	Thr	Val	Thr	Gly	Ala	Arg	Val	Met
		340						345					350		
Val	His	Gly	Gln	Asp	Glu	Pro	Ala	Phe	Met	Asp	Asp	Gly	Gly	Phe	Asn
		355				360						365			
Leu	Arg	Pro	Gly	Val	Glu	Thr	Ser	Ile	Ser	Met	Arg	Lys	Glu	Thr	Leu
	370					375					380				
Asp	Arg	Leu	Gly	Gly	Asp	Tyr	Gly	Asp	Cys	Thr	Lys	Asn	Gly	Ser	Asp
385				390						395				400	
Val	Pro	Val	Glu	Asn	Leu	Tyr	Pro	Ser	Lys	Tyr	Thr	Gln	Gln	Val	Cys

288

				405						410					415
Ile	His	Ser	Cys	Phe	Gln	Glu	Ser	Met	Ile	Lys	Glu	Cys	Gly	Cys	Ala
			420					425					430		
Tyr	Ile	Phe	Tyr	Pro	Arg	Pro	Gln	Asn	Val	Glu	Tyr	Cys	Asp	Tyr	Arg
		435					440					445			
Lys	His	Ser	Ser	Trp	Gly	Tyr	Cys	Tyr	Tyr	Lys	Leu	Gln	Val	Asp	Phe
	450				455						460				
Ser	Ser	Asp	His	Leu	Gly	Cys	Phe	Thr	Lys	Cys	Arg	Lys	Pro	Cys	Ser
465				470						475					480
Val	Thr	Ser	Tyr	Gln	Leu	Ser	Ala	Gly	Tyr	Ser	Arg	Trp	Pro	Ser	Val
			485						490					495	
Thr	Ser	Gln	Glu	Trp	Val	Phe	Gln	Met	Leu	Ser	Arg	Gln	Asn	Asn	Tyr
		500						505					510		
Thr	Val	Asn	Asn	Lys	Arg	Asn	Gly	Val	Ala	Lys	Val	Asn	Ile	Phe	Phe
	515						520					525			
Lys	Glu	Leu	Asn	Tyr	Lys	Thr	Asn	Ser	Glu	Ser	Pro	Ser	Val	Thr	Met
	530				535						540				
Val	Thr	Leu	Leu	Ser	Asn	Leu	Gly	Ser	Gln	Trp	Ser	Leu	Trp	Phe	Gly
545				550					555						560
Ser	Ser	Val	Leu	Ser	Val	Val	Glu	Met	Ala	Glu	Leu	Val	Phe	Asp	Leu
			565					570					575		
Leu	Val	Ile	Met	Phe	Leu	Met	Leu	Leu	Arg	Arg	Phe	Arg	Ser	Arg	Tyr
	580							585					590		
Trp	Ser	Pro	Gly	Arg	Gly	Gly	Arg	Gly	Ala	Gln	Glu	Val	Ala	Ser	Thr
	595						600					605			
Leu	Ala	Ser	Ser	Pro	Pro	Ser	His	Phe	Cys	Pro	His	Pro	Met	Ser	Leu
	610					615					620				
Ser	Leu	Ser	Gln	Pro	Gly	Pro	Ala	Pro	Ser	Pro	Ala	Leu	Thr	Ala	Pro
625				630					635						640
Pro	Pro	Ala	Tyr	Ala	Thr	Leu	Gly	Pro	Arg	Pro	Ser	Pro	Gly	Gly	Ser
			645					650					655		
Ala	Gly	Ala	Ser	Ser	Ser	Ala	Cys	Pro	Leu	Gly	Gly	Pro			
		660						665							

&lt;210&gt; 281

&lt;211&gt; 2892

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 281

```

gcggcggcgg cggcggcggc aggcgcccgg gaggcggagg cgggaggcgg cggcggcgcg 60
cggagacgca gcagcggcag cggcagcatg tcggccggcg gagcgtcagt cccgccgccc 120
ccgaaccccg ccgtgtcctt cccgccgccc cgggtcaccc tgcccgcggg ccccgacatc 180
ctgcggacct actcggggcg cttcgtctgc ctggagattc tgttcggggg tcttgtcttg 240
atcttggttg cctcctccaa tttcctcta cctctactac aaggatgggt catgtttgtg 300
tccgtgacag cgtttttctt ttcgctctc tttctgggca tgttcctctc tggcatggtg 360
gctcaaattg atgctaactg gaacttcctg gattttgcct accattttac agtatttgtc 420
ttctattttg gagccttttt attggaagca gcagccacat ccctgcatga tttgcattgc 480
aatacaacca taaccgggca gccactcctg agtgataacc agtataacat aaacgtagca 540
gcctcaattt ttgcctttat gacgacagct tgttatggtt gcagtttggt tctggcttta 600
cgaagatggc gaccgtaaca ctccctagaa actggcagtc gtatgttagt ttcacttgtc 660
tactttatat gtctgatcaa ttggatacc attttgtcca gatgcaaaaa cattccaaaa 720
gtaatgtgtt tagtagagag agactctaag ctcaagttct ggtttatttc atggatggaa 780
tgtaattttt attatgatat taaagaaatg gccttttatt ttacatctct cccctttttc 840
cctttccccc tttatttttc tccttttctt tctgaaagtt tccttttatg tccataaaat 900
acaaatatat tgttcataaa aaattagtat cccttttgtt tggttgctga gtcacctgaa 960
ccttaatttt aattggtaat tacagcccct aaaaaaaca catttcaaat aggcttccca 1020

```

```

ctaaactcta tatttttagtg taaaccagga attggcacac tttttttaga atggggccaga 1080
tggtaaatat ttatgcttca cgggccatac agtctctgtc acaactattc agttctgcta 1140
gtatagcgtg aaagcagcta tacacaatac agaaatgaat gagtgtgggtt atgttctaata 1200
aaaacttatt tataaaaaaca aggggagggt ggggttagcc tgtgggccaat agtttgtcaa 1260
ccactgggtg aaaaccttag ttatatatga tctgcatttt cttgaactga tcattgaaaa 1320
cttataaacc taacagaaaa gccacataat atttagtgctc attatgcaat aatcacattg 1380
cctttgtgtt aatagtcaaa tacttacctt tggagaatac ttaccttttg aggaatgtat 1440
aaaatttctc aggcagagtc ctggatatag gaaaaagtaa tttatgaagt aaacttcagt 1500
tgcttaatca aactaatgat agtctaacaa ctgagcaaga tcctcatctg agagtgtcta 1560
aaatgggatc ccagagagacc attaaccaat actggaactg gtatctagct actgatgtct 1620
tactttgagt ttatttatgc ttcagaatac agttgtttgc cctgtgcatg aatataccca 1680
tattttgtgtg tggatatgtg aagcttttcc aaatagagct ctcagaagaa ttaagttttt 1740
acttctaatt attttgcatt actttgagtt aaatttgaat agagtattaa atataaagtt 1800
gtagattctt atgtgttttt gtattagccc agacatctgt aatgtttttg cactggtgac 1860
agacaaaatc tgttttaaaa tcatatccag cacaaaaact atttctgggt gaatagcaca 1920
gaaaagtatt ttaacctacc tgtagagatc ctgctcatgg aaagggtgcca aactgttttg 1980
aatggaagga caagtaagag tgaggccaca gttcccacca cagcaggggt tttgtattgt 2040
tctacttttt cagcccttta ctttctgggt gaagcatccc cttggagtgc catgtataag 2100
ttgggtctatt agagttcatg gaacatagaa caaccatgaa tgagtggcat gatccgtgct 2160
taatgatcaa gtgttactta tctaataatc ctctagaaaag aacctgttta gatcttggtt 2220
tgtgataaaa atataaagac agaagacatg aggaaaaaca aaaggtttga ggaaatcagg 2280
catatgactt tatacttaac atcagatctt ttctataata tcctactact ttggttttcc 2340
tagctccata ccacacacct aaacctgtat tatgaattac atattacaaa gtcataaatg 2400
tgccatattg atatacagta cattctagtt ggaatcggtt actctgctag aatttaggtg 2460
tgagattttt tgtttcccag gtatagcagg cttatgtttg gtggcattaa attggtttct 2520
ttaaaatgct ttggtggcac ttttgtaaac agattgcttc tagattgtta caaaccaagc 2580
ctaagacaca tctgtgaata cttagatttg tagcttaatc acattctaga cttgtgagtt 2640
gaatgacaaa gcagttgaac aaaaattatg gcatttaaga attaacatg tcttagctgt 2700
aaaaatgaga aagtgttggt tggtttttaa atctggtaac tccatgatga aaagaaaatt 2760
attttatacg tgttatgtct ctaataaagt attcatttga taaaaaaaaa aaaaaaaagg 2820
gcggccgctc tagaggatcc aagcttacgt acgcgtgcat gcgacgtcat agctcttcta 2880
taggtcacc ta                                     2892

```

&lt;210&gt; 282

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 282

```

Met Ser Ala Gly Gly Ala Ser Val Pro Pro Pro Pro Asn Pro Ala Val
1          5          10          15
Ser Phe Pro Pro Arg Val Thr Leu Pro Ala Gly Pro Asp Ile Leu
20          25          30
Arg Thr Tyr Ser Gly Ala Phe Val Cys Leu Glu Ile Leu Phe Gly Gly
35          40          45
Leu Val Trp Ile Leu Val Ala Ser Ser Asn Val Pro Leu Pro Leu Leu
50          55          60
Gln Gly Trp Val Met Phe Val Ser Val Thr Ala Phe Phe Phe Ser Leu
65          70          75          80
Leu Phe Leu Gly Met Phe Leu Ser Gly Met Val Ala Gln Ile Asp Ala
85          90          95
Asn Trp Asn Phe Leu Asp Phe Ala Tyr His Phe Thr Val Phe Val Phe
100         105         110
Tyr Phe Gly Ala Phe Leu Leu Glu Ala Ala Ala Thr Ser Leu His Asp
115         120         125
Leu His Cys Asn Thr Thr Ile Thr Gly Gln Pro Leu Leu Ser Asp Asn
130         135         140
Gln Tyr Asn Ile Asn Val Ala Ala Ser Ile Phe Ala Phe Met Thr Thr

```

145	150	155	160
Ala Cys Tyr Gly Cys	Ser Leu Gly Leu Ala	Leu Arg Arg Trp Arg	Pro
165	170	175	

<210> 283  
 <211> 2530  
 <212> DNA  
 <213> Homo sapiens

<400> 283

ggaattccct	gcagcatggg	ctgggttaact	aggattgtct	gtcttttctg	gggagtatta	60
cttacagcaa	gagcaacta	tcagaatggg	aagaacaatg	tgccaaggct	gaaattatcc	120
tacaaagaaa	tggtggaatc	caacaatgtg	atcactttca	atggcttggc	caacagctcc	180
agttatcata	ccttcctttt	ggatgaggaa	cggagtaggc	tgtatgttgg	agcaaaggat	240
cacatatttt	cattcgacct	ggtaaatatc	aaggattttc	aaaagattgt	gtggccagta	300
tcttacacca	gaagagatga	atgcaagtgg	gctggaaaag	acatcctgaa	agaatgtgct	360
aatttcatca	aggtacttaa	ggcatataat	cagactcact	tgtacgcctg	tggaacgggg	420
gcttttcatc	caatttgcac	ctacattgaa	attggacatc	atcctgagga	caatattttt	480
aagctggaga	actcacattt	tgaaaacggc	cgtgggaaga	gtccatatga	ccctaagctg	540
ctgacagcat	cccttttaat	agatggagaa	ttatactctg	gaactgcagc	tgattttatg	600
ggcgagact	ttgctatctt	ccgaactcct	gggcaccacc	acccaatcag	gacagagcag	660
catgattcca	ggtggctcaa	tgatccaaag	ttcattagt	cccacctcat	ctcagagagt	720
gacaatcctg	aagatgacaa	agtatacttt	ttcttccgtg	aaaatgcaat	agatggagaa	780
cactctggaa	aagctactca	cgctagaata	ggtcagatat	gcaagaatga	ctttggaggg	840
cacagaagtc	tggtgaataa	atggacaaca	ttcctcaaag	ctcgtctgat	ttgctcagtg	900
ccaggtccaa	atggcattga	cactcatttt	gatgaactgc	aggatgtatt	cctaataaac	960
tttaaagatc	ctaaaaatcc	agttgtatat	ggagtgttta	cgacttccag	taacattttc	1020
aagggatcag	ccgtgtgtat	gtatagcatg	agtgtgtga	gaagggtgtt	ccttgggtcca	1080
tatgccca	gggatggacc	caactatcaa	tgggtgcctt	atcaagggaag	agtcccctat	1140
ccacggccag	gaacttgtcc	cagcaaaaaca	tttgggtggt	ttgactctac	aaaggacctt	1200
cctgatgatg	ttataacctt	tgcaagaagt	catccagcca	tgtacaatcc	agtgtttcct	1260
atgaacaatc	gcccaatagt	gatcaaaacg	gatgtaaatt	atcaatttac	acaaattgtc	1320
gtagaccgag	tggtatgcaga	agatggacag	tatgatgtta	tgtttatcgg	aacagatgtt	1380
gggaccgttc	ttaaagtagt	ttcaattcct	aaggagactt	ggtatgattt	agaagagggt	1440
ctgctggaag	aaatgacagt	ttttcgggaa	ccgactgcta	tttcagcaat	ggagcttttc	1500
actaagcagc	aacaactata	tatttggttca	acggctgggg	ttgccagct	ccctttacac	1560
cgggtgtgata	tttacgggaa	agcgtgtgct	gagtgttgcc	tcgcccagag	cccttactgt	1620
gcttgggatg	gttctgcatg	ttctcgctat	tttccactg	caaagagacg	cacaagacga	1680
caagatataa	gaaatggaga	cccaactgact	cactgttcag	acttacacca	tgataatcac	1740
catggccaca	gccctgaaga	gagaatcatc	tatggtgtag	agaatagtag	cacatttttg	1800
gaatgcagtc	cgaagtgcga	gagagcgctg	gtctattggc	aattccagag	gcgaaatgaa	1860
gagcgaaaag	aagagatcag	agtggatgat	catatcatca	ggacagatca	aggccttctg	1920
ctacgtagtc	tacaacagaa	ggattcaggc	aattacctct	gccatgcggt	ggaacatggg	1980
ttcatacaaa	ctcttcttaa	ggtaaccctg	gaagtcattg	acacagagca	tttgggaagaa	2040
cttcttcata	aagatgatga	tggagatggc	tctaagacca	aagaaatgtc	caatagcatg	2100
acacctagcc	agaaggtctg	gtacagagac	ttcatgcagc	tcatcaacca	ccccaatctc	2160
aacacgatgg	atgagttctg	tgaacaagtt	tggaaaaggg	accgaaaaca	acgtcggcaa	2220
aggccaggac	ataccccagg	gaacagtaac	aatgggaagc	acttacaaga	aaataagaaa	2280
ggtagaacaa	ggaggaccca	cgaatttgag	agggcaccca	ggagtgtctg	agctgcatta	2340
cctctagaaa	cctcaaacaa	gtagaaactt	gcctagacaa	taactggaaa	aacaaatgca	2400
atatacatga	acttttttca	tggcattatg	tggatgttta	caatgggtgg	aaattcagct	2460
gagttccacc	aattataaat	taaatccatg	agtaactttc	ctaataaggct	tttttttctt	2520
aataccaccg						2530

<210> 284  
 <211> 771  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 284

```

Met Gly Trp Leu Thr Arg Ile Val Cys Leu Phe Trp Gly Val Leu Leu
 1           5           10           15
Thr Ala Arg Ala Asn Tyr Gln Asn Gly Lys Asn Asn Val Pro Arg Leu
      20           25           30
Lys Leu Ser Tyr Lys Glu Met Leu Glu Ser Asn Asn Val Ile Thr Phe
      35           40           45
Asn Gly Leu Ala Asn Ser Ser Ser Tyr His Thr Phe Leu Leu Asp Glu
      50           55           60
Glu Arg Ser Arg Leu Tyr Val Gly Ala Lys Asp His Ile Phe Ser Phe
      65           70           75           80
Asp Leu Val Asn Ile Lys Asp Phe Gln Lys Ile Val Trp Pro Val Ser
      85           90           95
Tyr Thr Arg Arg Asp Glu Cys Lys Trp Ala Gly Lys Asp Ile Leu Lys
      100          105          110
Glu Cys Ala Asn Phe Ile Lys Val Leu Lys Ala Tyr Asn Gln Thr His
      115          120          125
Leu Tyr Ala Cys Gly Thr Gly Ala Phe His Pro Ile Cys Thr Tyr Ile
      130          135          140
Glu Ile Gly His His Pro Glu Asp Asn Ile Phe Lys Leu Glu Asn Ser
      145          150          155          160
His Phe Glu Asn Gly Arg Gly Lys Ser Pro Tyr Asp Pro Lys Leu Leu
      165          170          175
Thr Ala Ser Leu Leu Ile Asp Gly Glu Leu Tyr Ser Gly Thr Ala Ala
      180          185          190
Asp Phe Met Gly Arg Asp Phe Ala Ile Phe Arg Thr Leu Gly His His
      195          200          205
His Pro Ile Arg Thr Glu Gln His Asp Ser Arg Trp Leu Asn Asp Pro
      210          215          220
Lys Phe Ile Ser Ala His Leu Ile Ser Glu Ser Asp Asn Pro Glu Asp
      225          230          235          240
Asp Lys Val Tyr Phe Phe Arg Glu Asn Ala Ile Asp Gly Glu His
      245          250          255
Ser Gly Lys Ala Thr His Ala Arg Ile Gly Gln Ile Cys Lys Asn Asp
      260          265          270
Phe Gly Gly His Arg Ser Leu Val Asn Lys Trp Thr Thr Phe Leu Lys
      275          280          285
Ala Arg Leu Ile Cys Ser Val Pro Gly Pro Asn Gly Ile Asp Thr His
      290          295          300
Phe Asp Glu Leu Gln Asp Val Phe Leu Met Asn Phe Lys Asp Pro Lys
      305          310          315          320
Asn Pro Val Val Tyr Gly Val Phe Thr Thr Ser Ser Asn Ile Phe Lys
      325          330          335
Gly Ser Ala Val Cys Met Tyr Ser Met Ser Asp Val Arg Arg Val Phe
      340          345          350
Leu Gly Pro Tyr Ala His Arg Asp Gly Pro Asn Tyr Gln Trp Val Pro
      355          360          365
Tyr Gln Gly Arg Val Pro Tyr Pro Arg Pro Gly Thr Cys Pro Ser Lys
      370          375          380
Thr Phe Gly Gly Phe Asp Ser Thr Lys Asp Leu Pro Asp Asp Val Ile
      385          390          395          400
Thr Phe Ala Arg Ser His Pro Ala Met Tyr Asn Pro Val Phe Pro Met
      405          410          415
Asn Asn Arg Pro Ile Val Ile Lys Thr Asp Val Asn Tyr Gln Phe Thr
      420          425          430
Gln Ile Val Val Asp Arg Val Asp Ala Glu Asp Gly Gln Tyr Asp Val

```

292

435	440	445
Met Phe Ile Gly Thr Asp Val Gly Thr Val Leu Lys Val Val Ser Ile		
450	455	460
Pro Lys Glu Thr Trp Tyr Asp Leu Glu Glu Val Leu Leu Glu Glu Met		
465	470	475
Thr Val Phe Arg Glu Pro Thr Ala Ile Ser Ala Met Glu Leu Ser Thr		
485	490	495
Lys Gln Gln Gln Leu Tyr Ile Gly Ser Thr Ala Gly Val Ala Gln Leu		
500	505	510
Pro Leu His Arg Cys Asp Ile Tyr Gly Lys Ala Cys Ala Glu Cys Cys		
515	520	525
Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Ser Ala Cys Ser Arg		
530	535	540
Tyr Phe Pro Thr Ala Lys Arg Arg Thr Arg Arg Gln Asp Ile Arg Asn		
545	550	555
Gly Asp Pro Leu Thr His Cys Ser Asp Leu His His Asp Asn His His		
565	570	575
Gly His Ser Pro Glu Glu Arg Ile Ile Tyr Gly Val Glu Asn Ser Ser		
580	585	590
Thr Phe Leu Glu Cys Ser Pro Lys Ser Gln Arg Ala Leu Val Tyr Trp		
595	600	605
Gln Phe Gln Arg Arg Asn Glu Glu Arg Lys Glu Glu Ile Arg Val Asp		
610	615	620
Asp His Ile Ile Arg Thr Asp Gln Gly Leu Leu Leu Arg Ser Leu Gln		
625	630	635
Gln Lys Asp Ser Gly Asn Tyr Leu Cys His Ala Val Glu His Gly Phe		
645	650	655
Ile Gln Thr Leu Leu Lys Val Thr Leu Glu Val Ile Asp Thr Glu His		
660	665	670
Leu Glu Glu Leu Leu His Lys Asp Asp Asp Gly Asp Gly Ser Lys Thr		
675	680	685
Lys Glu Met Ser Asn Ser Met Thr Pro Ser Gln Lys Val Trp Tyr Arg		
690	695	700
Asp Phe Met Gln Leu Ile Asn His Pro Asn Leu Asn Thr Met Asp Glu		
705	710	715
Phe Cys Glu Gln Val Trp Lys Arg Asp Arg Lys Gln Arg Arg Gln Arg		
725	730	735
Pro Gly His Thr Pro Gly Asn Ser Asn Lys Trp Lys His Leu Gln Glu		
740	745	750
Asn Lys Lys Gly Arg Asn Arg Arg Thr His Glu Phe Glu Arg Ala Pro		
755	760	765
Arg Ser Val		
770		

&lt;210&gt; 285

&lt;211&gt; 3041

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 285

```

ggcaccacca ctgacctggg acagtgaatc gacaatgccg tcttctgtct cgtggggcat 60
cctcctgctg gcaggcctgt gctgcctggt ccctgtctcc ctggctgagg atccccaggg 120
agatgctgcc cagaagacag atacatccca ccatgatcag gatcacccaa ccttcaacaa 180
gatcaccccc aacctggctg agttgcctt cagcctatac cgccagctgg cacaccagtc 240
caacagcacc aatatcttct tctcccagc gagcatcgct acagcctttg caatgctctc 300
cctggggacc aaggctgaca ctcacgatga aatcctggag ggctgaatt tcaacctcac 360
ggagattccg gaggtcaga tccatgaagg cttccaggaa ctctccgta cctcaacca 420

```

```

gccagacagc cagctccagc tgaccaccgg caatggcctg ttcctcagcg agggcctgaa 480
gctagtggat aagtttttgg aggatgttaa aaagtgttac cactcagaag ccttcactgt 540
caacttcggg gacaccgaag aggccaagaa acagatcaac gattacgtgg agaagggtac 600
tcaagggaat atttgtgatt tgggtcaagga gcttgacaga gacacagttt ttgctctggt 660
gaattacatc ttcttttaaag gcaaatggga gagacccttt gaagtcaagg acaccgagga 720
agaggacttc cacgtggacc aggtgaccac cgtgaagggt cctatgatga agcgttttag 780
catgtttaac atccagcact gtaagaagct gtccagctgg gtgctgctga tgaaatacct 840
gggcaatgcc accgccatct tcttcctgcc tgatgagggg aaactacagc acctggaaaa 900
tgaactcacc cacgatatca tcaccaagtt cctggaaaat gaagacagaa ggtctgccag 960
cttacattta cccaaactgt ccattactgg aacctatgat ctgaagagcg tcctgggtca 1020
actgggcac ctaaggtct tcagcaatgg ggctgacctc tccggggtca cagaggaggc 1080
accctgaag ctctccaagg ccgtgcataa ggctgtgctg accatcgacg agaaagggac 1140
tgaagctgct ggggccatgt ttttagaggc catacccatg tctatcccc ccgaggtcaa 1200
gttcaacaaa ccctttgtct tcttaatgat tgaacaaaat accaagtctc ccctcttcat 1260
gggaaaagtg gtgaatccca cccaaaaata actgcctctc gtcctcaac ccctcccctc 1320
catccctggc cccctccctg gatgacatta aagaagggtt gagctggtec ctgcctgcat 1380
gtgactgtaa atccctccca tgttttctct gagtctccct ttgcctgctg aggctgtatg 1440
tgggctccag gtaacagtgc tgtcttcggg cccctgaac tgtgttcatg gagcatctgg 1500
ctgggtaggc acatrtctggg cttgaatcca ggggggactg aatcctcagc ttacggacct 1560
gggccatct ctttctggag ggctccagtc ttccttgctc tgtcttgag tccccaagaa 1620
ggaaacacag gggagggaacc agataccagc catgacccca ggctccacca agcatcttca 1680
tgtccccctg ctcatcccc actccccccc acccagagtt gctcatcctg ccagggtctg 1740
ctgtgccac cccaaggctg ccctcctggg ggccccagaa ctgcctgatc gtgccgtggc 1800
ccagttttgt ggcatctgca gcaacacaag agagaggaca atgtcctct cttgaccgc 1860
tgtcacctaa ccagactcgg gccctgcacc tctcaggcac ttctggaaaa tgactgaggc 1920
agattcttcc tgaagcccat tctccatggg gcaacaagga cacctattct gtccttgtcc 1980
ttccatcgct gccccagaaa gcctcacata tctcgttcta gaatcaggtc ccttctcccc 2040
agatgaagag gaggtctct gctttgtttt ctctatctcc tctcagact tgaccaggcc 2100
cagcaggccc cagaagacca ttaccctata tcccttctcc tcccagtc catggcata 2160
ggcctgctga tggctcagga aggccattgc aaggactcct cagctatggg agaggaagca 2220
catcaccat tgacccccgc aacccctccc tttcctcccc tgagtccga ctggggccac 2280
atgcagcctg acttctttgt gcctgttctg gtccctgcag tcttcagagg gccaccgcag 2340
ctccagtgc acggcaggag gctgttctg aatagcccct gtggttaagg ccaggagagt 2400
ccttccatcc tccaaggccc tgctaaagga cacagcagcc aggaagtccc ctgggcccct 2460
agctgaagga cagcctgctc cctccgtctc taccaggaat ggccttgtcc tatggaaggc 2520
actgccccat cccaaactaa tctaggaatc actgtctaac cactcactgt catgaatgtg 2580
tacttaaagg atgaggttga gtcataccaa atagtattt cgatagttca aaatggtgaa 2640
attagcaatt ctacatgatt cagtctaacc aatggatacc gactgtttcc cacacaagtc 2700
tctgtttctc ttaagcttac tcactgacag cctttcactc tccacaaata cattaaagat 2760
atggccatca ccaagccccc taggatgaca ccagacctga gagtctgaag acctggatcc 2820
aagttctgac ttttccccct gacagctgtg tgacctcgt gaagtcgcca aacctctctg 2880
agccccagtc attgctagta agacctgcct ttgagttggt atgatgttca agttagataa 2940
caaaatgttt ataccatta gaacagagaa taaatagaac tacatttctt gcaaaaaaaaa 3000
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 3041

```

&lt;210&gt; 286

&lt;211&gt; 418

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 286

```

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys
1           5           10          15
Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
20          25          30
Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
35          40          45
Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln

```

[illegible]

```
<210> 287
<211> 3928
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(3928)
<223> n = A,T,C or G
```



&lt;400&gt; 287

```

cacgcgtccg gcggcggggg cgaggtgagg tgttggcagt ggaaaggggt tcgggctcgg 60
ggggcggggg gacgcggagc gatggcccgc gccggccgca ggggcggata aaaagccgtc 120
gcgctgcggg agtgggcggg agggagaggg ggtgtccgag ggccacaaga gtatgacggg 180
gctgtacgag ctgggtgtgc ggggtgctga cgcgtgctc tgtctgcacc gcacgctcac 240
ctcctggctc cgcgttcggt tcggcacctg gaactggatc tggcggcgct gctgccgcgc 300
cgcctctgcc gcggtcctag cgccgctcgg ttccacgctc cgcaagcccc cggcagtcgg 360
caggaaccgc cgtcaccacc ggcacccgcg cgggggggtcg tgcctggcag ccgcacacca 420
ccgatgcgc tggcgcgcgg acggtcgttc cttggagaag ctgcctgtgc atatgggcct 480
ggtgatcacc gaggtggagc aggaaccag cttctcggac atcgcgagcc tcgtggtgtg 540
gtgtatggcc gtgggcatct cctacattag cgtctacgac caccaaggta ttttcaaaag 600
aaataattcc agattgatgg atgaaatttt aaaacaacag caagaacttc tgggcctaga 660
ttgttcaaaa tactcaccag aatttgcaaa tagtaatgac aaagatgatc aagttttaaa 720
ttgccatttg gcagtgaagg tgctgtctcc ggaagatgga aaagcagata ttgtaagagc 780
tgctcaggac ttttgccagt tagtagccca gaagcaaaag agaccacag atttggtatg 840
agatacgtta gccagtttac ttagttcaaa tggttgtcct gatcctgatt tagtattgaa 900
gttcggtcct gtggacagca cattaggctt tcttccctgg cacatcagat tgactgagat 960
tgtctctttg ccttcccacc taaacatcag ttatgaggac tttttctctg cccttcgtca 1020
atatgcagcc tgtgaacagc gtctgggaaa gtagtggta ttggttgcat aatttgattt 1080
gaggcttggt gaggaaggga accaagtgc tctgatgttt acaaagcacc tatgaaaccc 1140
tgtacacacc tatgaaaccc tgtacacacc tagttcataa tcctcataat ttatcaacaa 1200
acacaaaaaa gtgtcttact tgagagttag tgtgtgtgtg tgcgtgtgca cgtgcacaca 1260
tgtgcacggt tgtatgtatg gaaataaact tataaatggg gacgtatttg agaaggaaat 1320
acatagacct acaactttga gcaaatagca gtgatgtttt aggaactgaa atgtcacact 1380
taaagtcttc agcccagcta cttccctatt tttgtgggga gaagagggcc tgattagaac 1440
tgttctggtt gtgtttggcg ggaggggaat aatttttgtt cagtccttct tagtgacca 1500
actttaattt ttaagaataa tatattgact tactgaactg aagcattctg agttgaaagg 1560
agctccagag gagtggagtt ctgtgttgct cacatgttaa aatcttgctc accttcagag 1620
cagagggaat acctatcttc agatatccgt ccattttcat ctcttaattg tagtcaaaag 1680
tatgacttga gagtgttgct ctggtattct gggttctgaa gtctggtatt ctggtattct 1740
gggttcaaaa gtatgacttg agagtgttgc tctggtattc tgagagttag tctgtattct 1800
gggttctgaa gattatttga aaaataaact ctactacatt gaaatgcaga cttaaaaatt 1860
taaacatttg attaggcagt caaaaaaacc aagcaagcat aaaaggtcaa taagttgtaa 1920
tcttgatagt aaaggtggaa aacttattat aaatggaaag aaagttttat ttctttttt 1980
gtttgatggg cagtatgcca tattataccc aaagttcttt taaaaaatat ttccatcaac 2040
catttttatt taaaataaac atttgaggga agttaccaag gcagcttttt tcctcaaaag 2100
taacctgttc ctctttggaa tagcacattt taggggcatg gttaatacct gagattttta 2160
ctcagtaaat cctgatgggt actgtgtgta aaatatcttt aagtaggatt gaaggcctct 2220
gtgggggaat aaaatatatt caaagtctat aaaaataaat tttacatggt ctctttttatg 2280
acagagagca gcactgggtc tgttattttt aaaatgaata attgatttct tgataggtgt 2340
ttaatatatt ttccctcact gctgattctt agatagaaac cattctttat atttgataga 2400
ctgctttcag aaaaccctta tcaacaagtg tacaatactt atctaaaact atacatttag 2460
aatggagcag ttaataacta gatctcagaa gttttgaaaa atagcaaaga agactggatt 2520
tggaagcat ggtctacaat tgggtgttaa attctgaagc tatgaaagat aaatgtttca 2580
actttggatt atgaaacccc atttatgatt ttttaaatat acttgaaata afaatgatta 2640
aactaaaaaa aaaaamarwr amattacttt gcactgcata atccattata cgttgtacga 2700
cttttttttt tttgttttaa tttattactg agagttttgt gtgaagctac agcatatcta 2760
accagagaat ttctgattcc ttatactgtg attatattat attgaggcat ttgtagtga 2820
gctgaagact gaatttatgc cttttgtaaa catgataggt ataaatgtct tataaacatt 2880
ctggagtatg tatagcttta atgaatgaaa tttaatggac ctgattaaaa tgaagggtat 2940
taatcgttgt taaagttaag ttagtcaaat aaattadcta ctggaatata gcccaagcca 3000
gtaaaggttt aatatttgca ttttcgtgct tttattttct ccttccattc ataagtatat 3060
acttgaaagt acatctgtag cctatgattt gagtctcttg aagttctagg aagaggcaaa 3120
ctacaaacta ctagtattct gatttcagat gtagtcatte cagaaccttc tctttatgag 3180
ttcacctgct agtacaatct ccacaacttg aatggcattg gttgtttctg aattcctgcc 3240
aaaagcatca caagttgtac atcatcaagg ctccctttgc actccaaga agaactggta 3300
attttaacaa aaagtatgtg tctttatttg tattggaaaa tactgtctat aaattgtttc 3360

```

296

```

ttgttgacac tccccacaat ggaaaaatta ccaaattaaa cctgttttat ggatggcagc 3420
ttggagcata gcaagaagtt ggaggatttg aattccattc ccagttctca ttgygttttg 3480
tttcttaaaa ctataataat tggttactgt tataaagttt aaaaggtggt tttaatatga 3540
atagcaaatt ctggtatatt gtgactaacg cttagaatg cctgtctttg agaggaaggt 3600
gttataatat taatcaacag tgccaaatac actgtgcata tctacaattt aatctttgaa 3660
tgtttggtac tggattagct ccctcctcct tctgtgtgat ggtaccatgc atagagtcaa 3720
tcaaatcctt gtgatgtttt gtatggactt tgacaacatg taactaatgt gtaaagcaag 3780
tttttatgat taaggaatca aatttattga attttattat tgaaagttga aacttaacat 3840
gtataaaciaa aaaacaataa aataataaac tatttttcatt gacaaaaaaa aaaraaaaaa 3900
aaaaaaaaan aaaaaaaaaa aaaaaaaaaa 3928

```

&lt;210&gt; 288

&lt;211&gt; 293

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 288

```

Met Thr Gly Leu Tyr Glu Leu Val Trp Arg Val Leu His Ala Leu Leu
 1          5          10          15
Cys Leu His Arg Thr Leu Thr Ser Trp Leu Arg Val Arg Phe Gly Thr
 20          25          30
Trp Asn Trp Ile Trp Arg Arg Cys Cys Arg Ala Ala Ser Ala Ala Val
 35          40          45
Leu Ala Pro Leu Gly Phe Thr Leu Arg Lys Pro Pro Ala Val Gly Arg
 50          55          60
Asn Arg Arg His His Arg His Pro Arg Gly Gly Ser Cys Leu Ala Ala
 65          70          75          80
Ala His His Arg Met Arg Trp Arg Ala Asp Gly Arg Ser Leu Glu Lys
 85          90          95
Leu Pro Val His Met Gly Leu Val Ile Thr Glu Val Glu Gln Glu Pro
100          105          110
Ser Phe Ser Asp Ile Ala Ser Leu Val Val Trp Cys Met Ala Val Gly
115          120          125
Ile Ser Tyr Ile Ser Val Tyr Asp His Gln Gly Ile Phe Lys Arg Asn
130          135          140
Asn Ser Arg Leu Met Asp Glu Ile Leu Lys Gln Gln Gln Glu Leu Leu
145          150          155          160
Gly Leu Asp Cys Ser Lys Tyr Ser Pro Glu Phe Ala Asn Ser Asn Asp
165          170          175
Lys Asp Asp Gln Val Leu Asn Cys His Leu Ala Val Lys Val Leu Ser
180          185          190
Pro Glu Asp Gly Lys Ala Asp Ile Val Arg Ala Ala Gln Asp Phe Cys
195          200          205
Gln Leu Val Ala Gln Lys Gln Lys Arg Pro Thr Asp Leu Asp Val Asp
210          215          220
Thr Leu Ala Ser Leu Leu Ser Ser Asn Gly Cys Pro Asp Pro Asp Leu
225          230          235          240
Val Leu Lys Phe Gly Pro Val Asp Ser Thr Leu Gly Phe Leu Pro Trp
245          250          255
His Ile Arg Leu Thr Glu Ile Val Ser Leu Pro Ser His Leu Asn Ile
260          265          270
Ser Tyr Glu Asp Phe Phe Ser Ala Leu Arg Gln Tyr Ala Ala Cys Glu
275          280          285
Gln Arg Leu Gly Lys
290

```

&lt;210&gt; 289

<211> 936  
 <212> DNA  
 <213> Homo sapiens

<400> 289  
 gctccggggcc tggaaatccct acgcgtccct ttgggttttag cacgatgagc tcaatcggca 60  
 ctgggtatga cctgtcagcc tctacattct ctctgacgg aagagttttt caagttgaat 120  
 atgctatgaa ggctgtggaa aatagtagta cagctatttg aatcagatgc aaagatgggtg 180  
 ttgtcttttg ggtagaaaaa ttagtccttt ctaaacttta tgaagaagggt tccaacaaaa 240  
 gactttttta tggtgatcgg catgttggaa tggcagtagc aggtttgttg gcagatgctc 300  
 gttcttttagc agacatagca agagaagaag cttccaactt cagatctaac tttggctaca 360  
 acattccact aaaacatctt gcagacagag tggccatgta tgtgcatgca tatacactct 420  
 acagtgtctgt tagacctttt ggctgcagtg tgaatgacgg tgcgcaactc tacatgattg 480  
 acccatcagg tgtttcatac gggttattggg gctgtgccat cggcaaagcc aggcaagctg 540  
 caaagacgga aatagagaag cttcagatga aagaaatgac ctgccgtgat atcgttaaag 600  
 aagttgcaaa aataatttac atagtacatg acgaagttaa ggataaagct tttgaactag 660  
 aactcagctg ggttggtgaa ttaactaatg gaagacatga aattgttcca aaagatataa 720  
 gagaagaagc agagaaatat gctaaggaat ctctgaagga agaagatgaa tcagatgatg 780  
 ataatatgta acatttactc cagcatctat tgtattttta atttctactc cagtccaatg 840  
 taactattta gccctggatt atacatactg tccaattttc attaaatttt tgtcttataa 900  
 ctattaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 936

<210> 290  
 <211> 248  
 <212> PRT  
 <213> Homo sapiens

<400> 290  
 Met Ser Ser Ile Gly Thr Gly Tyr Asp Leu Ser Ala Ser Thr Phe Ser  
 1 5 10 15  
 Pro Asp Gly Arg Val Phe Gln Val Glu Tyr Ala Met Lys Ala Val Glu  
 20 25 30  
 Asn Ser Ser Thr Ala Ile Gly Ile Arg Cys Lys Asp Gly Val Val Phe  
 35 40 45  
 Gly Val Glu Lys Leu Val Leu Ser Lys Leu Tyr Glu Glu Gly Ser Asn  
 50 55 60  
 Lys Arg Leu Phe Asn Val Asp Arg His Val Gly Met Ala Val Ala Gly  
 65 70 75 80  
 Leu Leu Ala Asp Ala Arg Ser Leu Ala Asp Ile Ala Arg Glu Glu Ala  
 85 90 95  
 Ser Asn Phe Arg Ser Asn Phe Gly Tyr Asn Ile Pro Leu Lys His Leu  
 100 105 110  
 Ala Asp Arg Val Ala Met Tyr Val His Ala Tyr Thr Leu Tyr Ser Ala  
 115 120 125  
 Val Arg Pro Phe Gly Cys Ser Val Asn Asp Gly Ala Gln Leu Tyr Met  
 130 135 140  
 Ile Asp Pro Ser Gly Val Ser Tyr Gly Tyr Trp Gly Cys Ala Ile Gly  
 145 150 155 160  
 Lys Ala Arg Gln Ala Ala Lys Thr Glu Ile Glu Lys Leu Gln Met Lys  
 165 170 175  
 Glu Met Thr Cys Arg Asp Ile Val Lys Glu Val Ala Lys Ile Ile Tyr  
 180 185 190  
 Ile Val His Asp Glu Val Lys Asp Lys Ala Phe Glu Leu Glu Leu Ser  
 195 200 205  
 Trp Val Gly Glu Leu Thr Asn Gly Arg His Glu Ile Val Pro Lys Asp  
 210 215 220  
 Ile Arg Glu Glu Ala Glu Lys Tyr Ala Lys Glu Ser Leu Lys Glu Glu  
 225 230 235 240

Asp Glu Ser Asp Asp Asp Asn Met  
245

<210> 291  
<211> 2782  
<212> DNA  
<213> Homo sapiens

<400> 291  
ggcagcaggc ccacccgggc tcgcgtctcc gtttctccga gaggcccaag gtgtctccgc 60  
cgcagcctct gtcgcgccgt gacctgtaca ggctgcggga gtcgtagga ggacgccggg 120  
acacctggaa gccgagaaat ggattcagtg gcctttgagg atgtggctgt gaacttcacc 180  
ctggaggagt gggctttgct ggatccttcc cagaagaatc tctacagga tgtgatgcgg 240  
gaaaccttca ggaacctggc ttctgttaga aaacaatggg aagaccagaa cattgaagac 300  
ccattcaaaa ttcccaggag aaatataagt catattccag agagactctg tgaaagtaaa 360  
gaaggtggtc aaggtgaaga aaccttcagc cagattccag atggtattct gaacaagaaa 420  
actcctggag taaaaccgtg tgaaagcagt gtgtgtggag aagttggcat gggctccttca 480  
tcacttaata ggcacatcag agatcacact ggacgtgaac caaatgaata tcaggaatat 540  
ggaaagaagt catatacag taaccagtggt ggacgagcct tgagttatca tcgctctttt 600  
ccagtacgtg aaaggactca tcctggagga aagccctatg attgtaagga atgtggagaa 660  
acctttatct ctcttgtaag cattcgaaga cacatgttaa cgcatagggg aggtgtacct 720  
tacaatgta aggtgtgtgg gaaagccttt gattatccca gtttatttctg tatacatgaa 780  
agaagtcaca ctggagagaa accttatgaa tgcaagcaat gtgggaaagc cttcagttgt 840  
tccagttaca ttagaataca tgaaaggact cacactggag ataaacccta tgaatgcaag 900  
cagtggtgga aagctttcag ttgttccaag tacattcgaa tccatgaacg aactcacaca 960  
ggagagaaac cctacgaatg taaacagtgc ggtaaagcct ttaggtgcgc cagttctgtt 1020  
cgaagtcacg agaggactca caccggagag aaactttttg aatgtaagga atgcgggaag 1080  
gctttgactt gtcttgcaag tgttagaaga cacatgataa agcacactgg caatggacct 1140  
tataaatgta aggtgtgtgg gaaagccttt gatttcccca gttcatttctg aatccatgaa 1200  
aggaccaca ctggagagaa accctatgat tgtaagcaat gtgggaaagc cttcagttgt 1260  
tccagttcgt ttcgaaaaca tgaaagaatt cacactggag agaaacccta taaatgtaca 1320  
aaatgtggga aagccttcag tcgttccagt tacttccgaa tccatgaaag aactcacact 1380  
ggagagaaac cctatgaatg taagcaatgt gggaaagcct tcagtcgatc cacttacttt 1440  
cgagtacatg aaaaaattca tactggagag aaaccctatg agaaccctaa ccctaacgct 1500  
tcagttgtcc cagttctttc atgagcataa aaggagtcac atagagaaac cccatgaaag 1560  
taagaaattt gggaaagcct tcagtccttt ctgtttcttt caactacgtg aaaggattca 1620  
cagtggagaa agaccctgta agataatttg ctttaaatta cgagagactt gtgataggac 1680  
agtaaaacct agagttggag ttggatctct ggattgtgtt atgtcagttt tggtagggtta 1740  
ggaactagat ttcccagaat ccattccatt tgtgattcca tgatacaatt caccagtaac 1800  
ctatcttaca tgagattcgg aagtaagtta agaaggcatt agtcatggtt tggaagcacc 1860  
atacaggag acagctgtgt gaatacaggc tgtatggaca cttgcttcca tcccattttc 1920  
ctgcttcttt gggttgccaa tcaagagtat cctcaaaacg acttgacttt aattttctcg 1980  
gaggtgatag gcttccacac aggtctccag aagccctgca ttgaatatcc atccacactt 2040  
tggttttctt tcagacatta ttatgtctgt actaggcaac taattcagac tgtcctgggt 2100  
gggaatattc tgtgatgctc tgactcccct agtctgtaga cggaattggc atacggtcta 2160  
atttgtgtag taagcacctt tgttcatact agtagtgact gtattcttga ttcagcctga 2220  
tagctacat gctgctgtca aaaccaacca gaggggagct tgttcttctg ctgtagtgtg 2280  
cagtgactgg cctcaccag gactttgatg tgagaatgag cactttcctc tatcaggaaa 2340  
tttcaagtgt ttctgttat tcgtagctca atgtaatgcc tcagttcatt ttcagttgtt 2400  
tgattatatg tgactaatat gtatttttta ttcaaacaag acttctgtac atgtttcttc 2460  
aaaacagttt attaactgtc ttcagtcctg gattacatca agtttataat tttggcaaat 2520  
tgttaagaca ctgtgaagtc agcgttaacc atgtgcatac aacttaagga atttttctc 2580  
cctcatgtaa attttacttt tcatgcttat atagtttcaa cttttatctt catagtaatt 2640  
tctcatctac tcataatacc aaaagttaag tcatgctgtt ttgtgtgctc tcttgctaaa 2700  
gaccgcagag accatacctg ttgtcaaaga ggggtgaata aactgtaata ataatacatg 2760  
ccacaaaaaa aaaaaaaaaa aa 2782

299

&lt;210&gt; 292

&lt;211&gt; 461

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 292

```

Met Asp Ser Val Ala Phe Glu Asp Val Ala Val Asn Phe Thr Leu Glu
 1          5          10          15
Glu Trp Ala Leu Leu Asp Pro Ser Gln Lys Asn Leu Tyr Arg Asp Val
 20          25          30
Met Arg Glu Thr Phe Arg Asn Leu Ala Ser Val Gly Lys Gln Trp Glu
 35          40          45
Asp Gln Asn Ile Glu Asp Pro Phe Lys Ile Pro Arg Arg Asn Ile Ser
 50          55          60
His Ile Pro Glu Arg Leu Cys Glu Ser Lys Glu Gly Gly Gln Gly Glu
 65          70          75          80
Glu Thr Phe Ser Gln Ile Pro Asp Gly Ile Leu Asn Lys Lys Thr Pro
 85          90          95
Gly Val Lys Pro Cys Glu Ser Ser Val Cys Gly Glu Val Gly Met Gly
100          105          110
Pro Ser Ser Leu Asn Arg His Ile Arg Asp His Thr Gly Arg Glu Pro
115          120          125
Asn Glu Tyr Gln Glu Tyr Gly Lys Lys Ser Tyr Thr Arg Asn Gln Cys
130          135          140
Gly Arg Ala Leu Ser Tyr His Arg Ser Phe Pro Val Arg Glu Arg Thr
145          150          155          160
His Pro Gly Gly Lys Pro Tyr Asp Cys Lys Glu Cys Gly Glu Thr Phe
165          170          175
Ile Ser Leu Val Ser Ile Arg Arg His Met Leu Thr His Arg Gly Gly
180          185          190
Val Pro Tyr Lys Cys Lys Val Cys Gly Lys Ala Phe Asp Tyr Pro Ser
195          200          205
Ile Phe Arg Ile His Glu Arg Ser His Thr Gly Glu Lys Pro Tyr Glu
210          215          220
Cys Lys Gln Cys Gly Lys Ala Phe Ser Cys Ser Ser Tyr Ile Arg Ile
225          230          235          240
His Glu Arg Thr His Thr Gly Asp Lys Pro Tyr Glu Cys Lys Gln Cys
245          250          255
Gly Lys Ala Phe Ser Cys Ser Lys Tyr Ile Arg Ile His Glu Arg Thr
260          265          270
His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Gln Cys Gly Lys Ala Phe
275          280          285
Arg Cys Ala Ser Ser Val Arg Ser His Glu Arg Thr His Thr Gly Glu
290          295          300
Lys Leu Phe Glu Cys Lys Glu Cys Gly Lys Ala Leu Thr Cys Leu Ala
305          310          315          320
Ser Val Arg Arg His Met Ile Lys His Thr Gly Asn Gly Pro Tyr Lys
325          330          335
Cys Lys Val Cys Gly Lys Ala Phe Asp Phe Pro Ser Ser Phe Arg Ile
340          345          350
His Glu Arg Thr His Thr Gly Glu Lys Pro Tyr Asp Cys Lys Gln Cys
355          360          365
Gly Lys Ala Phe Ser Cys Ser Ser Ser Phe Arg Lys His Glu Arg Ile
370          375          380
His Thr Gly Glu Lys Pro Tyr Lys Cys Thr Lys Cys Gly Lys Ala Phe
385          390          395          400
Ser Arg Ser Ser Tyr Phe Arg Ile His Glu Arg Thr His Thr Gly Glu
405          410          415

```

300

Lys Pro Tyr Glu Cys Lys Gln Cys Gly Lys Ala Phe Ser Arg Ser Thr  
                   420                  425                  430  
 Tyr Phe Arg Val His Glu Lys Ile His Thr Gly Glu Lys Pro Tyr Glu  
                   435                  440                  445  
 Asn Pro Asn Pro Asn Ala Ser Val Val Pro Val Leu Ser  
                   450                  455                  460

<210> 293  
 <211> 666  
 <212> DNA  
 <213> Homo sapiens

<400> 293  
 actgagatgg cctctttaat caaccaactt cccaggccaa tctcttccct ttcttttctg 60  
 atagttgctg tgttgccctc atagccttac ctggcatagg aaagataaac aatctccttg 120  
 gtgtcaggat ttctggtctc tggctaggtt tctgtcttat gcaatagtag ctgggagagg 180  
 ccgaaagaat tctggtgggg ccacaccacac tggtgaaaga ataaatagtg aggtttggca 240  
 ttggccatca gagtcactcc tgccttcacc atgaagtcca gcggcctctt ccccttcctg 300  
 gtgctgcttg ccttggaac tctggcacct tgggctgtgg aaggctctgg aaagtgtgag 360  
 ttggagtcac tctggtctaa tctgggctgc agggctcagag gtggggtctc cttgtggtgt 420  
 ggggtgtgtcc ccttctgtag gctctgatcc ctcagcttag ttctgggaga cctccctgag 480  
 ggtggaatac atgtctggct gagctccaag gtttgtgtga cagtttgagc ttctggaaat 540  
 gcttctctta tgcagccatg ctgtcagccc aggtcccact ctctctctct ctctctctct 600  
 ctctctctct ctcatactcc gccttcttct tcacctgtct gcgactctca aaaaaaaaaa 660  
 aaaaaa 666

<210> 294  
 <211> 58  
 <212> PRT  
 <213> Homo sapiens

<400> 294  
 Met Lys Ser Ser Gly Leu Phe Pro Phe Leu Val Leu Leu Ala Leu Gly  
   1                  5                  10                  15  
 Thr Leu Ala Pro Trp Ala Val Glu Gly Ser Gly Lys Cys Lys Leu Glu  
                   20                  25                  30  
 Ser Leu Trp Ser Asn Leu Gly Cys Arg Val Arg Gly Gly Val Ser Leu  
                   35                  40                  45  
 Trp Cys Gly Cys Val Pro Phe Cys Arg Leu  
                   50                  55

<210> 295  
 <211> 594  
 <212> DNA  
 <213> Homo sapiens

<400> 295  
 gtcactcctg ccttcaccat gaagtcacgc ggctcttcc ccttcctggg gctgcttgcc 60  
 ctgggaactc tggcaccttg ggctgtggaa ggctctggaa agtccttcaa agctggagtc 120  
 tgtcctccta agaaatctgc ccagtgctt agatacaaga aacctgagtg ccagagtgc 180  
 tggcagtgct cagggaagaa gagatgttgt cctgacactt tgggcatcaa atgcctggat 240  
 cctgttgaca ccccaaacc aacaaggagg aagcctggga agtgcccagt gacttatggc 300  
 caatgtttga tgcttaaccc cccaatttc tgtgagatgg atggccagtg caagcgtgac 360  
 ttgaagtgtt gcatgggcat gtgtgggaaa tctgtcggtt cccctgtgaa agcttgattc 420  
 ctgccatatg gaggaggctc tggagtctgt ctctgtgtgg tccaggtoct ttccaccctg 480  
 agacttggct ccaccactga tatcctcctt tggggaaagg cttggcacac agcaggcttt 540

301

caagaagtgc cagttgatca atgaataaat aaacgagcct atttctcttt gcac 594

<210> 296

<211> 132

<212> PRT

<213> Homo sapiens

<400> 296

Met	Lys	Ser	Ser	Gly	Leu	Phe	Pro	Phe	Leu	Val	Leu	Leu	Ala	Leu	Gly
1				5					10					15	
Thr	Leu	Ala	Pro	Trp	Ala	Val	Glu	Gly	Ser	Gly	Lys	Ser	Phe	Lys	Ala
			20					25					30		
Gly	Val	Cys	Pro	Pro	Lys	Lys	Ser	Ala	Gln	Cys	Leu	Arg	Tyr	Lys	Lys
		35					40					45			
Pro	Glu	Cys	Gln	Ser	Asp	Trp	Gln	Cys	Pro	Gly	Lys	Lys	Arg	Cys	Cys
	50				55					60					
Pro	Asp	Thr	Cys	Gly	Ile	Lys	Cys	Leu	Asp	Pro	Val	Asp	Thr	Pro	Asn
65					70				75					80	
Pro	Thr	Arg	Arg	Lys	Pro	Gly	Lys	Cys	Pro	Val	Thr	Tyr	Gly	Gln	Cys
			85					90					95		
Leu	Met	Leu	Asn	Pro	Pro	Asn	Phe	Cys	Glu	Met	Asp	Gly	Gln	Cys	Lys
			100				105						110		
Arg	Asp	Leu	Lys	Cys	Cys	Met	Gly	Met	Cys	Gly	Lys	Ser	Cys	Val	Ser
		115					120					125			
Pro	Val	Lys	Ala												
			130												

<210> 297

<211> 720

<212> DNA

<213> Homo sapiens

<400> 297

cctgcgagct	cgtcctgcc	tgcagcagca	caaccctgca	caccacccat	ggatgtcttc	60
aagaagggtc	tctccatcgc	caaggagggc	gtggtgggtg	cggtggaaaa	gaccaagcag	120
gggggtgacg	aagcagctga	gaagaccaag	gaggggggtc	tgtatgtggg	agccaagacc	180
aaggagaatg	ttgtacagag	cgtgacctca	gtggccgaga	agaccaagga	gcaggccaac	240
gcggtgagcg	aggctgtggt	gagcagcgtc	aacactgtgg	ccaccaagac	cgtggaggag	300
gcggagaaca	tcgcggtcac	ctccgggggtg	gtgcgcaagg	aggacttgag	gccatctgcc	360
ccccaacagg	aggggtgtggc	atccaaagag	aaagaggaag	tggcagagga	ggcccagagt	420
gggggagact	agagggctac	aggccagcgt	ggatgacctg	aagagcgctc	ctctgccttg	480
gacaccatcc	cctcctagca	caaggagtgc	ccgccttgag	tgacatgcgg	ctgcccacgc	540
tcttgccctc	gtcttctctg	ccacccttgg	cctgtccacc	tgtgctgctg	caccaacctc	600
actgccctcc	ctcggcccca	cccaccctct	ggctctctctg	accccactta	tgctgctgtg	660
aatttttttt	ttaaatgatt	caaataaaaa	cttgagccca	ctcctaaaaa	aaaaaaaaaa	720

<210> 298

<211> 127

<212> PRT

<213> Homo sapiens

<400> 298

Met	Asp	Val	Phe	Lys	Lys	Gly	Phe	Ser	Ile	Ala	Lys	Glu	Gly	Val	Val
1				5					10					15	
Gly	Ala	Val	Glu	Lys	Thr	Lys	Gln	Gly	Val	Thr	Glu	Ala	Ala	Glu	Lys
			20					25					30		

Thr	Lys	Glu	Gly	Val	Met	Tyr	Val	Gly	Ala	Lys	Thr	Lys	Glu	Asn	Val
	35						40					45			
Val	Gln	Ser	Val	Thr	Ser	Val	Ala	Glu	Lys	Thr	Lys	Glu	Gln	Ala	Asn
	50					55					60				
Ala	Val	Ser	Glu	Ala	Val	Val	Ser	Ser	Val	Asn	Thr	Val	Ala	Thr	Lys
65					70					75					80
Thr	Val	Glu	Glu	Ala	Glu	Asn	Ile	Ala	Val	Thr	Ser	Gly	Val	Val	Arg
				85					90					95	
Lys	Glu	Asp	Leu	Arg	Pro	Ser	Ala	Pro	Gln	Gln	Glu	Gly	Val	Ala	Ser
			100					105					110		
Lys	Glu	Lys	Glu	Glu	Val	Ala	Glu	Glu	Ala	Gln	Ser	Gly	Gly	Asp	
	115						120					125			

&lt;210&gt; 299

&lt;211&gt; 6981

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 299

ttgctgcgtc	aactgtgttc	cctttggcct	ggctgagttt	gatactgtgg	ggattcagtt	60
taggcgctgg	cccaggata	tcccagcgg	ggtacttcgg	agacacctgt	ctgcatctga	120
ctgagccggc	tctcctggcc	tcgcgtgca	cattctctcc	tggcggcggc	gccacctgca	180
gtagcgttcg	cccgaaatg	gcgacacga	gcagcaggag	ggagtgcga	ctcccgttcc	240
tattcaccct	ggtcgcactg	ctgccgcccg	gagctctctg	cgaagtctgg	acgcagaggc	300
tgcacggcgg	cagcgcgcc	ttgccccagg	accggggcct	cctcgtgggt	cagggcgacc	360
cgcgcgagct	gcggctgtgg	gcgcgcgggg	atgccagggy	ggcgcgcgc	gcggacgaga	420
agccgctccg	gaggaacgg	agcgcctgcc	tgcagcccg	gccatcaag	gtgtacggac	480
aggttagtct	gaatgattcc	cacaatcaga	tgggtgggca	ctgggctgga	gagaaaagca	540
acgtgatcgt	ggccttgccc	cgagatagcc	tggcattggc	gaggcccaag	agcagtgatg	600
tgtacgtgtc	ttacgactat	ggaaaatcat	tcaagaaaat	ttcagacaag	ttaaactttg	660
gcttgggaaa	taggagtga	gctgttatcg	cccagttcta	ccacagccct	gcggacaaca	720
agcgggtacat	ctttgcagac	gcttatgccc	agtacctctg	gatcacgttt	gacttctgca	780
acactcttca	aggcttttcc	atcccatttc	gggcagctga	tctcctccta	cacagtaagg	840
cctccaacct	tctcttgggc	tttgacaggt	cccaccccaa	caagcagctg	tggagtcag	900
atgacttttg	ccagacctgg	atcatgattc	aggaacatgt	caagtccttt	tcttggggaa	960
ttgatcccta	tgacaaacca	aataccatct	acattgaacg	acacgaacct	tctggctact	1020
ccactgtctt	ccgaagtaca	gatttcttcc	agtcccggga	aaaccaggaa	gtgatccctg	1080
aggaagtgag	agattttcag	cttcggggaca	agtacatggt	tgtacaaaag	gtggtgcata	1140
tcttgggcag	tgaacagcag	tcttctgtcc	agctctgggt	ctcctttggc	cggagcccca	1200
tgagagcagc	ccagtttgtc	acaagacatc	ctattaatga	atattacatc	gcagatgcct	1260
ccgaggacca	ggtgtttgtg	tgtgtcagcc	acagtaacaa	ccgcaccaat	ttatacatct	1320
cagaggcaga	ggggctgaag	ttctccctgt	ccttgagaaa	cgtgctctat	tacagcccag	1380
gaggggcccg	cagtgcacac	ttggtgaggt	atthtgcaaa	tgaacctatt	gctgacttcc	1440
accgagtggg	aggattgcaa	ggagtctaca	ttgctactct	gattaatggt	tctatgaatg	1500
aggagaacat	gagatcggtc	atcacctttg	acaaaggggg	aacctgggag	tttcttcagg	1560
ctccagcctt	cacgggatat	ggagagaaaa	tcaattgtga	gctttcccag	ggctgttccc	1620
ttcatctggc	tcagcgcctc	agtcagctcc	tcaacctcca	gctccggaga	atgcccaccc	1680
tgtccaagga	gtcggctcca	ggcctcatca	tcgccactgg	ctcagtggga	aagaacttgg	1740
ctagcaagac	aaacgtgtac	atctctagca	gtgctggagc	caggtggcga	gaggcacttc	1800
ctggacctca	ctactacaca	tggggagacc	acggcggaat	catcacggcc	attgcccagg	1860
gcatggaaac	caacgagcta	aaatacagta	ccaatgaagg	ggagacctgg	aaaacattca	1920
tcttctctga	gaagccagtg	tttgtgtatg	gcctcctcac	agaacctggg	gagaagagca	1980
ctgtcttcc	catctttggc	tcgaacaaag	agaatgtcca	cagctggctg	atcctccagg	2040
tcaatgccac	ggatgccttg	ggagtccctt	gcacagagaa	tgactacaag	ctgtggtcac	2100
catctgatga	gcggggggaat	gagtggttgc	tgggacacaa	gactgttttc	aaacggcgga	2160
ccccccatgc	cacatgcttc	aatggagagg	actttgacag	gccggtgggt	gtgtccaact	2220
gctcctgcac	ccgggaggac	tatgagtgtg	acttcgggtt	caagatgagt	gaagatttgt	2280



cattagaggt	ttgtgttcca	gatccggaat	tttctggaaa	gtcatactcc	cctcctgtgc	2340
cttgccctgt	gggttctact	tacaggagaa	cgagaggcta	ccggaagatt	tctggggaca	2400
ctttagcg	aggagatgtt	gaagcgcgac	tggaggaga	gctggtcccc	tgtccctgg	2460
cagaagagaa	cgagttcatt	ctgtatgctg	tgaggaaatc	catctaccgc	tatgacctgg	2520
cctcgggagc	caccgagcag	ttgcctctca	ccgggctacg	ggcagcagtg	gccctggact	2580
ttgactatga	gcacaactgt	ttgtattggt	ccgacctggc	cttggacgtc	atccagcgcc	2640
tctgtttgaa	tggaaagcaca	gggcaagagg	tgatcatcaa	ttctggcctg	gagacagtag	2700
aagctttggc	ttttgaaccc	ctcagccagc	tgctttactg	ggtagatgca	ggcttcaaaa	2760
agattgaggt	agctaatacca	gatggcgact	tccgactcac	aatcgtcaat	tcctctgtgc	2820
ttgatcgctc	cagggtctctg	gtcctcgtgc	cccaagaggg	ggtgatgttc	tggacagact	2880
ggggagacct	gaagcctggg	atttatcgga	gcaatatgga	tggttctgct	gcctatcacc	2940
tggtgtctga	ggaatgtgaag	tggtccaatg	gcatctctgt	ggacgaccag	tggatttact	3000
ggacggatgc	ctacctggag	tgcatagagc	ggatcacgtt	cagtggccag	cagcgctctg	3060
tcattctgga	caacctcccg	cacctctatg	ccattgctgt	ctttaagaat	gaaatctact	3120
gggatgactg	gtcacagctc	agcatattcc	gagcttccaa	atacagtggg	tcccagatgg	3180
agattctggc	aaaccagctc	acggggctca	tggacatgaa	gattttctac	aaggggaaga	3240
acactggaag	caatgcctgt	gtgccagggc	catgcagcct	gctgtgcctg	cccaaggcca	3300
acaacagtag	aagctgcagg	tgtccagagg	atgtgtccag	cagtgtgctt	ccatcagggg	3360
acctgatgtg	tgactgcccc	cagggtatc	agctcaagaa	caatacctgt	gtcaaagaag	3420
agaacacctg	tcttcgcaac	cagtatcgct	gcagcaacgg	gaactgtatc	aacagcattt	3480
ggtggtgtga	ctttgacaac	gactgtggag	acatgagcga	tgagagaaac	tgccctacca	3540
ccatctgtga	cctggacacc	cagtttcgtt	gccaggagtc	tgggacttgt	atccactgt	3600
cctataaatg	tgaccttgag	gatgactgtg	gagacaacag	tgatgaaagt	cattgtgaaa	3660
tgcaccagtg	ccggagtgc	gagtacaact	gcagttccgg	catgtgcac	cgctcctcct	3720
gggtatgtga	cggggacaac	gactgcaggg	actggtctga	tgaagccaac	tgtaccgcca	3780
tctatcacac	ctgtgaggcc	tccaacttcc	agtgccgaaa	cgggcactgc	atccccagc	3840
ggtgggctgt	tgacggggat	acggactgcc	aggatggttc	cgatgaggat	ccagtcaact	3900
gtgagaagaa	gtgcaatgga	ttccgctgcc	caaacggcac	ttgcatccca	tccagcaaac	3960
attgtgatgg	tctgctgatg	tgctctgatg	gctccgatga	acagcactgc	gagcccctct	4020
gtacgcactt	catggacttt	gtgtgtaaga	accgccagca	gtgcctgttc	cactccatgg	4080
tctgtgacgg	aatcatccag	tgccgcgacg	ggtccgatga	ggatgcggcg	tttgcaggat	4140
gctcccaaga	tcctgagttc	cacaaggtat	gtgatgagtt	cggtttccag	tgtcagaatg	4200
gagtgtgcat	cagtttgatt	tggaaagtgc	acgggatgga	tgattgcggc	gattattctg	4260
atgaagccaa	ctgcgaaaac	cccacagaag	ccccaaactg	ctcccgtac	ttccagtttc	4320
ggtgtgagaa	tggccactgc	atcccccaaca	gatggaaatg	tgacagggag	aacgactgtg	4380
gggactggtc	tgatgagaag	gattgtggag	attcacatat	tcttcccttc	tgcactcctg	4440
ggcctccac	gtgtctgcc	aattactacc	gctgcagcag	tgggacctgc	gtgatggaca	4500
cctgggtgtg	cgacgggtac	cgagattgtg	cagatggctc	tgacgaggaa	gcctgcccct	4560
tgcttgcaaa	cgtaactgct	gcctccactc	ccaccaactg	tgggcgatgt	gaccgatttg	4620
agttcgaatg	ccaccaaccg	aagacgtgta	ttcccaactg	gaagcgctgt	gacggccacc	4680
aagattgcca	ggatggccgg	gacgaggcca	attgccccac	acacagcacc	ttgacttgca	4740
tgagcaggga	gttccagtg	gaggacgggg	aggcctgcat	tgtgctctcg	gagcgctgcg	4800
acggcttcct	ggactgctcg	gacgagagcg	atgaaaaggc	ctgcagtgat	gagttgactg	4860
tgtacaaagt	acagaatctt	cagtggacag	ctgacttctc	tggggatgtg	actttgacct	4920
ggatgaggcc	caaaaaaatg	ccctctgctt	cttgtgtata	taatgtctac	tacagggtgg	4980
ttggagagag	catatggaag	actctggaga	cccacagcaa	taagacaaac	actgtattaa	5040
aagtcttgaa	accagatacc	acgtatcagg	ttaaagtaca	ggttcagtgt	ctcagcaagg	5100
cacacaacac	caatgacttt	gtgacctga	ggaccccaga	gggattgcca	gatgccctc	5160
gaaatctcca	gctgtcactc	cccagggaag	cagaaggtgt	gattgtaggc	cactgggctc	5220
ctcccatcca	cacccatggc	ctcatccgtg	agtacattgt	agaatacagc	aggagtgggt	5280
ccaagatgtg	ggcctcccag	agggctgcta	gtaactttac	agaaatcaag	aacttattgg	5340
tcaacactct	atacaccgtc	agagtggctg	cggtgactag	tcgtggaata	ggaaactgga	5400
gcgattctaa	atccattacc	accataaaag	gaaaagtgat	cccaccacca	gatatccaca	5460
ttgacagcta	tgggtgaaaat	tatctaagct	tcacctgac	catggagagt	gatatcaagg	5520
tgaatggcta	tgtgggtgaa	ctttctggg	catttgacac	ccacaagcaa	gagaggagaa	5580
ctttgaaact	ccgaggaagc	atattgtcac	acaaagtgg	caatctgaca	gctcatacat	5640
cctatgagat	ttctgcctgg	gccaaagactg	acttggggga	tagccctctg	gcatttgagc	5700
atgttatgac	cagaggggtt	cgcccacctg	cacctagcct	caaggccaaa	gccatcaacc	5760

304

```

agactgcagt ggaatgtacc tggaccggcc cccggaatgt gggttatggt attttctatg 5820
ccacgtcctt tcttgacctc tatcgcaacc cgaagagctt gactacttca ctccacaaca 5880
agacggtcat tgtcagtaag gatgagcagt atttgtttct ggtccgtgta gtggtaccct 5940
accaggggcc atcctctgac tacgttgtag tgaagatgat cccggacagc aggottccac 6000
cccgtcacct gcatgtggtt catacgggca aaacctccgt ggtcatcaag tgggaatcac 6060
cgtatgactc tcctgaccag gacttggtgt atgcaattgc agtcaaagat ctcataagaa 6120
agactgacag gagctacaaa gtaaaatccc gtaacagcac tgtggaatac acccttaaca 6180
agttggagcc tggcggaaaa taccacatca ttgtccaact ggggaacatg agcaaagatt 6240
ccagcataaa aattaccaca gtttcattat cagcacctga tgccttaaaa atcataacag 6300
aaaatgatca tggtcttctg ttttggaaaa gcctggcttt aaaggaaaag cattttaatg 6360
aaagcagggg ctatgagata cacatgtttg atagtgccat gaatatcaca gtttaccttg 6420
ggaatactac tgacaatttc tttaaaattt ccaacctgaa gatgggtcat aattacacgt 6480
tcaccgtcca agcaagatgc ctttttggca accagatctg tggggagcct gccatcctgc 6540
tgtacgatga gctggggtct ggtgcagatg catctgcaac gcaggctgcc agatctacgg 6600
atgttgctgc tgtggtggtg cccatcttat tcttgatact gctgagcctg ggggtggggg 6660
ttgccatcct gtacacgaag caccggaggc tgcagagcag cttcaccgcc ttcgccaaca 6720
gccactacag ctccaggctg gggtcgcaa tcttctcctc tggggatgac ctgggggaag 6780
atgatgaaga tgccccatg ataactggat ttccagatga cgtcccatg gtgatagcct 6840
gaaagagctt tctcactag aaaccaaag gtgtaaatat tttatttgat aaagatagtt 6900
gatgggttat tttaaaagat gcactttgag ttgcaatatg ttatttttat atgggcaaaa 6960
aacaacaaaa aaaaaaaaaa a 6981

```

&lt;210&gt; 300

&lt;211&gt; 2214

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 300

```

Met Ala Thr Arg Ser Ser Arg Arg Glu Ser Arg Leu Pro Phe Leu Phe
 1          5          10          15
Thr Leu Val Ala Leu Leu Pro Pro Gly Ala Leu Cys Glu Val Trp Thr
          20          25          30
Gln Arg Leu His Gly Gly Ser Ala Pro Leu Pro Gln Asp Arg Gly Phe
          35          40          45
Leu Val Val Gln Gly Asp Pro Arg Glu Leu Arg Leu Trp Ala Arg Gly
          50          55          60
Asp Ala Arg Gly Ala Ser Arg Ala Asp Glu Lys Pro Leu Arg Arg Lys
65          70          75          80
Arg Ser Ala Ala Leu Gln Pro Glu Pro Ile Lys Val Tyr Gly Gln Val
          85          90          95
Ser Leu Asn Asp Ser His Asn Gln Met Val Val His Trp Ala Gly Glu
          100          105          110
Lys Ser Asn Val Ile Val Ala Leu Ala Arg Asp Ser Leu Ala Leu Ala
          115          120          125
Arg Pro Lys Ser Ser Asp Val Tyr Val Ser Tyr Asp Tyr Gly Lys Ser
          130          135          140
Phe Lys Lys Ile Ser Asp Lys Leu Asn Phe Gly Leu Gly Asn Arg Ser
145          150          155          160
Glu Ala Val Ile Ala Gln Phe Tyr His Ser Pro Ala Asp Asn Lys Arg
          165          170          175
Tyr Ile Phe Ala Asp Ala Tyr Ala Gln Tyr Leu Trp Ile Thr Phe Asp
          180          185          190
Phe Cys Asn Thr Leu Gln Gly Phe Ser Ile Pro Phe Arg Ala Ala Asp
          195          200          205
Leu Leu Leu His Ser Lys Ala Ser Asn Leu Leu Leu Gly Phe Asp Arg
          210          215          220
Ser His Pro Asn Lys Gln Leu Trp Lys Ser Asp Asp Phe Gly Gln Thr
225          230          235          240

```

Trp Ile Met Ile Gln Glu His Val Lys Ser Phe Ser Trp Gly Ile Asp  
 245 250 255  
 Pro Tyr Asp Lys Pro Asn Thr Ile Tyr Ile Glu Arg His Glu Pro Ser  
 260 265 270  
 Gly Tyr Ser Thr Val Phe Arg Ser Thr Asp Phe Phe Gln Ser Arg Glu  
 275 280 285  
 Asn Gln Glu Val Ile Leu Glu Glu Val Arg Asp Phe Gln Leu Arg Asp  
 290 295 300  
 Lys Tyr Met Phe Ala Thr Lys Val Val His Leu Gly Ser Glu Gln  
 305 310 315 320  
 Gln Ser Ser Val Gln Leu Trp Val Ser Phe Gly Arg Lys Pro Met Arg  
 325 330 335  
 Ala Ala Gln Phe Val Thr Arg His Pro Ile Asn Glu Tyr Tyr Ile Ala  
 340 345 350  
 Asp Ala Ser Glu Asp Gln Val Phe Val Cys Val Ser His Ser Asn Asn  
 355 360 365  
 Arg Thr Asn Leu Tyr Ile Ser Glu Ala Glu Gly Leu Lys Phe Ser Leu  
 370 375 380  
 Ser Leu Glu Asn Val Leu Tyr Tyr Ser Pro Gly Gly Ala Gly Ser Asp  
 385 390 395 400  
 Thr Leu Val Arg Tyr Phe Ala Asn Glu Pro Phe Ala Asp Phe His Arg  
 405 410 415  
 Val Glu Gly Leu Gln Gly Val Tyr Ile Ala Thr Leu Ile Asn Gly Ser  
 420 425 430  
 Met Asn Glu Glu Asn Met Arg Ser Val Ile Thr Phe Asp Lys Gly Gly  
 435 440 445  
 Thr Trp Glu Phe Leu Gln Ala Pro Ala Phe Thr Gly Tyr Gly Glu Lys  
 450 455 460  
 Ile Asn Cys Glu Leu Ser Gln Gly Cys Ser Leu His Leu Ala Gln Arg  
 465 470 475 480  
 Leu Ser Gln Leu Leu Asn Leu Gln Leu Arg Arg Met Pro Ile Leu Ser  
 485 490 495  
 Lys Glu Ser Ala Pro Gly Leu Ile Ile Ala Thr Gly Ser Val Gly Lys  
 500 505 510  
 Asn Leu Ala Ser Lys Thr Asn Val Tyr Ile Ser Ser Ser Ala Gly Ala  
 515 520 525  
 Arg Trp Arg Glu Ala Leu Pro Gly Pro His Tyr Tyr Thr Trp Gly Asp  
 530 535 540  
 His Gly Gly Ile Ile Thr Ala Ile Ala Gln Gly Met Glu Thr Asn Glu  
 545 550 555 560  
 Leu Lys Tyr Ser Thr Asn Glu Gly Glu Thr Trp Lys Thr Phe Ile Phe  
 565 570 575  
 Ser Glu Lys Pro Val Phe Val Tyr Gly Leu Leu Thr Glu Pro Gly Glu  
 580 585 590  
 Lys Ser Thr Val Phe Thr Ile Phe Gly Ser Asn Lys Glu Asn Val His  
 595 600 605  
 Ser Trp Leu Ile Leu Gln Val Asn Ala Thr Asp Ala Leu Gly Val Pro  
 610 615 620  
 Cys Thr Glu Asn Asp Tyr Lys Leu Trp Ser Pro Ser Asp Glu Arg Gly  
 625 630 635 640  
 Asn Glu Cys Leu Leu Gly His Lys Thr Val Phe Lys Arg Arg Thr Pro  
 645 650 655  
 His Ala Thr Cys Phe Asn Gly Glu Asp Phe Asp Arg Pro Val Val Val  
 660 665 670  
 Ser Asn Cys Ser Cys Thr Arg Glu Asp Tyr Glu Cys Asp Phe Gly Phe  
 675 680 685  
 Lys Met Ser Glu Asp Leu Ser Leu Glu Val Cys Val Pro Asp Pro Glu  
 690 695 700

306

Phe Ser Gly Lys Ser Tyr Ser Pro Pro Val Pro Cys Pro Val Gly Ser  
 705 710 715 720  
 Thr Tyr Arg Arg Thr Arg Gly Tyr Arg Lys Ile Ser Gly Asp Thr Cys  
 725 730 735  
 Ser Gly Gly Asp Val Glu Ala Arg Leu Glu Gly Glu Leu Val Pro Cys  
 740 745 750  
 Pro Leu Ala Glu Glu Asn Glu Phe Ile Leu Tyr Ala Val Arg Lys Ser  
 755 760 765  
 Ile Tyr Arg Tyr Asp Leu Ala Ser Gly Ala Thr Glu Gln Leu Pro Leu  
 770 775 780  
 Thr Gly Leu Arg Ala Ala Val Ala Leu Asp Phe Asp Tyr Glu His Asn  
 785 790 795 800  
 Cys Leu Tyr Trp Ser Asp Leu Ala Leu Asp Val Ile Gln Arg Leu Cys  
 805 810 815  
 Leu Asn Gly Ser Thr Gly Gln Glu Val Ile Ile Asn Ser Gly Leu Glu  
 820 825 830  
 Thr Val Glu Ala Leu Ala Phe Glu Pro Leu Ser Gln Leu Leu Tyr Trp  
 835 840 845  
 Val Asp Ala Gly Phe Lys Lys Ile Glu Val Ala Asn Pro Asp Gly Asp  
 850 855 860  
 Phe Arg Leu Thr Ile Val Asn Ser Ser Val Leu Asp Arg Pro Arg Ala  
 865 870 875 880  
 Leu Val Leu Val Pro Gln Glu Gly Val Met Phe Trp Thr Asp Trp Gly  
 885 890 895  
 Asp Leu Lys Pro Gly Ile Tyr Arg Ser Asn Met Asp Gly Ser Ala Ala  
 900 905 910  
 Tyr His Leu Val Ser Glu Asp Val Lys Trp Pro Asn Gly Ile Ser Val  
 915 920 925  
 Asp Asp Gln Trp Ile Tyr Trp Thr Asp Ala Tyr Leu Glu Cys Ile Glu  
 930 935 940  
 Arg Ile Thr Phe Ser Gly Gln Gln Arg Ser Val Ile Leu Asp Asn Leu  
 945 950 955 960  
 Pro His Pro Tyr Ala Ile Ala Val Phe Lys Asn Glu Ile Tyr Trp Asp  
 965 970 975  
 Asp Trp Ser Gln Leu Ser Ile Phe Arg Ala Ser Lys Tyr Ser Gly Ser  
 980 985 990  
 Gln Met Glu Ile Leu Ala Asn Gln Leu Thr Gly Leu Met Asp Met Lys  
 995 1000 1005  
 Ile Phe Tyr Lys Gly Lys Asn Thr Gly Ser Asn Ala Cys Val Pro Arg  
 1010 1015 1020  
 Pro Cys Ser Leu Leu Cys Leu Pro Lys Ala Asn Asn Ser Arg Ser Cys  
 1025 1030 1035 1040  
 Arg Cys Pro Glu Asp Val Ser Ser Ser Val Leu Pro Ser Gly Asp Leu  
 1045 1050 1055  
 Met Cys Asp Cys Pro Gln Gly Tyr Gln Leu Lys Asn Asn Thr Cys Val  
 1060 1065 1070  
 Lys Glu Glu Asn Thr Cys Leu Arg Asn Gln Tyr Arg Cys Ser Asn Gly  
 1075 1080 1085  
 Asn Cys Ile Asn Ser Ile Trp Trp Cys Asp Phe Asp Asn Asp Cys Gly  
 1090 1095 1100  
 Asp Met Ser Asp Glu Arg Asn Cys Pro Thr Thr Ile Cys Asp Leu Asp  
 1105 1110 1115 1120  
 Thr Gln Phe Arg Cys Gln Glu Ser Gly Thr Cys Ile Pro Leu Ser Tyr  
 1125 1130 1135  
 Lys Cys Asp Leu Glu Asp Asp Cys Gly Asp Asn Ser Asp Glu Ser His  
 1140 1145 1150  
 Cys Glu Met His Gln Cys Arg Ser Asp Glu Tyr Asn Cys Ser Ser Gly  
 1155 1160 1165

Met Cys Ile Arg Ser Ser Trp Val Cys Asp Gly Asp Asn Asp Cys Arg  
 1170 1175 1180  
 Asp Trp Ser Asp Glu Ala Asn Cys Thr Ala Ile Tyr His Thr Cys Glu  
 1185 1190 1195 1200  
 Ala Ser Asn Phe Gln Cys Arg Asn Gly His Cys Ile Pro Gln Arg Trp  
 1205 1210 1215  
 Ala Cys Asp Gly Asp Thr Asp Cys Gln Asp Gly Ser Asp Glu Asp Pro  
 1220 1225 1230  
 Val Asn Cys Glu Lys Lys Cys Asn Gly Phe Arg Cys Pro Asn Gly Thr  
 1235 1240 1245  
 Cys Ile Pro Ser Ser Lys His Cys Asp Gly Leu Arg Asp Cys Ser Asp  
 1250 1255 1260  
 Gly Ser Asp Glu Gln His Cys Glu Pro Leu Cys Thr His Phe Met Asp  
 1265 1270 1275 1280  
 Phe Val Cys Lys Asn Arg Gln Gln Cys Leu Phe His Ser Met Val Cys  
 1285 1290 1295  
 Asp Gly Ile Ile Gln Cys Arg Asp Gly Ser Asp Glu Asp Ala Ala Phe  
 1300 1305 1310  
 Ala Gly Cys Ser Gln Asp Pro Glu Phe His Lys Val Cys Asp Glu Phe  
 1315 1320 1325  
 Gly Phe Gln Cys Gln Asn Gly Val Cys Ile Ser Leu Ile Trp Lys Cys  
 1330 1335 1340  
 Asp Gly Met Asp Asp Cys Gly Asp Tyr Ser Asp Glu Ala Asn Cys Glu  
 1345 1350 1355 1360  
 Asn Pro Thr Glu Ala Pro Asn Cys Ser Arg Tyr Phe Gln Phe Arg Cys  
 1365 1370 1375  
 Glu Asn Gly His Cys Ile Pro Asn Arg Trp Lys Cys Asp Arg Glu Asn  
 1380 1385 1390  
 Asp Cys Gly Asp Trp Ser Asp Glu Lys Asp Cys Gly Asp Ser His Ile  
 1395 1400 1405  
 Leu Pro Phe Ser Thr Pro Gly Pro Ser Thr Cys Leu Pro Asn Tyr Tyr  
 1410 1415 1420  
 Arg Cys Ser Ser Gly Thr Cys Val Met Asp Thr Trp Val Cys Asp Gly  
 1425 1430 1435 1440  
 Tyr Arg Asp Cys Ala Asp Gly Ser Asp Glu Glu Ala Cys Pro Leu Leu  
 1445 1450 1455  
 Ala Asn Val Thr Ala Ala Ser Thr Pro Thr Gln Leu Gly Arg Cys Asp  
 1460 1465 1470  
 Arg Phe Glu Phe Glu Cys His Gln Pro Lys Thr Cys Ile Pro Asn Trp  
 1475 1480 1485  
 Lys Arg Cys Asp Gly His Gln Asp Cys Gln Asp Gly Arg Asp Glu Ala  
 1490 1495 1500  
 Asn Cys Pro Thr His Ser Thr Leu Thr Cys Met Ser Arg Glu Phe Gln  
 1505 1510 1515 1520  
 Cys Glu Asp Gly Glu Ala Cys Ile Val Leu Ser Glu Arg Cys Asp Gly  
 1525 1530 1535  
 Phe Leu Asp Cys Ser Asp Glu Ser Asp Glu Lys Ala Cys Ser Asp Glu  
 1540 1545 1550  
 Leu Thr Val Tyr Lys Val Gln Asn Leu Gln Trp Thr Ala Asp Phe Ser  
 1555 1560 1565  
 Gly Asp Val Thr Leu Thr Trp Met Arg Pro Lys Lys Met Pro Ser Ala  
 1570 1575 1580  
 Ser Cys Val Tyr Asn Val Tyr Tyr Arg Val Val Gly Glu Ser Ile Trp  
 1585 1590 1595 1600  
 Lys Thr Leu Glu Thr His Ser Asn Lys Thr Asn Thr Val Leu Lys Val  
 1605 1610 1615  
 Leu Lys Pro Asp Thr Thr Tyr Gln Val Lys Val Gln Val Gln Cys Leu  
 1620 1625 1630

Ser Lys Ala His Asn Thr Asn Asp Phe Val Thr Leu Arg Thr Pro Glu  
 1635 1640 1645  
 Gly Leu Pro Asp Ala Pro Arg Asn Leu Gln Leu Ser Leu Pro Arg Glu  
 1650 1655 1660  
 Ala Glu Gly Val Ile Val Gly His Trp Ala Pro Pro Ile His Thr His  
 1665 1670 1675 1680  
 Gly Leu Ile Arg Glu Tyr Ile Val Glu Tyr Ser Arg Ser Gly Ser Lys  
 1685 1690 1695  
 Met Trp Ala Ser Gln Arg Ala Ala Ser Asn Phe Thr Glu Ile Lys Asn  
 1700 1705 1710  
 Leu Leu Val Asn Thr Leu Tyr Thr Val Arg Val Ala Ala Val Thr Ser  
 1715 1720 1725  
 Arg Gly Ile Gly Asn Trp Ser Asp Ser Lys Ser Ile Thr Thr Ile Lys  
 1730 1735 1740  
 Gly Lys Val Ile Pro Pro Pro Asp Ile His Ile Asp Ser Tyr Gly Glu  
 1745 1750 1755 1760  
 Asn Tyr Leu Ser Phe Thr Leu Thr Met Glu Ser Asp Ile Lys Val Asn  
 1765 1770 1775  
 Gly Tyr Val Val Asn Leu Phe Trp Ala Phe Asp Thr His Lys Gln Glu  
 1780 1785 1790  
 Arg Arg Thr Leu Asn Phe Arg Gly Ser Ile Leu Ser His Lys Val Gly  
 1795 1800 1805  
 Asn Leu Thr Ala His Thr Ser Tyr Glu Ile Ser Ala Trp Ala Lys Thr  
 1810 1815 1820  
 Asp Leu Gly Asp Ser Pro Leu Ala Phe Glu His Val Met Thr Arg Gly  
 1825 1830 1835 1840  
 Val Arg Pro Pro Ala Pro Ser Leu Lys Ala Lys Ala Ile Asn Gln Thr  
 1845 1850 1855  
 Ala Val Glu Cys Thr Trp Thr Gly Pro Arg Asn Val Val Tyr Gly Ile  
 1860 1865 1870  
 Phe Tyr Ala Thr Ser Phe Leu Asp Leu Tyr Arg Asn Pro Lys Ser Leu  
 1875 1880 1885  
 Thr Thr Ser Leu His Asn Lys Thr Val Ile Val Ser Lys Asp Glu Gln  
 1890 1895 1900  
 Tyr Leu Phe Leu Val Arg Val Val Val Pro Tyr Gln Gly Pro Ser Ser  
 1905 1910 1915 1920  
 Asp Tyr Val Val Val Lys Met Ile Pro Asp Ser Arg Leu Pro Pro Arg  
 1925 1930 1935  
 His Leu His Val Val His Thr Gly Lys Thr Ser Val Val Ile Lys Trp  
 1940 1945 1950  
 Glu Ser Pro Tyr Asp Ser Pro Asp Gln Asp Leu Leu Tyr Ala Ile Ala  
 1955 1960 1965  
 Val Lys Asp Leu Ile Arg Lys Thr Asp Arg Ser Tyr Lys Val Lys Ser  
 1970 1975 1980  
 Arg Asn Ser Thr Val Glu Tyr Thr Leu Asn Lys Leu Glu Pro Gly Gly  
 1985 1990 1995 2000  
 Lys Tyr His Ile Ile Val Gln Leu Gly Asn Met Ser Lys Asp Ser Ser  
 2005 2010 2015  
 Ile Lys Ile Thr Thr Val Ser Leu Ser Ala Pro Asp Ala Leu Lys Ile  
 2020 2025 2030  
 Ile Thr Glu Asn Asp His Val Leu Leu Phe Trp Lys Ser Leu Ala Leu  
 2035 2040 2045  
 Lys Glu Lys His Phe Asn Glu Ser Arg Gly Tyr Glu Ile His Met Phe  
 2050 2055 2060  
 Asp Ser Ala Met Asn Ile Thr Ala Tyr Leu Gly Asn Thr Thr Asp Asn  
 2065 2070 2075 2080  
 Phe Phe Lys Ile Ser Asn Leu Lys Met Gly His Asn Tyr Thr Phe Thr  
 2085 2090 2095

309

Val Gln Ala Arg Cys Leu Phe Gly Asn Gln Ile Cys Gly Glu Pro Ala  
 2100 2105 2110  
 Ile Leu Leu Tyr Asp Glu Leu Gly Ser Gly Ala Asp Ala Ser Ala Thr  
 2115 2120 2125  
 Gln Ala Ala Arg Ser Thr Asp Val Ala Ala Val Val Val Pro Ile Leu  
 2130 2135 2140  
 Phe Leu Ile Leu Leu Ser Leu Gly Val Gly Phe Ala Ile Leu Tyr Thr  
 2145 2150 2155 2160  
 Lys His Arg Arg Leu Gln Ser Ser Phe Thr Ala Phe Ala Asn Ser His  
 2165 2170 2175  
 Tyr Ser Ser Arg Leu Gly Ser Ala Ile Phe Ser Ser Gly Asp Asp Leu  
 2180 2185 2190  
 Gly Glu Asp Asp Glu Asp Ala Pro Met Ile Thr Gly Phe Ser Asp Asp  
 2195 2200 2205  
 Val Pro Met Val Ile Ala  
 2210

<210> 301  
 <211> 1544  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(1544)  
 <223> n = A,T,C or G

<400> 301  
 gcacgagttg ggaggtgtag cgcggtctctg aacgcgctga gggccgttga gtgtcgcagg 60  
 cggcgagggc gcgagttagg agcagaccca ggcacgcgc gccgagaagg ccggggtcc 120  
 ccacactgaa ggtccgga aa ggcgacttcc gggggctttg gcacctggcg gacctccc 180  
 gagcgtcggc acctgaacgc gaggcgtcc attgcgctg cgcgttgagg ggcttcccgc 240  
 acctgatcgc gagaccccaa cggctggttg cgtcgcctgc gcgtctcggc tgagctggcc 300  
 atggcgcagc tgtgcgggct gaggcggagc cgggcgtttc tcgccctgct gggatcgctg 360  
 ctctctctg gggctcctggc ggccgaccga gaacgcagca tccacgactt ctgcctgggtg 420  
 tcgaagggtg tgggcagatg ccgggcctcc atgcctaggt ggtggtacaa tgtcactgac 480  
 ggatcctgcc agctgtttgt gtatgggggc tgtgacgaa acagcaataa ttacctgacc 540  
 aaggaggagt gcctcaagaa atgtgccact gtcacagaga atgccacggg tgacctggcc 600  
 accagcagga atgcagcgga ttctctgtc ccaagtgtc ccagaaggca ggattctgaa 660  
 gaccactcca gcgatatgtt caactatgaa gaatactgca ccgccaacgc agtcactggg 720  
 ccttgccgtg catccttccc acgtgggtac tttgacgtg agaggaactc ctgcaataac 780  
 ttcatctatg gaggtgccc gggcaataag aacagctacc gctctgagga ggcctgcatg 840  
 ctccgctgct tccgccagca ggagaatcct cccctgcccc ttggtcaaa ggtggtggtt 900  
 ctggcgggc tgttcgtgat ggtgtgatc ctcttcttg gagcctccat ggtctacctg 960  
 atccgggtg caccgaggaa ccaggagcgt gccctgcgca ccgtctggag ctccggagat 1020  
 gacaaggagc agctggtgaa gaacacatat gtctgtgac cgccctgtcg ccaaggaggac 1080  
 tggggaagg aggggagact atgtgtgagc tttttttaa tagagggatt gactcggatt 1140  
 tgagtgatca ttagggctga ggtctgtttc tctgggaggt aggacggctg cttcctggtc 1200  
 tggcagggat gggtttgctt tggaaatcct ctaggaggct cctctctgca tggctgcag 1260  
 tctggcagca gcccogagtt gtttctcgc tgatcgattt ctttctcca ggtagagttt 1320  
 tctttgctta tgttgaaatc cattgcctcc ttttctcnat cacagaagtg atgttggaat 1380  
 cgtttctttt gtttgtctga tttatggttt ttttaagtat aaacaaaagt tttttattag 1440  
 cattctgaaa gaaggaaagt aaaatgtaca agtttaataa aaagggcct tcccctttag 1500  
 aataaatttc cagcatgttg ctttcaaaaa aaaaaaaaaa aaaa 1544

<210> 302  
 <211> 252

310

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 302

```

Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu Ala Leu
 1           5           10           15
Leu Gly Ser Leu Leu Leu Ser Gly Val Leu Ala Ala Asp Arg Glu Arg
      20           25           30
Ser Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg
      35           40           45
Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln
 50           55           60
Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr
65           70           75           80
Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr
      85           90           95
Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser
      100           105           110
Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn
      115           120           125
Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala
      130           135           140
Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn
145           150           155           160
Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu
      165           170           175
Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro Pro Leu
      180           185           190
Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly Leu Phe Val Met Val
      195           200           205
Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala
      210           215           220
Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val Trp Ser Ser Gly Asp
225           230           235           240
Asp Lys Glu Gln Leu Val Lys Asn Thr Tyr Val Leu
      245           250

```

&lt;210&gt; 303

&lt;211&gt; 1558

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1558)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 303

```

agggagtcga cccacgcgtc cgggcgacct ccgcgcgttg ggagggtgtag gcgcggctct 60
gaacgcgctg agggccgttg agtgtcgag gcggcgaggg cgcgagtgag gagcagaccc 120
aggcatcgcg cgccgagaag gccgggcgtc cccacactga aggtccggaa aggcgacttc 180
cgggggcttt ggacacctggc ggacctctcc ggagcgctcg cacctgaacg cgaggcgctc 240
cattgcgcgt gcgcgttgag gggcttcccg cacctgateg cgagacccca acggtggtg 300
gcgtgcctg cgcgtctcgg ctgagctggc catggcgag ctgtgcgggc tgaggcggag 360
ccgggcgttt ctgcacctgc tgggatcgct gctcctctct ggggtcctgg cggccgaccg 420
agaacgcagc atccacgaga atgccacggg tgacctggcc accagcagga atgcagcgga 480
ttcctctgtc ccaagtgtc ccagaaggca ggattctgaa gacctactca gcgatatgtt 540

```



311

```

caactatgaa gaatactgca ccgccaacgc agtcactggg ccttgccgtg catccttccc 600
acgctggtagc tttagcgtgg agaggaaactc ctgcaataac ttcatctatg gaggctgccg 660
gggcaataag aacagctacc gctctgagga ggcttgcacg ctccgctgct tccgccagca 720
ggagaatcct cccctgcccc ttggctcaaa ggtggtggtt ctggcggggc tgttcgtgat 780
ggtgttgatc ctcttcctgg gagcctccat ggtctacctg atccgggtgg cacggaggaa 840
ccaggagcgt gccctgcgca ccgtctggag ctccggagat gacaaggagc agctggtgaa 900
gaacacatat gtcctgtgac cgccctgtcg ccaagaggac tggggaaggg aggggagact 960
atgtgtgagc tttttttaaa tagagggatt gactcggatt tgagtgatca ttagggctga 1020
ggtctgtttc tctgggagggt aggacggctg ctctcctggtc tggcagggat gggtttgctt 1080
tggaatcct ctaggagggt cctcctcgca tggcctgcag tctggcagca gccccgagtt 1140
gtttcctcgc tgatcgattt ctttcctcca ggtagagttt tctttgctta tgttgaattc 1200
cattgcctct tttctcatca cagaagtgat gttggaatcg tttcttttgt ttgtctgatt 1260
tatggttttt ttaagtataa acaaaagtgt tttattagca ttctgaaaga aggaaagtaa 1320
aatgtacctn cgcccgnnnc gancrcctcg amcbttccch htaraawaaa wwwmarmawr 1380
tgctttcttt atgggagtc taatttcaac cctaccaaaa tgatcacaag acactatctg 1440
aggtgtccca ttctagaaat agaccctca aaatagcgtc tttcagatct ttttgaatga 1500
atccacaaga tgaataaat gtcctattac tgaaaaaaaa aaaaaaaagg gcggccgc 1558

```

&lt;210&gt; 304

&lt;211&gt; 195

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(195)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 304

```

Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu Ala Leu
1          5          10          15
Leu Gly Ser Leu Leu Leu Ser Gly Val Leu Ala Ala Asp Arg Glu Arg
20          25          30
Ser Ile His Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala
35          40          45
Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp
50          55          60
His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala
65          70          75          80
Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val
85          90          95
Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn
100         105         110
Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg
115         120         125
Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Xaa Leu
130         135         140
Ala Gly Leu Phe Val Met Val Leu Ile Leu Phe Leu Gly Ala Ser Met
145         150         155         160
Val Tyr Leu Ile Arg Val Ala Arg Arg Asn Gln Glu Arg Ala Leu Arg
165         170         175
Thr Val Trp Ser Ser Gly Asp Asp Lys Glu Gln Leu Val Lys Asn Thr
180         185         190
Tyr Val Leu
195

```

&lt;210&gt; 305

&lt;211&gt; 3079

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 305

```

ggcacaaagt tggggggccgc gaagatgagg ctgtccccgg cggccctgaa gctgagccgg 60
actccggcac tgctggccct ggcgctgccc ctggccgchg cgctggcctt ctccgacgag 120
accctggaca aagtgcccaa gtcagagggc tactgtagcc gtatcctgcg cgcccagggc 180
acggggcgcg agggctacac cgagttcagc ctccgchggt agggcgaccc cgactttctac 240
aagccgggaa ccagctaccg cgtaacactt tcagctgctc ctccctccta cttcagagga 300
ttcacattaa ttgccctcag agagaacaga gagggtgata aggaagaaga ccatgctggg 360
accttcaga tcatagacga agaagaaact cagtttatga gcaattgccc tgttgagtc 420
actgaaagca ctccacggag gaggacccgg atccagggtt tttggatagc accaccagcg 480
ggaacaggct gcgtgattct gaaggccagc atcgtacaaa aacgcattat ttattttcaa 540
gatgagggct ctctgacca gaaactttgt gaacaagatt ccacatttga tggggtgact 600
gacaaaccca tcttagactg ctgtgcctgc ggaactgcca agtacagact cacattttat 660
gggaatttgt ccgagaagac acacccaaag gattaccctc gtcgggcca cactggtct 720
gcgatcatcg gaggatccca ctccaagaat tatgtactgt gggaatatgg aggatatgcc 780
agcgaaggcg tcaaacaagt tgcagaattg ggctcaccgg tgaaaatgga ggaagaaatt 840
cgacaacaga gtgatgagg cctcaccgtc atcaaagcca aagcccaatg gccagcctgg 900
cagcctctca acgtgagagc agcaccttca gctgaatttt ccgtggacag aacgcgccat 960
ttaatgtcct tcctgaccat gatgggccct agtcccgact ggaacgtagg cttatctgca 1020
gaagatctgt gcaccaagga atgtggctgg gtccagaagg tggtgcaaga cctgattccc 1080
tgggacgctg gcaccgacag cggggtgacc tatgagtcac ccaacaaacc caccattccc 1140
caggagaaaa tccggcccct gaccagcctg gaccatcctc agagtccttt ctatgacca 1200
gaggggtggg ccatcactca agtagccaga gttgtcatcg agagaatcgc acggaagggg 1260
gaacaatgca atattgtacc tgacaatgtc gatgatattg tagctgacct ggctccagaa 1320
gagaaagatg aagatgacac ccctgaaacc tgcatctact ccaactggtc ccatgggtcc 1380
gcctgcagct cctccacctg tgacaagagc aagaggatgc gacagcgc atgctgaaaga 1440
cagctggacc tcagcgtccc ctgccctgac acccaggact tccagccctg catgggccct 1500
ggctgcagtg acgaagacgg ctccacctgc accatgtccg agtggatcac ctggtcgccc 1560
tgcaqcatct cctgcggcat gggcatgagg tcccgggaga ggtatgtgaa gcagttcccg 1620
gaggacggct ccgtgtgcac gctgccact gaggaatgg agaagtgcac ggtcaacgag 1680
gagtgtcttc ccagcagctg cctgatgacc gagtgggchg agtgggacga gtgcagcgcc 1740
acctgchgca tgggcatgaa gaagcggcac cgcgatgatc agatgaacct cgcagatggc 1800
tccatgtgca aagccgagac atcacaggca gagaagtgca tgatgccaga gtgccacacc 1860
atcccatgct tgctgtcccc atggtccgag tggagtgcac gcagcgtgac ctgcgggaag 1920
ggcatgcgaa cccgacagcg gatgtcgaag tctctggcag aacttgga ga ctgcaatgag 1980
gatctggagc aggtggagaa gtgcatgtc cctgaatgcc ccattgactg tgagctcacc 2040
gagtgggtccc agtgggtcga atgtaacaag tcatgtggga aaggccacgt gattcgaacc 2100
cggatgatcc aaatggagcc tcagtttgga ggtgcaccct gccagagac tgtgcagcga 2160
aaaaagtgcc gcatccgaaa atgccttcga aatccatcca tccaaaagcc acgctggagg 2220
gaggcccgag agagccggcg gagtgaagcag ctgaaggaag agtctgaagg ggagcagttc 2280
ccaggttgta ggatgcgccc atggacggcc tggtcagaat gcaccaaact gtgcggagg 2340
ggaattcagg aacgttacat gactgtaaag aagagattca aaagctccca gtttaccagc 2400
tgcaaagaca agaaggagat cagagcatgc aatgttcac cttgttagca aggtacgag 2460
ttccccaggg ctgcactcta gattccagag taccaatgg ctggattatt tgcttgttta 2520
agacaattta aattgtgtac gctagttttc atttttgcag tgtggttcgc ccagtagtct 2580
tgtggatgcc agagacatcc tttctgaata cttcttgatg ggtacaggct gagggggchg 2640
ccctcacctc cagccagcct cttcctgcag aggagtagtg tcagccacct tgtactaagc 2700
tgaaacatgt ccctctggag cttccacctg gccagggagg acggagactt tgacctactc 2760
cacatggaga ggcaaccatg tctggaagtg actatgcctg agtcccaggg tgcggcagg 2820
aggaaacatt cacagatgaa gacagcagat tccccacatt ctcatctttg gcctgttcaa 2880
tgaaacatt gtttgcccat ctcttcttag tggaacttta ggtctctttt caagtctcct 2940
cagtcattca tagttcctgg ggaaaaacag agctggtaga cttgaagagg agcattgatg 3000
ttgggtggct tttgttcttt cactgagaaa ttcggaatac atttgtctca cccctgatat 3060
tggttctctga tgccccagc

```

313

<210> 306  
 <211> 807  
 <212> PRT  
 <213> Homo sapiens

<400> 306

Met	Arg	Leu	Ser	Pro	Ala	Pro	Leu	Lys	Leu	Ser	Arg	Thr	Pro	Ala	Leu
1				5					10					15	
Leu	Ala	Leu	Ala	Leu	Pro	Leu	Ala	Ala	Leu	Ala	Phe	Ser	Asp	Glu	
			20					25				30			
Thr	Leu	Asp	Lys	Val	Pro	Lys	Ser	Glu	Gly	Tyr	Cys	Ser	Arg	Ile	Leu
		35					40					45			
Arg	Ala	Gln	Gly	Thr	Arg	Arg	Glu	Gly	Tyr	Thr	Glu	Phe	Ser	Leu	Arg
	50					55					60				
Val	Glu	Gly	Asp	Pro	Asp	Phe	Tyr	Lys	Pro	Gly	Thr	Ser	Tyr	Arg	Val
65					70					75				80	
Thr	Leu	Ser	Ala	Ala	Pro	Pro	Ser	Tyr	Phe	Arg	Gly	Phe	Thr	Leu	Ile
				85					90					95	
Ala	Leu	Arg	Glu	Asn	Arg	Glu	Gly	Asp	Lys	Glu	Glu	Asp	His	Ala	Gly
			100					105					110		
Thr	Phe	Gln	Ile	Ile	Asp	Glu	Glu	Glu	Thr	Gln	Phe	Met	Ser	Asn	Cys
		115					120					125			
Pro	Val	Ala	Val	Thr	Glu	Ser	Thr	Pro	Arg	Arg	Arg	Thr	Arg	Ile	Gln
	130					135					140				
Val	Phe	Trp	Ile	Ala	Pro	Pro	Ala	Gly	Thr	Gly	Cys	Val	Ile	Leu	Lys
145					150					155				160	
Ala	Ser	Ile	Val	Gln	Lys	Arg	Ile	Ile	Tyr	Phe	Gln	Asp	Glu	Gly	Ser
				165					170					175	
Leu	Thr	Lys	Lys	Leu	Cys	Glu	Gln	Asp	Ser	Thr	Phe	Asp	Gly	Val	Thr
			180					185					190		
Asp	Lys	Pro	Ile	Leu	Asp	Cys	Cys	Ala	Cys	Gly	Thr	Ala	Lys	Tyr	Arg
	195					200						205			
Leu	Thr	Phe	Tyr	Gly	Asn	Trp	Ser	Glu	Lys	Thr	His	Pro	Lys	Asp	Tyr
	210				215						220				
Pro	Arg	Arg	Ala	Asn	His	Trp	Ser	Ala	Ile	Ile	Gly	Gly	Ser	His	Ser
225					230						235				240
Lys	Asn	Tyr	Val	Leu	Trp	Glu	Tyr	Gly	Gly	Tyr	Ala	Ser	Glu	Gly	Val
			245						250					255	
Lys	Gln	Val	Ala	Glu	Leu	Gly	Ser	Pro	Val	Lys	Met	Glu	Glu	Glu	Ile
			260					265					270		
Arg	Gln	Gln	Ser	Asp	Glu	Val	Leu	Thr	Val	Ile	Lys	Ala	Lys	Ala	Gln
	275						280					285			
Trp	Pro	Ala	Trp	Gln	Pro	Leu	Asn	Val	Arg	Ala	Ala	Pro	Ser	Ala	Glu
	290					295					300				
Phe	Ser	Val	Asp	Arg	Thr	Arg	His	Leu	Met	Ser	Phe	Leu	Thr	Met	Met
305					310					315					320
Gly	Pro	Ser	Pro	Asp	Trp	Asn	Val	Gly	Leu	Ser	Ala	Glu	Asp	Leu	Cys
			325						330					335	
Thr	Lys	Glu	Cys	Gly	Trp	Val	Gln	Lys	Val	Val	Gln	Asp	Leu	Ile	Pro
		340						345					350		
Trp	Asp	Ala	Gly	Thr	Asp	Ser	Gly	Val	Thr	Tyr	Glu	Ser	Pro	Asn	Lys
	355						360					365			
Pro	Thr	Ile	Pro	Gln	Glu	Lys	Ile	Arg	Pro	Leu	Thr	Ser	Leu	Asp	His
	370					375					380				
Pro	Gln	Ser	Pro	Phe	Tyr	Asp	Pro	Glu	Gly	Gly	Ser	Ile	Thr	Gln	Val
385					390					395					400
Ala	Arg	Val	Val	Ile	Glu	Arg	Ile	Ala	Arg	Lys	Gly	Glu	Gln	Cys	Asn
				405					410					415	

314

Ile Val Pro Asp Asn Val Asp Asp Ile Val Ala Asp Leu Ala Pro Glu  
 420 425 430  
 Glu Lys Asp Glu Asp Asp Thr Pro Glu Thr Cys Ile Tyr Ser Asn Trp  
 435 440 445  
 Ser Pro Trp Ser Ala Cys Ser Ser Ser Thr Cys Asp Lys Gly Lys Arg  
 450 455 460  
 Met Arg Gln Arg Met Leu Lys Ala Gln Leu Asp Leu Ser Val Pro Cys  
 465 470 475 480  
 Pro Asp Thr Gln Asp Phe Gln Pro Cys Met Gly Pro Gly Cys Ser Asp  
 485 490 495  
 Glu Asp Gly Ser Thr Cys Thr Met Ser Glu Trp Ile Thr Trp Ser Pro  
 500 505 510  
 Cys Ser Ile Ser Cys Gly Met Gly Met Arg Ser Arg Glu Arg Tyr Val  
 515 520 525  
 Lys Gln Phe Pro Glu Asp Gly Ser Val Cys Thr Leu Pro Thr Glu Glu  
 530 535 540  
 Met Glu Lys Cys Thr Val Asn Glu Glu Cys Ser Pro Ser Ser Cys Leu  
 545 550 555 560  
 Met Thr Glu Trp Gly Glu Trp Asp Glu Cys Ser Ala Thr Cys Gly Met  
 565 570 575  
 Gly Met Lys Lys Arg His Arg Met Ile Lys Met Asn Pro Ala Asp Gly  
 580 585 590  
 Ser Met Cys Lys Ala Glu Thr Ser Gln Ala Glu Lys Cys Met Met Pro  
 595 600 605  
 Glu Cys His Thr Ile Pro Cys Leu Leu Ser Pro Trp Ser Glu Trp Ser  
 610 615 620  
 Asp Cys Ser Val Thr Cys Gly Lys Gly Met Arg Thr Arg Gln Arg Met  
 625 630 635 640  
 Leu Lys Ser Leu Ala Glu Leu Gly Asp Cys Asn Glu Asp Leu Glu Gln  
 645 650 655  
 Val Glu Lys Cys Met Leu Pro Glu Cys Pro Ile Asp Cys Glu Leu Thr  
 660 665 670  
 Glu Trp Ser Gln Trp Ser Glu Cys Asn Lys Ser Cys Gly Lys Gly His  
 675 680 685  
 Val Ile Arg Thr Arg Met Ile Gln Met Glu Pro Gln Phe Gly Gly Ala  
 690 695 700  
 Pro Cys Pro Glu Thr Val Gln Arg Lys Lys Cys Arg Ile Arg Lys Cys  
 705 710 715 720  
 Leu Arg Asn Pro Ser Ile Gln Lys Pro Arg Trp Arg Glu Ala Arg Glu  
 725 730 735  
 Ser Arg Arg Ser Glu Gln Leu Lys Glu Glu Ser Glu Gly Glu Gln Phe  
 740 745 750  
 Pro Gly Cys Arg Met Arg Pro Trp Thr Ala Trp Ser Glu Cys Thr Lys  
 755 760 765  
 Leu Cys Gly Gly Gly Ile Gln Glu Arg Tyr Met Thr Val Lys Lys Arg  
 770 775 780  
 Phe Lys Ser Ser Gln Phe Thr Ser Cys Lys Asp Lys Lys Glu Ile Arg  
 785 790 795 800  
 Ala Cys Asn Val His Pro Cys  
 805

&lt;210&gt; 307

&lt;211&gt; 5108

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 307

gcgagtcgat	acagtaagta	agccgcgaag	catattgcta	ggcacagagc	aggtgtgcaa	60
caaaagttat	ttctcaggct	ttccctcctc	tgagcgccgt	cctccagagg	gtccggagtg	120
tagctggggg	ttggagcagc	agcctcctag	gcgatgggac	agagcccaca	gggtccggta	180
tgccacggtt	ttctcgtcag	accctgggaa	tccaacgtcg	caaaataaac	acggccgcgc	240
cgctaatacg	cagttcggag	gaaacaaaac	agcgtcgcgc	tgggggatct	gggcaaaatc	300
agccctccct	cctcccgcct	cttcgcgcgc	gccctccctc	cctcgcgcgt	ctctcgttcg	360
cttggtcag	ctcagctcag	ctcagcgcag	ctccgcggcc	gccaagccga	ggcgggcacg	420
gtctccgagt	cgcgagcgcc	agctccgagc	tccctctctc	cgccgcgcct	ccgccaggtc	480
gcgccttcgt	cgggaccact	tcgggcagga	gtcgcgtggc	gaaggcctgc	ggccgcggca	540
caaagtggg	ggccgcgaag	atgaggctgt	ccccggcgcc	cctgaagctg	agccggactc	600
cggcaactgct	ggccctggcg	ctgcccctgg	cgcggcgct	ggccttctcc	gacgagaccc	660
tggacaaaagt	gccaagtca	gagggctact	cgagccgtat	cctgcgcgcc	cagggcacgc	720
ggcgcgaggg	ctacaccgag	ttcagcctcc	gcgtggaggg	cgaccccgac	ttctacaagc	780
cgggaaccag	ctaccgcgta	acactttcag	ctgctcctcc	ctcctacttc	agaggattca	840
cattaattgc	cctcagagag	aacagagagg	gtgataagga	agaagaccat	gctgggacct	900
tcagatcat	agacgaagaa	gaaactcagt	ttatgagcaa	ttgccctgtt	gcagtcactg	960
aaagcactcc	acggaggagg	acccggatcc	aggtgttttg	gatagcacca	ccagcgggaa	1020
caggctgctg	gattctgaag	gccagcatcg	tacaaaaacg	cattatttat	tttcaagatg	1080
agggctctct	gaccaagaaa	ctttgtgaac	aagattccac	atttgatggg	gtgactgaca	1140
aacctactct	agactcgtgt	gcctgcggaa	ctgccaaagta	cagactcaca	ttttatggga	1200
attgggtccga	gaagacacac	ccaaaggatt	accctcgtcg	ggccaaccac	tgggtctgca	1260
tcacgcgagg	atcccactcc	aagaattatg	tactgtggga	atatggagga	tatgccagcg	1320
aaggcgtcaa	acaagttgca	gaattgggct	caccctgtaa	aatggaggaa	gaaattcgac	1380
aacagagtga	tgaggtcctc	acogtcatca	aagccaaagc	ccaatggcca	gcctggcagc	1440
ctctcaacgt	gagagcagca	ccttcagctg	aattttccgt	ggacagaacg	cgccatttaa	1500
tgtccttcct	gaccatgatg	ggccctagtc	ccgactggaa	cgtaggctta	tctgcagaag	1560
atctgtgcac	caaggaatgt	ggctgggtcc	agaaggtggt	gcaagacctg	attccctggg	1620
acgtcggcac	cgacagcggg	ytgacctatg	agtcacccaa	caaaccacc	attccccagg	1680
agaaaatccg	ggccctgacc	agcctggacc	atcctcagag	tcctttctat	gaccagagg	1740
gtgggtccat	cactcaagta	gccagagttg	tcacgcagag	aatcgcacyg	aagggtgaac	1800
aatgcaatat	tgtacctgac	aatgtcgatg	atattgtagc	tgacctggct	ccagaagaga	1860
aagatgaaga	tgacaccctc	gaaacctgca	tctactccaa	ctgggtccca	tgggtccgct	1920
gcagctcctc	cacctgtgac	aaaggcaaga	ggatgcgaca	gcgcagtctg	aaagcacagc	1980
tggacctcag	cgtcccctgc	cctgacaccc	aggacttcca	gccctgcagt	ggccctggct	2040
gcagtgaaga	agacggctcc	acctgcacca	tgtccgagtg	gatcacctgg	tcgccctgca	2100
gcactcctct	cggcatgggc	atgaggtccc	gggagaggta	tgtgaagcag	ttcccgagg	2160
acggctcctg	gtgcacgctg	ccactgagg	aaacggagaa	gtgcacggtc	aacgaggagt	2220
gctctcccag	cagctgcctg	atgaccgagt	ggggcgagtg	ggacgagtgc	agcgcacact	2280
gcggcatggg	catgaagaag	cggcaccgca	tgatcaagat	gaaccccgca	gatggctcca	2340
tgtgcaaaag	cgagacatca	caggcagaga	agtgcagtgc	gccagagtgc	cacaccatcc	2400
catgcttgct	gtccccatgg	tcagagtggg	gtgactgcag	cgtgacctgc	gggaagggca	2460
tgcgaacccg	acagcggatg	ctcaagtctc	tggcagaact	tggagactgc	aatgaggatc	2520
tggagcaggt	ggagaagtgc	atgctccctg	aatgccccat	tgactgtgag	ctcaccgagt	2580
ggtcccagtg	gtcgaatgt	aacaagtcac	gtgggaaagg	ccacgtgatt	cgaacccgga	2640
tgatccaaat	ggagcctcag	tttgagggtg	caccctgccc	agagactgtg	cagcgaaaaa	2700
agtgcgcgat	ccgaaaatgc	cttcgaaatc	catccatcca	aaagctacgc	tggaggagg	2760
cccagagagag	ccggcggagt	gagcagctga	aggaagagtc	tgaaggggag	cagttcccag	2820
gttgtaggat	gcgcccctgg	acggcctggg	cagaatgcac	caaactgtgc	ggagggtgaa	2880
ttcaggaacg	ttacatgact	gtaaagaaga	gattcaaaag	ctcccagttt	accagctgca	2940
aagacaagaa	ggagatcaga	gcatgcaatg	ttcatccttg	ttagcaaggg	tacgagttcc	3000
ccagggtctgc	actctagatt	ccagagtcac	caatggctgg	attatttgct	tgtttaagac	3060
aatttaaatt	gtgtacgcta	gttttcattt	ttgcagtgtg	gttcgccag	tagtcttggt	3120
gatgccagag	acatcctttc	tgaatacttc	ttgatgggta	caggctgagt	ggggcgccct	3180
cacctccagc	cagcctcttc	ctgcagagga	gtagtgtcag	ccaccttgta	ctaagctgaa	3240
acatgtccct	ctggagcttc	cacctggcca	gggaggacgg	agactttgac	ctactccaca	3300
tggagaggca	accatgtctg	gaagtgacta	tgctctgagtc	ccagggtgcg	gcaggtagga	3360
aacattcaca	gatgaagaca	gcagattccc	cacattctca	tctttggcct	gttcaatgaa	3420
accattgttt	gcccactctc	tcttagtgga	acttttaggtc	tcttttcaag	tctcctcagt	3480

```

catcaatagt tcctggggaa aaacagagct ggtagacttg aagaggagca ttgatgttg 3540
gtgggcttttgc ttctttcact gagaaattcg gaatacattt gtctcaccoc tgatattggt 3600
tcctgatgcc cccccaacaa aaataaataa ataaattatg gctgctttat ttaaataata 3660
ggtagctagt ttttacacct gagataaata ataagcttag agtgtatttt tcccttgctt 3720
ttgggggttc agaggagtat gtacaattct tctgggaagc cagccttctg aactttttg 3780
tactaaatcc ttattggaac caagacaaag gaagcaaaat tggctctctt agagaccaat 3840
ttgcctaaat tttaaaatct tctacacac atctagacgt tcaagtttg aaatcagttt 3900
ttagcaagaa aacatttttg ctatacaaac attttgctaa gtctgcccac agcccccca 3960
atgcattcct tcaacaaaat acaatctctg tacttttaag ttatttttagt catgaaattt 4020
tatatgcaga gagaaaaagt taccgagaca gaaaacaaat ctaagggaag ggaatattat 4080
gggattaagc tgagcaagca attctggtgg aaagtcaaac ctgtcagtgc tccacaccag 4140
ggctgtggtc ctcccagaca tgcataaggaa tggccacagg tttacactgc cttcccagca 4200
attataagca caccagattc agggagactg accaccaagg gatagtgtaa aaggacattt 4260
tctcagtttg gtccatcagc agtttttctt cctgcattta ttgttgaaaa ctattgtttc 4320
atttcttctt ttataggcct tattactgct taatccaaat gtgtaccatt ggtgagacac 4380
atacaatgct ctgaatacac tacgaatttg tattaaacac atcagaatat ttccaaatac 4440
aacatagtat agtctgaat atgtactttt aacacaagag agactattca ataaaaactc 4500
actgggtctt tcatgtcttt aagctaagta agtggtcaga aggttctttt ttatattgtc 4560
ctccacctcc atcattttca ataaaagata gggcttttgc tcccttgctt ttggagggac 4620
cattattaca tctctgaact acctttgtat ccaacatggt ttaaatcctt aaatgaattg 4680
ctttctccca aaaaaagcac aatataaaga aacacaagat ttaattattt ttctacttgg 4740
ggggaaaaaa gtctcatgt agaagcacc ctttttgcaa tgttgttcta agctatctat 4800
ctaactctca gcccatgata aagttcctta agctggtgat tcctaataca ggacaagcca 4860
ccctagtgtc tcatgtttgt atttggtccc agttgggtac attttaaaat cctgattttg 4920
gagacttaaa accaggttaa tggctaagaa tgggtaacat gactcttgtt ggattgttat 4980
tttttgttt caatggggaa tttataagaa gcatcaagtc tctttcttac caaagtctt 5040
ttaggtggtt tatagtctt ttggctaaca aatcattttg gaaataaaga ttttttacta 5100
caaaaatg 5108

```

&lt;210&gt; 308

&lt;211&gt; 934

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 308

```

Met Pro Arg Phe Leu Arg Gln Thr Leu Gly Ile Gln Arg Arg Lys Ile
1 5 10 15
Asn Thr Ala Ala Pro Leu Ile Ala Ser Ser Glu Glu Thr Lys Gln Arg
20 25 30
Cys Ala Gly Gly Ser Gly Gln Asn Gln Pro Ser Leu Leu Pro Leu Leu
35 40 45
Arg Arg Gly Pro Pro Leu Leu Ala Leu Leu Ser Phe Ala Trp Leu Ser
50 55 60
Ser Ala Gln Leu Ser Ala Ala Pro Arg Pro Pro Ser Arg Gly Gly His
65 70 75 80
Gly Leu Arg Val Ala Asp Ala Ser Ser Glu Leu Pro Leu Ser Ala Ala
85 90 95
Pro Pro Pro Gly Arg Ala Phe Val Gly Thr Thr Ser Gly Arg Ser Arg
100 105 110
Val Ala Lys Ala Cys Gly Arg Gly Thr Lys Leu Gly Ala Ala Lys Met
115 120 125
Arg Leu Ser Pro Ala Pro Leu Lys Leu Ser Arg Thr Pro Ala Leu Leu
130 135 140
Ala Leu Ala Leu Pro Leu Ala Ala Ala Leu Ala Phe Ser Asp Glu Thr
145 150 155 160
Leu Asp Lys Val Pro Lys Ser Glu Gly Tyr Cys Ser Arg Ile Leu Arg
165 170 175
Ala Gln Gly Thr Arg Arg Glu Gly Tyr Thr Glu Phe Ser Leu Arg Val

```

				180					185					190	
Glu	Gly	Asp	Pro	Asp	Phe	Tyr	Lys	Pro	Gly	Thr	Ser	Tyr	Arg	Val	Thr
				195					200					205	
Leu	Ser	Ala	Ala	Pro	Pro	Ser	Tyr	Phe	Arg	Gly	Phe	Thr	Leu	Ile	Ala
				210					215					220	
Leu	Arg	Glu	Asn	Arg	Glu	Gly	Asp	Lys	Glu	Glu	Asp	His	Ala	Gly	Thr
				225					230					235	240
Phe	Gln	Ile	Ile	Asp	Glu	Glu	Glu	Thr	Gln	Phe	Met	Ser	Asn	Cys	Pro
				245					250					255	
Val	Ala	Val	Thr	Glu	Ser	Thr	Pro	Arg	Arg	Arg	Thr	Arg	Ile	Gln	Val
				260					265					270	
Phe	Trp	Ile	Ala	Pro	Pro	Ala	Gly	Thr	Gly	Cys	Val	Ile	Leu	Lys	Ala
				275					280					285	
Ser	Ile	Val	Gln	Lys	Arg	Ile	Ile	Tyr	Phe	Gln	Asp	Glu	Gly	Ser	Leu
				290					295					300	
Thr	Lys	Lys	Leu	Cys	Glu	Gln	Asp	Ser	Thr	Phe	Asp	Gly	Val	Thr	Asp
				305					310					315	320
Lys	Pro	Ile	Leu	Asp	Cys	Cys	Ala	Cys	Gly	Thr	Ala	Lys	Tyr	Arg	Leu
				325					330					335	
Thr	Phe	Tyr	Gly	Asn	Trp	Ser	Glu	Lys	Thr	His	Pro	Lys	Asp	Tyr	Pro
				340					345					350	
Arg	Arg	Ala	Asn	His	Trp	Ser	Ala	Ile	Ile	Gly	Gly	Ser	His	Ser	Lys
				355					360					365	
Asn	Tyr	Val	Leu	Trp	Glu	Tyr	Gly	Gly	Tyr	Ala	Ser	Glu	Gly	Val	Lys
				370					375					380	
Gln	Val	Ala	Glu	Leu	Gly	Ser	Pro	Val	Lys	Met	Glu	Glu	Glu	Ile	Arg
				385					390					395	400
Gln	Gln	Ser	Asp	Glu	Val	Leu	Thr	Val	Ile	Lys	Ala	Lys	Ala	Gln	Trp
				405					410					415	
Pro	Ala	Trp	Gln	Pro	Leu	Asn	Val	Arg	Ala	Ala	Pro	Ser	Ala	Glu	Phe
				420					425					430	
Ser	Val	Asp	Arg	Thr	Arg	His	Leu	Met	Ser	Phe	Leu	Thr	Met	Met	Gly
				435					440					445	
Pro	Ser	Pro	Asp	Trp	Asn	Val	Gly	Leu	Ser	Ala	Glu	Asp	Leu	Cys	Thr
				450					455					460	
Lys	Glu	Cys	Gly	Trp	Val	Gln	Lys	Val	Val	Gln	Asp	Leu	Ile	Pro	Trp
				465					470					475	480
Asp	Ala	Gly	Thr	Asp	Ser	Gly	Val	Thr	Tyr	Glu	Ser	Pro	Asn	Lys	Pro
				485					490					495	
Thr	Ile	Pro	Gln	Glu	Lys	Ile	Arg	Pro	Leu	Thr	Ser	Leu	Asp	His	Pro
				500					505					510	
Gln	Ser	Pro	Phe	Tyr	Asp	Pro	Glu	Gly	Gly	Ser	Ile	Thr	Gln	Val	Ala
				515					520					525	
Arg	Val	Val	Ile	Glu	Arg	Ile	Ala	Arg	Lys	Gly	Glu	Gln	Cys	Asn	Ile
				530					535					540	
Val	Pro	Asp	Asn	Val	Asp	Asp	Ile	Val	Ala	Asp	Leu	Ala	Pro	Glu	Glu
				545					550					555	560
Lys	Asp	Glu	Asp	Asp	Thr	Pro	Glu	Thr	Cys	Ile	Tyr	Ser	Asn	Trp	Ser
				565					570					575	
Pro	Trp	Ser	Ala	Cys	Ser	Ser	Ser	Thr	Cys	Asp	Lys	Gly	Lys	Arg	Met
				580					585					590	
Arg	Gln	Arg	Met	Leu	Lys	Ala	Gln	Leu	Asp	Leu	Ser	Val	Pro	Cys	Pro
				595					600					605	
Asp	Thr	Gln	Asp	Phe	Gln	Pro	Cys	Met	Gly	Pro	Gly	Cys	Ser	Asp	Glu
				610					615					620	
Asp	Gly	Ser	Thr	Cys	Thr	Met	Ser	Glu	Trp	Ile	Thr	Trp	Ser	Pro	Cys
				625					630					635	640
Ser	Ile	Ser	Cys	Gly	Met	Gly	Met	Arg	Ser	Arg	Glu	Arg	Tyr	Val	Lys

```
<210> 309
<211> 5471
<212> DNA
<213> Homo sapiens
```

<400> 309							
gcgagtcgat	acagtaagta	agccgccaag	catattgcta	ggcacagagc	aggtgtgcaa	60	
caaaagttat	ttctcaggct	ttccctcctc	tgagcgccgt	cctccagagg	gtccggagtg	120	
tagctggggg	ttggagcagc	agcctcctag	gcgatgggac	agagccca	gggtccggtg	180	
tgccacggtt	tcttcgtcag	accctgggaa	tccaacgtcg	caaaataaac	acggccgcgc	240	
cgctaatacg	cagttccggg	gaacaaaaac	agcgtctgcg	tgggggatct	gggcaaatc	300	
agccctccct	cctcccgcct	cttcgcgcgc	gcctccctcc	cctgcgcgtg	ctctcgttcg	360	
cttggctcag	ctcagctcag	ctcagcgcag	ctccgcgcgc	gccaaagccg	ggcgggcaag	420	
gtctccgagt	cgcggaagcc	agctccgagc	tccctctctc	cgccgcgcct	ccgccaggtc	480	
gcgccttcgt	cgggaccact	tcgggcagga	gtcgcgtggc	gaaggcctgc	ggccgcggca	540	
caaagttagg	ggccgcgaag	atgaggtctg	ccccggcgcc	cctgaagctg	agccggaactc	600	
cggcaactgt	ggccctggcg	ctgccccctg	ccgcggcgct	ggcctctctc	gacgagacc	660	
tggcaaaagt	gcccaagtca	gagggtactg	gcagccgat	cctgcgcgcc	cagggcacgc	720	
ggcgcgaggg	ctacaccgag	ttcagcctcc	cgctggaggg	cgaccgccgac	ttctacaagc	780	



cggaaccag	ctaccgcgta	acacttttcag	ctgctcctcc	ctcctacttc	agaggattca	840
cattaattgc	cctcagagag	aacagagagg	gtgataagga	agaagaccat	gctgggacct	900
tccagatcat	agacgaagaa	gaaactcagt	ttatgagcaa	ttgccctgtt	gcagtactg	960
aaagcactcc	acggaggagg	acccgatcc	aggtgttttg	gatagcacca	ccagcgggaa	1020
caggctgcgt	gattctgaag	gccagcatcg	tacaaaaacg	cattatttat	tttcaagatg	1080
agggctctct	gaccaagaaa	ctttgtgaac	aagattccac	atttgatggg	gtgactgaca	1140
aacccatctt	agactgctgt	gcctgcgga	ctgccaaagta	cagactcaca	ttttatggga	1200
attggtccga	gaagacacac	ccaaaggatt	accctcgctg	ggccaaccac	tggtctgcga	1260
tcacgcgagg	atcccactcc	aagaattatg	tactgtggga	atatggagga	tatgccagcg	1320
aaggcgtcaa	acaagttgca	gaattgggct	caccctgtaa	aatggaggaa	gaaattcgac	1380
aacagagtga	tgaggtcctc	accgtcatca	aagccaaagc	ccaatggcca	gcctggcagc	1440
ctctcaacgt	gagagcagca	ccttcagctg	aattttccgt	ggacagaacg	cgccatttaa	1500
tgtccttcct	gaccatgatg	ggccctagtc	ccgactggaa	cgtaggctta	tctgcagaag	1560
atctgtgcac	caaggaatgt	ggctgggtcc	agaaggtggt	gcaagacctg	attccctggg	1620
acgctggcac	cgacagcggg	gtgacctatg	agtcacccaa	caaaccacc	attcccagag	1680
agaaaatccg	gcccctgacc	agcctggacc	atcctcagag	tcctttctat	gaccagagg	1740
gtgggtccat	cactcaagta	gccagagttg	tcacgcagag	aatcgacgg	aaggggtaac	1800
aatgcaatat	tgtacctgac	aatgtcgatg	atattgtagc	tgacctggct	ccagaagaga	1860
aagatgaaga	tgacaccctc	gaaacctgca	tctactccaa	ctgggtccca	tggtccgcct	1920
gcagctcctc	cacctgtgac	aaaggcaaga	ggatgctgaca	gcgcatgctg	aaagcacagc	1980
tggacctcag	cgtcccctgc	cctgacaccc	aggacttcca	gccctgcatg	ggccctggct	2040
gcagtgcga	agacggctcc	acctgcacca	tgtccgagtg	gatcacctgg	tcgccctgca	2100
gcattctctg	cggcattggc	atgaggtccc	gggagaggta	tgtgaagcag	ttcccgagg	2160
acggctccgt	gtgcacgctg	cccactgagg	aaacggagaa	gtgcacggtc	aacgaggagt	2220
gctctcccag	cagctgcctg	atgaccgagt	ggggcgagtg	ggacgagtg	agcgccacct	2280
gcgcatggg	catgaagaag	cggcaccgca	tgatcaagat	gaaccccgca	gatggctcca	2340
tgtgcaaagc	cgagacatca	caggcagaga	agtgcagatg	gccagagtgc	cacaccatcc	2400
catgcttgct	gtccccctgg	tccgagtggg	gtgactgcag	cgtgacctgc	gggaagggca	2460
tgcgaacccg	acagcggatg	ctcaagtctc	tggcagaact	tggagactgc	aatgaggatc	2520
tggagcaggt	ggagaagtgc	atgctccctg	aatgccccat	tgactgtgag	ctcaccgagt	2580
ggtcccagtg	gtcggaatgt	aacaagtcac	gtgggaaagg	ccacgtgatt	cgaacccgga	2640
tgatccaaat	ggagcctcag	ttcctccaaa	gccttcttga	gtcatagagg	gagcatagaa	2700
tgggtgatga	cctggcacca	atcctgcctc	tgtgtcttac	caaccacacg	ggctgaagtc	2760
agcctgcctc	tttggagcct	cagtttcttc	ttctgtaaaa	tagcatgaca	cagcaccctgc	2820
tttgcattccc	tcattaggctt	gttgagatgt	tcaaaggaga	gcgtgaccat	atcttgtttc	2880
agacatgtga	tacactcatg	cccatctgtg	tcttgccagc	cattgactgt	gagctcaccg	2940
agtgggtccca	gtggctggaa	tgtaacaagt	catgtgggaa	aggccacgtg	attcgaaccc	3000
ggatgatcca	aatggagcct	cagtttgagg	gtgcaccctg	cccagagact	gtgcagcgaa	3060
aaaagtgcg	catccgaaaa	tgccttcgaa	atccatccat	ccaaaagcta	cgctggaggg	3120
aggcccgaga	gagccggcgg	agtgagcagc	tgaagggaaga	gtctgaaggg	gagcagttcc	3180
caggttgtag	gatgcgcccc	tggacggcct	ggtcagaatg	caccaaactg	tgcgagggtg	3240
gaattcagga	acgttacatg	actgtaaaaga	agagattcaa	aagctcccag	tttaccagct	3300
gcaaagacaa	gaaggagatc	agagcatgca	atgttcatcc	ttgttagcaa	gggtacgagt	3360
tccccagggc	tgcaactctag	attccagagt	caccaatggc	tggattattt	gcttgtttta	3420
gacaatttaa	attgtgtacg	ctagttttca	tttttgagct	gtggttcgcc	cagtagtctt	3480
gtggatgcca	gagacatcct	ttctgaatac	ttcttgatgg	gtacaggctg	agtggggcgc	3540
cctcacctcc	agccagcctc	ttcctgcaga	ggagttagtg	cagccacctt	gtactaagtc	3600
gaaacatgtc	cctctggagc	ttccacctgg	ccaggaggga	cggagacttt	gacctactcc	3660
acatggagag	gcaaccatgt	ctggaagtga	ctatgcctga	gtcccagggt	gcggcaggta	3720
ggaaacattc	acagatgaag	acagcagatt	ccccacattc	tcattctttg	cctgttcaat	3780
gaaaccattg	tttgcccatc	tcttcttagt	ggaactttag	gtctcttttc	aagtctcctc	3840
agtcattcaat	agttcctggg	gaaaaacaga	gctggttagac	ttgaagagga	gcattgatgt	3900
tgggtggctt	ttgttctttc	actgagaaat	tcggaataca	tttgtctcac	ccctgatatt	3960
ggttctctgat	gcccccccaa	caaaaataaa	taaataaatt	atggctgctt	tatttaaata	4020
taaggtagct	agttttttaca	cctgagataa	ataataagct	tagagtgtat	ttttcccttg	4080
cttttggggg	ttcagaggag	tatgtacaa	ttctctggga	agccagcctt	ctgaactttt	4140
tggtactaaa	tccttatttg	aaccaagaca	aaggaagcaa	aattggtctc	tttagagacc	4200
aatttgccta	aatttttaaaa	tcttctctaca	cacatctaga	cgttcaagtt	tgcaaatcag	4260

320

```

tttttagcaa gaaaacattt ttgctataca aacattttgc taagtctgcc caaagccccc 4320
ccaatgcatt ccttcaacaa aatacaatct ctgtacttta aagttatttt agtcatgaaa 4380
ttttatatgc agagagaaaa agttaccgag acagaaaaca aatctaaggg aaaggaatat 4440
tatgggatta agctgagcaa gcaattctgg tggaaagtca aacctgtcag tgctccacac 4500
cagggtctgt gtctctccag acatgcatag gaatggccac aggtttacac tgccttccca 4560
gcaattataa gcacaccaga ttcagggaga ctgaccacca agggatagtg taaaaggaca 4620
ttttctcagt tgggtccatc agcagttttt ctctctgcat ttattgttga aaactattgt 4680
ttcattttctt cttttatagg ctttattact gcttaatcca aatgtgtacc attggtgaga 4740
cacatacaat gctctgaata cactacgaat ttgtattaaa cacatcagaa tttttccaaa 4800
tacaacatag tatagtctctg aatatgtact ttttaacacaa gagagactat tcaataaaaa 4860
ctcactgggt ctttcatgtc ttttaagctaa gtaagtgttc agaaggttct tttttatatt 4920
gtctctccacc tccatcattt tcaataaaaag atagggtttt tgctcccttg ttcttggagg 4980
gaccattatt acatctctga actacctttg tatccaacat gttttaaatc cttaaatgaa 5040
ttgcttttctc ccaaaaaaag cacaatataa agaaacacaa gatttaatta tttttctact 5100
tgggggggaaa aaagtcctca tgtagaagca cccacttttg caatgttgtt ctaagctatc 5160
tatctaactc tcagcccatg ataaagttcc ttaagctggg gattcctaata caaggacaag 5220
ccaccctagt gtctcatgtt tgtatttggg cccagttggg tacattttta aatcctgatt 5280
ttggagactt aaaaccaggt taatggctaa gaatgggtaa catgactctt gttggattgt 5340
tattttttgt ttgcaatggg gaatttataa gaagcatcaa gtctctttct taccaaagtc 5400
ttgtaggtg gtttatagtt cttttggcta acaaatcatt ttggaaataa agatttttta 5460
ctacaaaaat g

```

&lt;210&gt; 310

&lt;211&gt; 835

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 310

```

Met Pro Arg Phe Leu Arg Gln Thr Leu Gly Ile Gln Arg Arg Lys Ile
 1           5           10           15
Asn Thr Ala Ala Pro Leu Ile Ala Ser Ser Glu Glu Thr Lys Gln Arg
          20           25           30
Cys Ala Gly Gly Ser Gly Gln Asn Gln Pro Ser Leu Leu Pro Leu Leu
          35           40           45
Arg Arg Gly Pro Pro Leu Leu Ala Leu Leu Ser Phe Ala Trp Leu Ser
          50           55           60
Ser Ala Gln Leu Ser Ala Ala Pro Arg Pro Pro Ser Arg Gly Gly His
          65           70           75           80
Gly Leu Arg Val Ala Asp Ala Ser Ser Glu Leu Pro Leu Ser Ala Ala
          85           90           95
Pro Pro Pro Gly Arg Ala Phe Val Gly Thr Thr Ser Gly Arg Ser Arg
          100          105          110
Val Ala Lys Ala Cys Gly Arg Gly Thr Lys Leu Gly Ala Ala Lys Met
          115          120          125
Arg Leu Ser Pro Ala Pro Leu Lys Leu Ser Arg Thr Pro Ala Leu Leu
          130          135          140
Ala Leu Ala Leu Pro Leu Ala Ala Ala Leu Ala Phe Ser Asp Glu Thr
          145          150          155          160
Leu Asp Lys Val Pro Lys Ser Glu Gly Tyr Cys Ser Arg Ile Leu Arg
          165          170          175
Ala Gln Gly Thr Arg Arg Glu Gly Tyr Thr Glu Phe Ser Leu Arg Val
          180          185          190
Glu Gly Asp Pro Asp Phe Tyr Lys Pro Gly Thr Ser Tyr Arg Val Thr
          195          200          205
Leu Ser Ala Ala Pro Pro Ser Tyr Phe Arg Gly Phe Thr Leu Ile Ala
          210          215          220
Leu Arg Glu Asn Arg Glu Gly Asp Lys Glu Glu Asp His Ala Gly Thr
          225          230          235          240

```

321

Phe	Gln	Ile	Ile	Asp	Glu	Glu	Glu	Thr	Gln	Phe	Met	Ser	Asn	Cys	Pro	245	250	255
Val	Ala	Val	Thr	Glu	Ser	Thr	Pro	Arg	Arg	Arg	Thr	Arg	Ile	Gln	Val	260	265	270
Phe	Trp	Ile	Ala	Pro	Pro	Ala	Gly	Thr	Gly	Cys	Val	Ile	Leu	Lys	Ala	275	280	285
Ser	Ile	Val	Gln	Lys	Arg	Ile	Ile	Tyr	Phe	Gln	Asp	Glu	Gly	Ser	Leu	290	295	300
Thr	Lys	Lys	Leu	Cys	Glu	Gln	Asp	Ser	Thr	Phe	Asp	Gly	Val	Thr	Asp	305	310	315
Lys	Pro	Ile	Leu	Asp	Cys	Cys	Ala	Cys	Gly	Thr	Ala	Lys	Tyr	Arg	Leu	325	330	335
Thr	Phe	Tyr	Gly	Asn	Trp	Ser	Glu	Lys	Thr	His	Pro	Lys	Asp	Tyr	Pro	340	345	350
Arg	Arg	Ala	Asn	His	Trp	Ser	Ala	Ile	Ile	Gly	Gly	Ser	His	Ser	Lys	355	360	365
Asn	Tyr	Val	Leu	Trp	Glu	Tyr	Gly	Gly	Tyr	Ala	Ser	Glu	Gly	Val	Lys	370	375	380
Gln	Val	Ala	Glu	Leu	Gly	Ser	Pro	Val	Lys	Met	Glu	Glu	Glu	Ile	Arg	385	390	395
Gln	Gln	Ser	Asp	Glu	Val	Leu	Thr	Val	Ile	Lys	Ala	Lys	Ala	Gln	Trp	405	410	415
Pro	Ala	Trp	Gln	Pro	Leu	Asn	Val	Arg	Ala	Ala	Pro	Ser	Ala	Glu	Phe	420	425	430
Ser	Val	Asp	Arg	Thr	Arg	His	Leu	Met	Ser	Phe	Leu	Thr	Met	Met	Gly	435	440	445
Pro	Ser	Pro	Asp	Trp	Asn	Val	Gly	Leu	Ser	Ala	Glu	Asp	Leu	Cys	Thr	450	455	460
Lys	Glu	Cys	Gly	Trp	Val	Gln	Lys	Val	Val	Gln	Asp	Leu	Ile	Pro	Trp	465	470	475
Asp	Ala	Gly	Thr	Asp	Ser	Gly	Val	Thr	Tyr	Glu	Ser	Pro	Asn	Lys	Pro	485	490	495
Thr	Ile	Pro	Gln	Glu	Lys	Ile	Arg	Pro	Leu	Thr	Ser	Leu	Asp	His	Pro	500	505	510
Gln	Ser	Pro	Phe	Tyr	Asp	Pro	Glu	Gly	Gly	Ser	Ile	Thr	Gln	Val	Ala	515	520	525
Arg	Val	Val	Ile	Glu	Arg	Ile	Ala	Arg	Lys	Gly	Glu	Gln	Cys	Asn	Ile	530	535	540
Val	Pro	Asp	Asn	Val	Asp	Asp	Ile	Val	Ala	Asp	Leu	Ala	Pro	Glu	Glu	545	550	555
Lys	Asp	Glu	Asp	Asp	Thr	Pro	Glu	Thr	Cys	Ile	Tyr	Ser	Asn	Trp	Ser	565	570	575
Pro	Trp	Ser	Ala	Cys	Ser	Ser	Ser	Thr	Cys	Asp	Lys	Gly	Lys	Arg	Met	580	585	590
Arg	Gln	Arg	Met	Leu	Lys	Ala	Gln	Leu	Asp	Leu	Ser	Val	Pro	Cys	Pro	595	600	605
Asp	Thr	Gln	Asp	Phe	Gln	Pro	Cys	Met	Gly	Pro	Gly	Cys	Ser	Asp	Glu	610	615	620
Asp	Gly	Ser	Thr	Cys	Thr	Met	Ser	Glu	Trp	Ile	Thr	Trp	Ser	Pro	Cys	625	630	635
Ser	Ile	Ser	Cys	Gly	Met	Gly	Met	Arg	Ser	Arg	Glu	Arg	Tyr	Val	Lys	645	650	655
Gln	Phe	Pro	Glu	Asp	Gly	Ser	Val	Cys	Thr	Leu	Pro	Thr	Glu	Glu	Thr	660	665	670
Glu	Lys	Cys	Thr	Val	Asn	Glu	Glu	Cys	Ser	Pro	Ser	Ser	Cys	Leu	Met	675	680	685
Thr	Glu	Trp	Gly	Glu	Trp	Asp	Glu	Cys	Ser	Ala	Thr	Cys	Gly	Met	Gly	690	695	700

322

Met Lys Lys Arg His Arg Met Ile Lys Met Asn Pro Ala Asp Gly Ser  
 705 710 715 720  
 Met Cys Lys Ala Glu Thr Ser Gln Ala Glu Lys Cys Met Met Pro Glu  
 725 730 735  
 Cys His Thr Ile Pro Cys Leu Leu Ser Pro Trp Ser Glu Trp Ser Asp  
 740 745 750  
 Cys Ser Val Thr Cys Gly Lys Gly Met Arg Thr Arg Gln Arg Met Leu  
 755 760 765  
 Lys Ser Leu Ala Glu Leu Gly Asp Cys Asn Glu Asp Leu Glu Gln Val  
 770 775 780  
 Glu Lys Cys Met Leu Pro Glu Cys Pro Ile Asp Cys Glu Leu Thr Glu  
 785 790 795 800  
 Trp Ser Gln Trp Ser Glu Cys Asn Lys Ser Cys Gly Lys Gly His Val  
 805 810 815  
 Ile Arg Thr Arg Met Ile Gln Met Glu Pro Gln Phe Leu Gln Ser Leu  
 820 825 830  
 Leu Glu Ser  
 835

&lt;210&gt; 311

&lt;211&gt; 3112

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 311

cacgcgtccg cggacgcgtg ggctgcagcc ggagaaagag gaagagggag agagagcgcg 60  
 ccagggcgag ggcaccgccc ccggtcgggc gcgctgggcc tgcccggaaat cccgcgcgct 120  
 gcgccccgcg ccccgcgccc tgccggccat gggagccgyc cgccggcagg gacgacgcct 180  
 gtgagaccgc cgagcgccct cggggaccat ggggagcgat cgggcccgcg agggcggagg 240  
 gggcccgaag gacttcggcg cgggactcaa gtacaactcc cggcacgaga aagtgaatgg 300  
 cttggaggaa ggcgtggagt tcctgccagt caacaacgtc aagaaggtgg aaaagcatgg 360  
 cccggggcgc tgggtggtgc tggcagccgt gctgatcgcc ctctcttgg tcttgcctgg 420  
 gatcggtctc ctggtgtggc atttgagta ccgggacgtg cgtgtccaga aggtcttcaa 480  
 tggctacatg aggatcacaa atgagaatgt tgtggatgcc tacgagaact ccaactccac 540  
 tgagtttgta agcctggcca gcaaggtgaa ggacgcgctg aagctgctgt acagcggagt 600  
 cccattctctg ggccttacc acaaggagtc ggctgtgacg gccttcagcg agggcagcgt 660  
 catcgctac tactggtctg agttcagcat cccgcagcac ctggtggagg aggccgagcg 720  
 cgtcatggcc gaggagcgcg tagtcatgct gccccgcgg gcgcgctccc tgaagtcctt 780  
 tgtggtcacc tcagtgggtg ctttccccac ggaactccaa acagtacaga ggaccacgga 840  
 caacagctgc agctttggcc tgcacgcccg cgggtgtggag ctgatgcgct tcaccacgcc 900  
 cggcttccct gacagcccct accccgctca tgcccgtgc cagtgggccc tgcgggggga 960  
 cgccgactca gtgtgagcc tcacctccg cagctttgac cttgcgtcct gcgacgagcg 1020  
 cggcagcgac ctggtgacgg tgtacaacac cctgagcccc atggagcccc acgccctggg 1080  
 gcagttgtgt ggcacctacc ctccctccta caacctgacc ttccactcct cccagaacgt 1140  
 cctgtcatc aactgataa ccaactga ggcgggcat cccggctttg aggccacctt 1200  
 cttccagctg cctaggatga gcagctgtgg aggcgctta cgtaaagccc aggggacatt 1260  
 caacagcccc tactaccag gccactacc acccaacatt gactgcacat ggaacattga 1320  
 ggtgcccaac aaccagcatg tgaaggtgcg cttcaaatc ttctacctgc tggagcccgg 1380  
 cgtgcctgcg ggcacctgcc ccaaggacta cgtggagatc aatggggaga aatactgagg 1440  
 agagaggtcc cagttcgtcg tcaccagcaa cagcaacaag atcacagttc gcttccactc 1500  
 agatcagtc tacaccgaca ccggttctt agctgaatac ctctcctacg actccagtga 1560  
 ccgttgcgac gccggccacc agttcacgtg caagaacaag ttctgcaagc ccctcttctg 1620  
 ggtctgcgac agtgtgaacg actgcggaga caacagcgac gagcaggggt gcatgaacgt 1680  
 cgtcacttgt accaaacaca cctaccgctg cctcaatggg ctctgcttga gcaagggcaa 1740  
 ccctgagtgt gacgggaagg aggactgtag cgacggctca gatgagaagg actgcgactg 1800  
 tgggctgcgg tcattcacga gacaggctcg tgttgttggg ggcacggatg cggatgaggg 1860  
 cgagtggccc tggcaggtaa gcctgcatgc tctgggcccag ggccacatct gcggtgcttc 1920

323

```

cctcatctct cccaactggc tgggtctctgc cgcacactgc tacatcgatg acagaggatt 1980
cagggtactca gacccacgc agtggacggc cttcctgggc ttgcacgacc agagccagcg 2040
cagcgcccct ggggtgcagg agcgaggct caagcgcatc atctcccacc ctttcttcaa 2100
tgacttcacc ttcgactatg acatcgcgct gctggagctg gagaaaccgg cagagtacag 2160
ctccatggtg cggcccatct gcctgccgga cgcctcccat gtcttccctg ccggcaaggc 2220
catctgggtc acgggctggg gacacaccca gtatggaggc actggcgcg c tgatcctgca 2280
aaaggggtgag atccgcgtca tcaaccagac cacctgcgag aacctcctgc cgcagcagat 2340
cacgcgcgcg atgatgtgag tgggcttcct cagcggcggc gtggactcct gccaggggtga 2400
ttccggggga cccctgtcca gcgtggaggc ggatgggagg atcttccagg ccggtgtggt 2460
gagctgggga gacggctgag ctacagaggaa caagccaggc gtgtacacaa ggctccctct 2520
gtttcgggac tggatcaaag agaacactgg ggtatagggg ccggggccac ccaaagtgtg 2580
acacctgcgg gggcaccocat cgtccacccc agtgtgcacg cctgcaggct ggagactgga 2640
ccgctgactg caccagcgcc cccagaacat acactgtgaa ctcaatctcc agggctccaa 2700
atctgcctag aaaacctctc gcttccctcag cctccaaagt ggagctggga ggtagaaggg 2760
gaggacactg gtggttctac tgacccaact gggggcaaag gtttgaagac acagcctccc 2820
ccgccagccc caagctgggc cgaggcgctg ttgtgcatat ctgcctcccc tgtctctaag 2880
gagcagcggg aacggagctt cggggcctcc tcagtgaagg tgggtggggct gccggatctg 2940
ggctgtgggg cccttggggc acgctcttga ggaagcccag gctcggagga ccctggaaaa 3000
cagacgggtc tgagactgaa attgttttac cagctcccag ggtggacttc agtgtgtgta 3060
tttgtgtaaa tgagtaaaac attttatttc tttttaaaaa aaaaaaaaaa aa 3112

```

&lt;210&gt; 312

&lt;211&gt; 782

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 312

```

Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1           5           10           15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
 20           25           30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
 35           40           45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Val Leu Ile Gly
 50           55           60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
 65           70           75           80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
 85           90           95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
100          105          110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
115          120          125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
130          135          140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145          150          155          160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
165          170          175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
180          185          190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
195          200          205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
210          215          220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225          230          235          240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu

```

324

					245					250					255
Ser	Leu	Thr	Phe	Arg	Ser	Phe	Asp	Leu	Ala	Ser	Cys	Asp	Glu	Arg	Gly
			260					265					270		
Ser	Asp	Leu	Val	Thr	Val	Tyr	Asn	Thr	Leu	Ser	Pro	Met	Glu	Pro	His
		275					280					285			
Ala	Leu	Val	Gln	Leu	Cys	Gly	Thr	Tyr	Pro	Pro	Ser	Tyr	Asn	Leu	Thr
		290				295					300				
Phe	His	Ser	Ser	Gln	Asn	Val	Leu	Leu	Ile	Thr	Leu	Ile	Thr	Asn	Thr
305					310					315					320
Glu	Arg	Arg	His	Pro	Gly	Phe	Glu	Ala	Thr	Phe	Phe	Gln	Leu	Pro	Arg
				325					330					335	
Met	Ser	Ser	Cys	Gly	Gly	Arg	Leu	Arg	Lys	Ala	Gln	Gly	Thr	Phe	Asn
			340					345					350		
Ser	Pro	Tyr	Tyr	Pro	Gly	His	Tyr	Pro	Pro	Asn	Ile	Asp	Cys	Thr	Trp
		355					360					365			
Asn	Ile	Glu	Val	Pro	Asn	Asn	Gln	His	Val	Lys	Val	Arg	Phe	Lys	Phe
		370				375					380				
Phe	Tyr	Leu	Leu	Glu	Pro	Gly	Val	Pro	Ala	Gly	Thr	Cys	Pro	Lys	Asp
385					390					395					400
Tyr	Val	Glu	Ile	Asn	Gly	Glu	Lys	Tyr	Cys	Gly	Glu	Arg	Ser	Gln	Phe
				405					410					415	
Val	Val	Thr	Ser	Asn	Ser	Asn	Lys	Ile	Thr	Val	Arg	Phe	His	Ser	Asp
			420					425					430		
Gln	Ser	Tyr	Thr	Asp	Thr	Gly	Phe	Leu	Ala	Glu	Tyr	Leu	Ser	Tyr	Asp
		435				440						445			
Ser	Ser	Asp	Arg	Cys	Asp	Ala	Gly	His	Gln	Phe	Thr	Cys	Lys	Asn	Lys
		450				455					460				
Phe	Cys	Lys	Pro	Leu	Phe	Trp	Val	Cys	Asp	Ser	Val	Asn	Asp	Cys	Gly
465					470					475					480
Asp	Asn	Ser	Asp	Glu	Gln	Gly	Cys	Met	Asn	Val	Val	Thr	Cys	Thr	Lys
			485						490				495		
His	Thr	Tyr	Arg	Cys	Leu	Asn	Gly	Leu	Cys	Leu	Ser	Lys	Gly	Asn	Pro
			500					505					510		
Glu	Cys	Asp	Gly	Lys	Glu	Asp	Cys	Ser	Asp	Gly	Ser	Asp	Glu	Lys	Asp
		515					520					525			
Cys	Asp	Cys	Gly	Leu	Arg	Ser	Phe	Thr	Arg	Gln	Ala	Arg	Val	Val	Gly
		530				535					540				
Gly	Thr	Asp	Ala	Asp	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Val	Ser	Leu	His
545					550					555					560
Ala	Leu	Gly	Gln	Gly	His	Ile	Cys	Gly	Ala	Ser	Leu	Ile	Ser	Pro	Asn
			565						570					575	
Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Tyr	Ile	Asp	Asp	Arg	Gly	Phe	Arg
			580					585					590		
Tyr	Ser	Asp	Pro	Thr	Gln	Trp	Thr	Ala	Phe	Leu	Gly	Leu	His	Asp	Gln
		595													

325

705		710		715		720
Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu						
		725		730		735
Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly Val Val Ser						
		740		745		750
Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val Tyr Thr Arg						
		755		760		765
Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly Val						
		770		775		780

<210> 313  
 <211> 2805  
 <212> DNA  
 <213> Homo sapiens

<400> 313

cgggtctgat	agtcacctacc	tgtcaggact	ggtgttagga	tgagataatg	tttgtgaact	60
gtaaaccatat	ataaacgtgt	gctactgtga	gaactggaac	aaagaagaga	gggagtgaga	120
gaaatcaagg	gagggctggg	gctgggaaag	aacgaaaagg	gagtcgcgta	tagaggagag	180
gcgacagtcg	cgagccacac	tttgcaatga	aactctttag	actttctgcc	gggagagcgg	240
cccagacgcg	ccaggtctgt	agcaggaggc	cgcgaggggc	ggtccccaga	agcctacagg	300
tgagtatcgg	ttctccctt	cccggctt	ggtccggagg	aggcgggagc	agcttccctg	360
ttctgatcct	atcgcgggcg	gcgcaggggc	ggcttggcct	tccgtgggac	ggggaggggg	420
gcgggatgtg	tcacccaaat	accagtggg	acggtcgggt	gtggaaccag	ccgggcaggt	480
cgggtagagt	ataagagccg	gagggagcgg	ccggggcgca	gacgcctgca	gaccatccca	540
gacgccggag	cccagagcccc	gacgagtc	cgcgccctcat	ccgcccgcgt	ccggtccgcg	600
ttcctccg	ccaccatggc	tcggggcccc	ggcctcgcc	cgccaccgct	gcggctgccg	660
ctgctgctgc	tggtgctggc	ggcggtgacc	ggccacacgg	ccgcgcagga	caactgcacg	720
tgtcccacca	acaagatgac	cgtgtgcagc	ccgcacggcc	ccggcgcccg	ctgccagtcg	780
cgcgcgctgg	gctcgggcat	ggcggtcgac	tgtccacgc	tgacctcaa	gtgtctgctg	840
ctcaaggcgc	gcatgagcgc	ccccaaagaac	gcccgcacgc	tggtgcggcc	gagtgcac	900
gcgctcgtgg	acaacgatgg	cctctacgac	ccgactgcg	accccgagg	ccgcttcaag	960
gcgcgccagt	gcaaccagac	gtcgggtgtg	tggtgcgtga	actcgggtgg	cgtgcgccgc	1020
acggacaagg	gcgacctgag	cctacgctgc	gatgagctgg	tgccgaccca	ccacatcctc	1080
attgacctgc	gccaccgccc	caccgcggc	gccttcaacc	actcagacct	ggacgccgag	1140
ctgaggcggc	tcttcgcgca	gcgctatcgg	ctgcaccca	agttcgtggc	ggccgtgcac	1200
tacgagcagc	ccaccatcca	gatcgagctg	cggcagaaca	cgtctcagaa	ggccgcgggt	1260
gaagtggata	tcggcgatgc	cgccactact	ttcgagagg	acatcaagg	cgagtctcta	1320
ttccagggcc	gcggcgccct	ggacttgcgc	gtgcgcggag	aaaccctgca	ggtggagcgc	1380
acgctcatct	attacctgga	cgagattccc	ccgaagtct	ccatgaagcg	cctcaccgcc	1440
ggcctcatcg	ccgtcatcgt	ggtggtcgtg	gtggccctcg	tcgccggcat	ggccgtcctg	1500
gtgatcacca	accggagaaa	gtcggggaag	tacaagaagg	tgagatcaa	ggaactggg	1560
gagttgagaa	aggaaccgag	cttgtaggta	ccggcgggg	caggggatgg	ggtgggttac	1620
cggatttcgg	tatcgtccca	gacccaagt	agtcacgctt	cctgattcct	cggcgcaaa	1680
gagacgttta	tcctttcaaa	ttcctgcctt	ccccctccct	tttgcgcaca	caccaggttt	1740
aatagatcct	ggcctcagg	tctccttct	ttctcacttc	tgtcttgagg	gaagcatttc	1800
taaaatgtat	cccctttcgg	tccaacaaca	ggaaacctga	ctggggcagt	gaaggaagg	1860
atggcacagc	gttatgtgta	aaaaacaagt	atctgtatga	caaccggga	tcgtttgcaa	1920
gtaactgaat	ccattgcgac	attgtgaagg	cttaaatgag	tttagatggg	aaatagcgtt	1980
gttatcgcct	tgggtttaaa	ttatttgatg	agttccactt	gtatcatggc	ctaccgagg	2040
agaagaggag	tttgtaact	gggcctatgt	agtagcctca	tttaccatcg	tttgtattac	2100
tgaccacata	tgcttgtcac	tggaagaa	gcctgtttca	gctgcctgaa	cgagtttg	2160
atgtctttga	ggacagacat	tgcccgaaa	ctcagtcctat	ttattcttca	gcttgcctt	2220
actgccactg	atattggtaa	tgctctttt	tgtaaaatgt	ttgtacatat	gttgtctttg	2280
ataatgttgc	tgtaattttt	taaaataaaa	cacgaattta	ataaaatag	ggaaaggcac	2340
aaaccagaag	tcggcatttg	tgaaaagtcc	ctccagattt	ctatcacttt	ggtctcta	2400
ttcccaagac	ttgtattttt	tttttatttc	aaattataac	actttttttt	cccccagaag	2460

326

```

tgggtgtttc atgttgctac tctgggtgtgt cccaagatat cctaactggc cagtgtaaat 2520
gctattcttt ctaaataaga ttatttgga acttccttca aactgcagga gggcgagctc 2580
tgagggcacg agaagctaaa actagctgct tttgatgaaa aagagtgcc gtctttggtc 2640
atctctaaac aaggcttata accaatggag acagaaaact ctagttcaag agctgtacct 2700
cctttgaatc ccagccctac tcgaaataag tgggtactatt tccatttagc ctttgagcaa 2760
atcacttaac tcaaaggcgt tgtggctcta agattaaacg acttt 2805

```

&lt;210&gt; 314

&lt;211&gt; 323

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 314

```

Met Ala Arg Gly Pro Gly Leu Ala Pro Pro Pro Leu Arg Leu Pro Leu
 1          5          10          15
Leu Leu Leu Val Leu Ala Ala Val Thr Gly His Thr Ala Ala Gln Asp
 20          25          30
Asn Cys Thr Cys Pro Thr Asn Lys Met Thr Val Cys Ser Pro Asp Gly
 35          40          45
Pro Gly Gly Arg Cys Gln Cys Arg Ala Leu Gly Ser Gly Met Ala Val
 50          55          60
Asp Cys Ser Thr Leu Thr Ser Lys Cys Leu Leu Leu Lys Ala Arg Met
 65          70          75          80
Ser Ala Pro Lys Asn Ala Arg Thr Leu Val Arg Pro Ser Glu His Ala
 85          90          95
Leu Val Asp Asn Asp Gly Leu Tyr Asp Pro Asp Cys Asp Pro Glu Gly
100          105          110
Arg Phe Lys Ala Arg Gln Cys Asn Gln Thr Ser Val Cys Trp Cys Val
115          120          125
Asn Ser Val Gly Val Arg Arg Thr Asp Lys Gly Asp Leu Ser Leu Arg
130          135          140
Cys Asp Glu Leu Val Arg Thr His His Ile Leu Ile Asp Leu Arg His
145          150          155          160
Arg Pro Thr Ala Gly Ala Phe Asn His Ser Asp Leu Asp Ala Glu Leu
165          170          175
Arg Arg Leu Phe Arg Glu Arg Tyr Arg Leu His Pro Lys Phe Val Ala
180          185          190
Ala Val His Tyr Glu Gln Pro Thr Ile Gln Ile Glu Leu Arg Gln Asn
195          200          205
Thr Ser Gln Lys Ala Ala Gly Glu Val Asp Ile Gly Asp Ala Ala Tyr
210          215          220
Tyr Phe Glu Arg Asp Ile Lys Gly Glu Ser Leu Phe Gln Gly Arg Gly
225          230          235          240
Gly Leu Asp Leu Arg Val Arg Gly Glu Pro Leu Gln Val Glu Arg Thr
245          250          255
Leu Ile Tyr Tyr Leu Asp Glu Ile Pro Pro Lys Phe Ser Met Lys Arg
260          265          270
Leu Thr Ala Gly Leu Ile Ala Val Ile Val Val Val Val Val Ala Leu
275          280          285
Val Ala Gly Met Ala Val Leu Val Ile Thr Asn Arg Arg Lys Ser Gly
290          295          300
Lys Tyr Lys Lys Val Glu Ile Lys Glu Leu Gly Glu Leu Arg Lys Glu
305          310          315          320
Pro Ser Leu

```

&lt;210&gt; 315



327

<211> 1142  
 <212> DNA  
 <213> Homo sapiens

<400> 315  
 gccgccagcg gctttctcgg acgccttgcc cagcggggccg cccgaccccc tgcaccatgg 60  
 accccgctcg cccctctggg ctgtcgattc tgctgctttt cctgacggag gctgcactgg 120  
 gcgatgctgc tcaggagcca acaggaaata acgcggagat ctgtctcctg cccctagact 180  
 acggaccctg ccggggcccta cttctccgtt actactacga caggtacacg cagagctgcc 240  
 gccagttcct gtacggggggc tgcgagggca acgccaacaa tttctacacc tgggaggctt 300  
 ggcacgatgc ttgctggagg atagaaaaag ttcccaaagt ttgcccggctg caagtgagtg 360  
 tggacgacca gtgtgagggg tccacagaaa agtatttctt taatctaagt tccatgacat 420  
 gtgaaaaatt cttttccggg ggggtgcacc ggaaccggat tgagaacagg tttccagatg 480  
 aagctacttg tatgggcttc tgcgcaccaa agaaaattcc atcattttgc tacagtccaa 540  
 aagatgaggg actgtgctct gccaatgtga ctgcgtatta ttttaattca agatacagaa 600  
 cctgtgatgc tttcacctat actggctgtg gaggggaatga caataacttt gttagcaggg 660  
 aggattgcaa acgtgcatgt gcaaaaagctt tgaaaaagaa aaagaagatg ccaaagcttc 720  
 gctttgccag tagaatccgg aaaattcggg agaagcaatt ttaaaccattc ttaatatgtc 780  
 atcttggttg tctttatggc ttatttgctt ttatgggtgt atctgaagaa taatatgaca 840  
 gcatgaggaa acaaatcatt ggtgatttat tcaccagttt ttattaatac aagtcacttt 900  
 ttcaaaaatt tggatttttt tatatataac tagctgctat tcaaattgtg gtctaccatt 960  
 ttttaatttat gggttcaactg tttgtgagac gaattcctgc aatgcataag atataaaagc 1020  
 aaatatgact cactcatttc ttggggctcg attcctgatt tcagaagagg atcataactg 1080  
 aaacaacata agacaatata atcatgtgct tttaacatat ttgagaataa aaaggactag 1140  
 cc 1142

<210> 316  
 <211> 235  
 <212> PRT  
 <213> Homo sapiens

<400> 316  
 Met Asp Pro Ala Arg Pro Leu Gly Leu Ser Ile Leu Leu Leu Phe Leu  
 1 5 10 15  
 Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn  
 20 25 30  
 Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu  
 35 40 45  
 Leu Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe  
 50 55 60  
 Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu  
 65 70 75 80  
 Ala Cys Asp Asp Ala Cys Trp Arg Ile Glu Lys Val Pro Lys Val Cys  
 85 90 95  
 Arg Leu Gln Val Ser Val Asp Asp Gln Cys Glu Gly Ser Thr Glu Lys  
 100 105 110  
 Tyr Phe Phe Asn Leu Ser Ser Met Thr Cys Glu Lys Phe Phe Ser Gly  
 115 120 125  
 Gly Cys His Arg Asn Arg Ile Glu Asn Arg Phe Pro Asp Glu Ala Thr  
 130 135 140  
 Cys Met Gly Phe Cys Ala Pro Lys Lys Ile Pro Ser Phe Cys Tyr Ser  
 145 150 155 160  
 Pro Lys Asp Glu Gly Leu Cys Ser Ala Asn Val Thr Arg Tyr Tyr Phe  
 165 170 175  
 Asn Pro Arg Tyr Arg Thr Cys Asp Ala Phe Thr Tyr Thr Gly Cys Gly  
 180 185 190  
 Gly Asn Asp Asn Asn Phe Val Ser Arg Glu Asp Cys Lys Arg Ala Cys  
 195 200 205

328

Ala Lys Ala Leu Lys Lys Lys Lys Lys Met Pro Lys Leu Arg Phe Ala  
 210 215 220  
 Ser Arg Ile Arg Lys Ile Arg Lys Lys Gln Phe  
 225 230 235

<210> 317  
 <211> 2307  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(2307)  
 <223> n = A,T,C or G

<400> 317  
 agtcgacccc gcgtccgggt ttaatcaagc tgcccaaagt cccccaatca ctccctggaat 60  
 acacagagag aggcagcagc ttgctcagcg gacaaggatg ctgggcgtga gggaccaagg 120  
 cctgccctgc actcgggcct cctccagcca gtgctgacca gggacttctg acctgctggc 180  
 cagccaggac ctgtgtgggg aggcctcct gctgccttg ggtagacaatc tcagctccag 240  
 gctacaggga gaccgggagg atcacagagc cagcatgtta caggatcctg acagtgatca 300  
 acctctgaac agcctcgatg tcaaaccct gcgcaaacc cgtatcccca tggagacctt 360  
 cagaaagggtg gggatcccca tcatcatagc actactgagc ctggcgagta tcatcattgt 420  
 ggttgctcctc atcaaagggtga ttctggataa atactacttc ctctgcgggc agcctctcca 480  
 cttcatcccg aggaagcagc tgtgtgacgg agagctggac tgtcccttg gggaggacga 540  
 ggagcactgt gtcaagagct tcccgaagg gcctgcagtg gcagtcggcc tctccaagga 600  
 ccgatccaca ctgcagggtgc tggactcggc cacagggaac tggttctctg cctgtttcga 660  
 caacttcaca gaagctctcg ctgagacagc ctgtaggcag atgggctaca gcagcaaac 720  
 cactttcaga gctgtggaga ttggccaga ccaggatctg gatgtgttg aaatcacaga 780  
 aaacagccag gagcttcgca tgcggaactc aagtgggccc tgtctctcag gctccctggt 840  
 ctccctgcac tgtcttgctt gtgggaagag cctgaagacc ccccggtgtg tgggtgggga 900  
 ggaggcctct gtggattctt ggccttggca ggtcagcatc cagtacgaca aacagcacgt 960  
 ctgtggaggg agcatcctgg acccccactg ggtcctcacg gcagcccact gcttcaggaa 1020  
 acataccgat gtgttcaact ggaagggtcg ggcagggtca gacaaactgg gcagcttccc 1080  
 atccctggct gtggccaaga tcatcatcat tgaattcaac cccatgtacc ccaaagacaa 1140  
 tgacatcgcc ctcatgaagc tgcagttccc actcatttc tcaggcacag tcaggcccat 1200  
 ctgtctgccc ttctttgatg aggaagctcac tccagccacc ccactctgga tcattggatg 1260  
 gggctttacg aagcagaatg gaggaagat gtctgacata ctgctgcagg cgtcagttcca 1320  
 ggtcattgac agcacacggt gcaatgcaga cgatgcgtac cagggggaag tcacccagaa 1380  
 gatgatgtgt gcaggcatcc cggaaggggg tgtggacacc tgccagggtg acagtgggtg 1440  
 gcccctgatg taccaatctg accagtggca tgtgggtggc atcgttagct ggggctatgg 1500  
 ctgcgggggc ccgagcaccc caggagtata caccaaggtc tcagcctatc tcaactggat 1560  
 ctacaatgtc tgggaaggctg agctgtaatg ctgctgcccc tttgcagtgc tgggagccgc 1620  
 ttcttctctg ccttgcccac ctggggatcc cccaaagtca gacacagagc aagagtcccc 1680  
 ttgggtacac nccctctngc ccacnagnnc ctncagnanc ttttcttngg agncagcaaa 1740  
 ngggcncntc aattncctgt aagagacccn tcgncagccc agaggcgccc nagagggaag 1800  
 cnagcagccc tagctcggcc nacacttggg gctcccangc atcccaggga gagacnacna 1860  
 gccnactga acaagggtctc aggggtattg ctaagccaag aaggaaactt tcccacacta 1920  
 ctgaatggaa gcaggctgtc ttgtaaaagc ccagatcanc tgtgggctgg agaggagaag 1980  
 gaaagggctc gcgccangcc ctgtccgtct tncacccatc cccaagccta ctagagcnaa 2040  
 gaaaccagtt gtaatatata atgcaactgcc ctactgttgg tatgactacc gttacctact 2100  
 gttgtcattg ttattacagc tatggccact attattaaag agnctgtgta acatcaaaaa 2160  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa ataaataaaa aaaaactcga gggggggccc 2220  
 gttacccaat tcgccctata gtgagtcgta ttacaattca ctggccgtcg ttttacaacg 2280  
 tcgtgactgg gaaaaccctg gcgttac 2307

<210> 318

329

&lt;211&gt; 428

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 318

```

Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp Val
 1          5          10          15
Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg Lys Val
          20          25          30
Gly Ile Pro Ile Ile Ile Ala Leu Ser Leu Ala Ser Ile Ile Ile
 35          40          45
Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr Tyr Phe Leu Cys
 50          55          60
Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln Leu Cys Asp Gly Glu
 65          70          75          80
Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu His Cys Val Lys Ser Phe
          85          90          95
Pro Glu Gly Pro Ala Val Ala Val Arg Leu Ser Lys Asp Arg Ser Thr
 100          105          110
Leu Gln Val Leu Asp Ser Ala Thr Gly Asn Trp Phe Ser Ala Cys Phe
 115          120          125
Asp Asn Phe Thr Glu Ala Leu Ala Glu Thr Ala Cys Arg Gln Met Gly
 130          135          140
Tyr Ser Ser Lys Pro Thr Phe Arg Ala Val Glu Ile Gly Pro Asp Gln
 145          150          155          160
Asp Leu Asp Val Val Glu Ile Thr Glu Asn Ser Gln Glu Leu Arg Met
          165          170          175
Arg Asn Ser Ser Gly Pro Cys Leu Ser Gly Ser Leu Val Ser Leu His
          180          185          190
Cys Leu Ala Cys Gly Lys Ser Leu Lys Thr Pro Arg Val Val Gly Gly
 195          200          205
Glu Glu Ala Ser Val Asp Ser Trp Pro Trp Gln Val Ser Ile Gln Tyr
 210          215          220
Asp Lys Gln His Val Cys Gly Gly Ser Ile Leu Asp Pro His Trp Val
 225          230          235          240
Leu Thr Ala Ala His Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp
          245          250          255
Lys Val Arg Ala Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala
 260          265          270
Val Ala Lys Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp
 275          280          285
Asn Asp Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly
 290          295          300
Thr Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro
 305          310          315          320
Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn Gly
          325          330          335
Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val Ile Asp
 340          345          350
Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu Val Thr Glu
 355          360          365
Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val Asp Thr Cys Gln
 370          375          380
Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser Asp Gln Trp His Val
 385          390          395          400
Val Gly Ile Val Ser Trp Gly Tyr Gly Cys Gly Gly Pro Ser Thr Pro
          405          410          415
Gly Val Tyr Thr Lys Val Ser Ala Tyr Leu Asn Trp

```

420

425

<210> 319  
<211> 3529  
<212> DNA  
<213> Homo sapiens

&lt;400&gt; 319

atgattgaag	acaataagga	gaacaaagac	cattccttag	aaaggggaag	agcaagtctc	60
atTTTTTcct	taaagaatga	agttggagga	cttataaaaag	ccctgaaaat	ctttcaggag	120
aagcatgtga	atctgtttaca	tatcgagtc	cgaaaatcaa	aaagaagaaa	ctcagaattt	180
gagatTTTTg	ttgactgtga	catcaacaga	gaacaattga	atgataTTTT	tcatctgctg	240
aagtctcata	ccaatgttct	ctctgtgaat	ctaccagata	atTTTacttt	gaaggaagat	300
ggtatggaaa	ctgttccttg	gtttccaaag	aagatttctg	acctggacca	ttgtgccaac	360
agagttctga	tgtatggatc	tgaactagat	gcagaccatc	ctggcttcaa	agacaatgtc	420
taccgtaaac	gtcgaaagta	TTTTgcggac	ttggctatga	actataaaca	tggagacccc	480
attccaaagg	ttgaattcac	tgaagaggag	attaagacct	ggggaaccgt	attccaagag	540
ctcaacaaac	tctacccaac	ccatgcttgc	agagagtatc	tcaaaaactt	acctttgctt	600
tctaaatatt	gtggatatcg	ggaggataat	atcccacaat	tggaagatgt	ctccaacttt	660
ttaaaagagc	gtacaggttt	ttccatccgt	cctgtggctg	gttacttatc	accaagagat	720
ttcttatcag	gttttagcct	tcgagttttt	cactgcactc	aatatgtgag	acacagttca	780
gatcccttct	ataccccaga	gccagatacc	tgccatgaac	tcttaggtca	tgtcccgtt	840
ttggctgaac	ctagttttgc	ccaattctcc	caagaaattg	gcttggcttc	tcttggcgct	900
tcagaggagg	ctgttcaaaa	actggcaacg	tgctactttt	tcactgtgga	gtttgggtcta	960
tgtaaacaaag	atggacagct	aagagtcttt	ggtgctggct	tactttcttc	tatcagtga	1020
ctcaaacatg	cactttctgg	acatgccaaa	gtaaagccct	ttgatcccaa	gattacctgc	1080
aaacaggaat	gtcttatcac	aacttttcaa	gatgtctact	ttgtatctga	aagttttgaa	1140
gatgcaaagg	agaagatgag	agaatttacc	aaaacaatta	agcgtccatt	tggagtgaag	1200
tataatccat	atacacggag	tattcagatc	ctgaaagaca	ccaagagcat	aaccagtgc	1260
atgaatgagc	tcgacgatga	tctcgatgtt	gtcagtgatg	cccttgctaa	ggtcagcagg	1320
aagccgagta	tctaatact	aaatgaagat	gttcttcaag	tttctgtctt	tgcacttcta	1380
ctctttttgc	catctcttca	tggggaatgt	caccagata	catgacttca	gttcttattt	1440
tgaatgactc	ctctatttgc	agttataacc	ctgacatctt	tcttgaattt	ttttgcccct	1500
taattccaac	gaactcctgg	atgtctatgt	agatgtctca	taatttaggc	caatgctgta	1560
caacttcatg	tggcatcatc	cacatagaat	gaataggggt	tgttcaatat	gacagccctg	1620
ccaagcatct	caaattgaac	aggtctataa	aggaactcag	aatcacttga	atatcacagt	1680
ccatcagctt	cctttcccag	taatttaatt	tccattaatg	gtatattaaa	catcgtattt	1740
tcaatcattt	ttaggtttag	tcagctactt	aaaaataggc	tttttcttca	cataaataaa	1800
ttgtatacca	tttaattgtg	tttatttcaa	cagactaata	gatcttttaa	cacttcttag	1860
tcctcaaaat	aaattattaa	aaactttgta	tttcatgtca	tattatataa	ggaaatagaa	1920
ttttgaagaa	taattcatgc	tgttttaaat	ttttacattg	tacattttta	tagctaataca	1980
actcttaagt	atacatttga	tggtaaatag	atgctagcta	atctagaatc	atttgaaata	2040
ttgattatct	gatttatagt	ttggttgcaa	ggaaatctac	tgtaagcaaa	tcataataga	2100
tagcaaatct	tagaacatgt	agaaaaaag	aaattaaaaa	aagcaaatct	tagaacatgt	2160
agaaaaagga	aattdaaaaa	tagatagcaa	ataacacaaa	ttatgcatac	tatatatggt	2220
tattttcata	caactttgat	aacggtgaag	aatcatactt	attgaatttt	aaaatgatga	2280
tgtttaaaat	cactctatga	ctaaagcaca	tggaataaaa	tgtaaaggc	acagccttat	2340
aatccacaac	ttcagaacaa	tggaaatttt	tttttttttt	tttttttttt	tttttttttt	2400
tttttttgag	acggagtctt	gctctgtcgc	ccaggctgga	gtgcagtggt	gcatcttgg	2460
ctcactgcaa	gctccacctc	ccaggttcac	ggcatttctc	tgctctgtc	tcctgagtag	2520
ctgggactac	aggcgccgc	caccacgtcc	ggctcatttt	ttgtattttt	agtagagaca	2580
aggtttcacc	gtgttagcca	ggatggtttc	aatctcctga	cattgtgatc	tgccacctc	2640
ggcctcccaa	agtgtctgga	ttacaggcgt	gagccactgc	acccggccaa	acattggaaa	2700
tttttaatat	tggatttcag	ttcttctcac	ctctgggtat	ttgtaatat	tggtaaatca	2760
ggagtctga	gagtcttaga	atttcatgc	attttaataa	tatgtcttca	aagcacctag	2820
gaatatgtaa	atagttaccc	aaatgtgaga	acagaattga	actaaaagct	tcgtttataa	2880
tttttttttt	tttgagacag	agtctcactc	tgttgccag	gctggagcgc	agttgcgtga	2940

331

```

tttcagctcg ctgcaacctg ggactgcagg cgtgcttcac catgccccgc taatttttgt 3000
tttttttagta gagatggggg ttcgccatgt tggccaggct ggtctcgaac ttctgaccgc 3060
aggatgatcca tccgcctcgg cctcccaaaag tgctgggatt acaagcatga gccaccatgc 3120
ccagccgggtt aataattctt aatcagtaaa tcattattca aagacatagt taatatcttc 3180
atgacttctt aaggatgctc aaaagctggt cttcagaata cctacatttc tttatctaca 3240
tattctgtca tttggagtta tacaagtagt aatgacacac caaaatgtaa ataattattg 3300
ttagctttta agttggcttc caaattcaaa aaagaaaaaa atcctgaatt ctctaaagga 3360
acatatgata gattccatat gttaattcat aggaagtgtt taaggtaacta tgggtctattt 3420
tgggtctaata tttgttttac tatgtaatat atatttatga ttacaagtt tggtattcag 3480
tgggataata aatgaacaca aaatttaaaa aaaaaaaaaa aaataaaaaa 3529

```

&lt;210&gt; 320

&lt;211&gt; 444

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 320

```

Met Ile Glu Asp Asn Lys Glu Asn Lys Asp His Ser Leu Glu Arg Gly
1      5      10      15
Arg Ala Ser Leu Ile Phe Ser Leu Lys Asn Glu Val Gly Gly Leu Ile
20     25     30
Lys Ala Leu Lys Ile Phe Gln Glu Lys His Val Asn Leu Leu His Ile
35     40     45
Glu Ser Arg Lys Ser Lys Arg Arg Asn Ser Glu Phe Glu Ile Phe Val
50     55     60
Asp Cys Asp Ile Asn Arg Glu Gln Leu Asn Asp Ile Phe His Leu Leu
65     70     75     80
Lys Ser His Thr Asn Val Leu Ser Val Asn Leu Pro Asp Asn Phe Thr
85     90     95
Leu Lys Glu Asp Gly Met Glu Thr Val Pro Trp Phe Pro Lys Lys Ile
100    105    110
Ser Asp Leu Asp His Cys Ala Asn Arg Val Leu Met Tyr Gly Ser Glu
115    120    125
Leu Asp Ala Asp His Pro Gly Phe Lys Asp Asn Val Tyr Arg Lys Arg
130    135    140
Arg Lys Tyr Phe Ala Asp Leu Ala Met Asn Tyr Lys His Gly Asp Pro
145    150    155    160
Ile Pro Lys Val Glu Phe Thr Glu Glu Glu Ile Lys Thr Trp Gly Thr
165    170    175
Val Phe Gln Glu Leu Asn Lys Leu Tyr Pro Thr His Ala Cys Arg Glu
180    185    190
Tyr Leu Lys Asn Leu Pro Leu Leu Ser Lys Tyr Cys Gly Tyr Arg Glu
195    200    205
Asp Asn Ile Pro Gln Leu Glu Asp Val Ser Asn Phe Leu Lys Glu Arg
210    215    220
Thr Gly Phe Ser Ile Arg Pro Val Ala Gly Tyr Leu Ser Pro Arg Asp
225    230    235    240
Phe Leu Ser Gly Leu Ala Phe Arg Val Phe His Cys Thr Gln Tyr Val
245    250    255
Arg His Ser Ser Asp Pro Phe Tyr Thr Pro Glu Pro Asp Thr Cys His
260    265    270
Glu Leu Leu Gly His Val Pro Leu Leu Ala Glu Pro Ser Phe Ala Gln
275    280    285
Phe Ser Gln Glu Ile Gly Leu Ala Ser Leu Gly Ala Ser Glu Glu Ala
290    295    300
Val Gln Lys Leu Ala Thr Cys Tyr Phe Phe Thr Val Glu Phe Gly Leu
305    310    315    320
Cys Lys Gln Asp Gly Gln Leu Arg Val Phe Gly Ala Gly Leu Leu Ser

```

332

			325					330				335			
Ser	Ile	Ser	Glu	Leu	Lys	His	Ala	Leu	Ser	Gly	His	Ala	Lys	Val	Lys
			340					345				350			
Pro	Phe	Asp	Pro	Lys	Ile	Thr	Cys	Lys	Gln	Glu	Cys	Leu	Ile	Thr	Thr
			355				360				365				
Phe	Gln	Asp	Val	Tyr	Phe	Val	Ser	Glu	Ser	Phe	Glu	Asp	Ala	Lys	Glu
			370				375				380				
Lys	Met	Arg	Glu	Phe	Thr	Lys	Thr	Ile	Lys	Arg	Pro	Phe	Gly	Val	Lys
			385			390			395					400	
Tyr	Asn	Pro	Tyr	Thr	Arg	Ser	Ile	Gln	Ile	Leu	Lys	Asp	Thr	Lys	Ser
			405					410					415		
Ile	Thr	Ser	Ala	Met	Asn	Glu	Leu	Gln	His	Asp	Leu	Asp	Val	Val	Ser
			420					425					430		
Asp	Ala	Leu	Ala	Lys	Val	Ser	Arg	Lys	Pro	Ser	Ile				
			435				440								

&lt;210&gt; 321

&lt;211&gt; 3505

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 321

```

atgattgaag acaataagga gaacaaagac cattccttag aaaggggaag agcaagtctc 60
attttttcct taaagaatga agttggagga cttataaaag ccctgaaaat ctttcaggag 120
aagcatgtga atctgtttaca tatcgagtcc cgaaaatcaa aaagaagaaa ctcagaattt 180
gagatTTTTg ttgactgtga catcaacaga gaacaattga atgatatttt tcatctgctg 240
aagtctcata ccaatgttct ctctgtgaat ctaccagata attttacttt gaaggaagat 300
ggtatggaaa ctgttccttg gttccaaag aagatttctg acctggacca ttgtgccaac 360
agagttctga tgtatggatc tgaactagat gcagaccatc ctggcttcaa agacaatgtc 420
taccgtaaac gtcgaaagta tttgctgac ttggctatga actataaaca tggagacccc 480
attccaaagg ttgaattcac tgaagaggag attaagacct ggggaaccgt attccaagag 540
ctcaacaac tctacccaac ccatgcttgc agagagtatc tcaaaaactt acctttgctt 600
tctaaatatt gtggatatcg ggaggataat atcccacaat tggaagatgt ctccaacttt 660
ttaaagagc gtacaggttt ttccatccgt cctgtggctg gttacttate accaagagat 720
ttcttatcag gtttagcctt tcgagttttt cactgcactc aatatgtgag acacagtcca 780
gatcccttct ataccccaga gccagatacc tgccatgaac tcttaggtca tgtcccgctt 840
ttggctgaac ctagttttgc ccaattctcc caagaaattg gcttggcttc tcttggcgct 900
tcagaggagg ctgttcaaaa actggcaacg tgctactttt tcaactgtgga gtttggctta 960
tgtaacaag atggacagct aagagtcttt ggtgctggct tactttcttc tatcagtga 1020
ctcaaacatg cactttcttg acatgccaaa gtaaagccct ttgatcccaa gattacctgc 1080
aaacaggaat gtcttatcac aacttttcaa gatgtctact ttgtatctga aagttttgaa 1140
gatgcaaagg agaagatgag agaatttacc aaaacaatta agcgtocatt tggagtgaag 1200
tataatccat atacacggag tattcagatc ctgaaagaca ccaagagcat aaccagtgcc 1260
atgaatgagc tgcagcatga tctcgatgtt gtcagtgatg cccttgctaa gtcactaaat 1320
gaagatgttc ttcaagtttc tgtctttgca cttctactct ttttgccatc tcttcattgg 1380
gaatgtcacc cagatacatg acttcagttc ttattttgaa tgactcctct atttgcagtt 1440
ataacctga catctttctt gaattttttt gcccttaaat tccaacgaac tcctggatgt 1500
ctatgtagat gtctcataat ttaggccaat gctgtacaac ttcatgtggc atcatccaca 1560
tagaatgaat aggggttggt caatatgaca gccctgcaa gcactcctcaa ttgaacaggt 1620
ctataaagga actcagaatc acttgaatat cacagtccat cagcttcctt tcccagtaat 1680
ttaatttcca ttaattggtat attaaacatc gtattttcaa tcatttttag gtttagtcag 1740
ctacttaaaa ataggctttt tcttcacata aataaattgt ataccattta atgtgtttta 1800
tttcaacaga ctaatagatc ttttaacact tcttagtctt caaaataaat tattaataac 1860
tttgtatttc atgtcatatt atataaggaa atagaatttt gaagaataat tcatgctgtt 1920
ttaaattttt acattgtaca ttttaatagc taatcaactc ttaagtatac atttgatggt 1980
aaatagatgc tagctaattc agaatcattt gaaatattga ttatctgatt tatagtttgg 2040
ttgcaaggaa atctactgta agcaaatcat aatagatagc aaatcttaga acatgtagaa 2100

```

333

```

aaaaagaaat taaaaaaagc aaatcttaga acatgtagaa aaaggaaatt aaaaaataga 2160
tagcaaataa cacaaattat gcatactata tatggttatt ttcatacaac tttgataacg 2220
gtgaagaatc atacttattg aattttaaaa tgatgatgtt taaaatcact ctatgactaa 2280
agcacatgag aataaatgtt aaaggcacag ccttataatc cacaacttca gaacaatgga 2340
atTTTTTTTT tTTTTTTTTT tTTTTTTTTT tTTTTTTTTT tttgagacgg agtcttgctc 2400
tgTgGcccag gctggagtgc agtggtgcga tcttggtcga ctgcaagctc cacctcccag 2460
gttcacggca ttctctgcc tctgtctcct gagtagctgg gactacaggc gcccgccacc 2520
acgtccggct cattttttgt attttttagta gagacaaggT ttcaccgtgt tagccaggat 2580
ggtttcaatc tcctgacatt gtgatctgcc cacctcggcc tcccaaagtG ctgggattac 2640
aggcgtgagc cactgcaccc ggccaaacat tggaattttt taatgatgga tttcagttct 2700
tctcacctct gggatattgt aatatttggt aaatcaggag tcctgagagt cttagaattt 2760
tcatgcattt taaatatatg tcttcaaagc acctaggaat atgtaaatag ttacccaaat 2820
gtgagaacag aattgaacta aaagcttcgt ttataatttt tttttttttg agacagagtc 2880
tactctgtt gcccgagctg gagcgagctt gcgtgatttc agctcgctgc aacctgggac 2940
tgcaggcgtg cttaccatg ccccgctaatt ttttgTTTTT ttagtagaga tggggtttcg 3000
ccatgttggc caggctggtc tcgaacttct gaccgcaggt gatccatccg cctcggcctc 3060
ccaaagtgct gggattacaa gcatgagcca ccatgccagc ccggttaata attcttaatc 3120
agtaaatacat tattcaaaga catagttaat atcttcatga cttcttaagg atgctcaaaa 3180
gctggctctc agaataccta catttcttta tctacatatt ctgtcatttg gagttatata 3240
agtagtaatg acacaccaaa atgtaaataa ttattgtagt cttttaagtt ggcttccaaa 3300
ttcaaaaaag aaaaaaatcc tgaattctct aaaggaacat atgatagagt ccatatgtta 3360
attcatagga agtgtttaag gtactatggt ctattttggt ctaatctttg ttttactatg 3420
taatatatat ttatgattta caagtttggt attcagtggtg ataataaatg aacacaaaat 3480
ttaaaaaaaa aaaaaaaat aaaaa 3505

```

&lt;210&gt; 322

&lt;211&gt; 466

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 322

```

Met Ile Glu Asp Asn Lys Glu Asn Lys Asp His Ser Leu Glu Arg Gly
  1             5             10             15
Arg Ala Ser Leu Ile Phe Ser Leu Lys Asn Glu Val Gly Gly Leu Ile
      20             25             30
Lys Ala Leu Lys Ile Phe Gln Glu Lys His Val Asn Leu Leu His Ile
      35             40             45
Glu Ser Arg Lys Ser Lys Arg Arg Asn Ser Glu Phe Glu Ile Phe Val
      50             55             60
Asp Cys Asp Ile Asn Arg Glu Gln Leu Asn Asp Ile Phe His Leu Leu
      65             70             75             80
Lys Ser His Thr Asn Val Leu Ser Val Asn Leu Pro Asp Asn Phe Thr
      85             90             95
Leu Lys Glu Asp Gly Met Glu Thr Val Pro Trp Phe Pro Lys Lys Ile
      100            105            110
Ser Asp Leu Asp His Cys Ala Asn Arg Val Leu Met Tyr Gly Ser Glu
      115            120            125
Leu Asp Ala Asp His Pro Gly Phe Lys Asp Asn Val Tyr Arg Lys Arg
      130            135            140
Arg Lys Tyr Phe Ala Asp Leu Ala Met Asn Tyr Lys His Gly Asp Pro
      145            150            155            160
Ile Pro Lys Val Glu Phe Thr Glu Glu Glu Ile Lys Thr Trp Gly Thr
      165            170            175
Val Phe Gln Glu Leu Asn Lys Leu Tyr Pro Thr His Ala Cys Arg Glu
      180            185            190
Tyr Leu Lys Asn Leu Pro Leu Leu Ser Lys Tyr Cys Gly Tyr Arg Glu
      195            200            205
Asp Asn Ile Pro Gln Leu Glu Asp Val Ser Asn Phe Leu Lys Glu Arg

```

334

210	215	220
Thr Gly Phe Ser Ile Arg	Pro Val Ala Gly Tyr	Leu Ser Pro Arg Asp
225	230	235
Phe Leu Ser Gly Leu Ala	Phe Arg Val Phe His	Cys Thr Gln Tyr Val
245	250	255
Arg His Ser Ser Asp Pro	Phe Tyr Thr Pro Glu	Pro Asp Thr Cys His
260	265	270
Glu Leu Leu Gly His Val	Pro Leu Leu Ala Glu	Pro Ser Phe Ala Gln
275	280	285
Phe Ser Gln Glu Ile Gly	Leu Ala Ser Leu Gly	Ala Ser Glu Glu Ala
290	295	300
Val Gln Lys Leu Ala Thr	Cys Tyr Phe Phe Thr	Val Glu Phe Gly Leu
305	310	315
Cys Lys Gln Asp Gly Gln	Leu Arg Val Phe Gly	Ala Gly Leu Leu Ser
325	330	335
Ser Ile Ser Glu Leu Lys	His Ala Leu Ser Gly	His Ala Lys Val Lys
340	345	350
Pro Phe Asp Pro Lys Ile	Thr Cys Lys Gln Glu	Cys Leu Ile Thr Thr
355	360	365
Phe Gln Asp Val Tyr Phe	Val Ser Glu Ser Phe	Glu Asp Ala Lys Glu
370	375	380
Lys Met Arg Glu Phe Thr	Lys Thr Ile Lys Arg	Pro Phe Gly Val Lys
385	390	395
Tyr Asn Pro Tyr Thr Arg	Ser Ile Gln Ile Leu	Lys Asp Thr Lys Ser
405	410	415
Ile Thr Ser Ala Met Asn	Glu Leu Gln His Asp	Leu Asp Val Val Ser
420	425	430
Asp Ala Leu Ala Lys Ser	Leu Asn Glu Asp Val	Leu Gln Val Ser Val
435	440	445
Phe Ala Leu Leu Leu Phe	Leu Pro Ser Leu His	Gly Glu Cys His Pro
450	455	460
Asp Thr		
465		

&lt;210&gt; 323

&lt;211&gt; 1154

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 323

```

cacgagggcg tccctctgcc tgcccactca gtggcaacac ccgggagctg ttttgcctt 60
tgtggagcct cagcagttcc ctctttcaga actcactgcc aagagccctg aacaggagcc 120
accatgcagt gcttcagctt cattaagacc atgatgatcc tcttcaattt gctcatcttt 180
ctgtgtggtg cagccctgtt ggcagtgggc atctgggtgt caatcgatgg ggcacccctt 240
ctgaagatct tcgggccact gtcgtccagt gccatgcagt ttgtcaacgt gggctacttc 300
ctcatcgag ccggcgttgt ggtctttgct cttgggttcc tgggctgcta tgggtgtaag 360
actgagagca agtgtgccct cgtgacgttc ttcttcatcc tctcctcat cttcattgct 420
gaggttgcag ctgctgtggt cgccttggtg tacaccacaa tggctgagca cttcctgacg 480
ttgctggtag tgccctgccat caagaaagat tatgggtccc aggaagactt cactcaagtg 540
tggaacacca ccatgaaagg gctcaagtgc tgtggcttca ccaactatac ggattttgag 600
gactcaccct acttcaaaga gaacagtgcc tttcccccct tctgttgcaa tgacaacgtc 660
accaacacag ccaatgaaac ctgcaccaag caaaaggctc acgacaaaaa agtagagggt 720
tgcttcaatc agcttttgta tgacatccga actaatgcag tcaccgtggg tgggtgtggc 780
gctggaattg ggggocctga gttcttttcc aactcagctc gaaggccacc tcttccagaa 840
agcctctata gcactcccat cagaagagat cagctcttcc tacaaccctc ccctccatga 900
ctttcatggc tcttagagcc tctgctgtct ctgcttcatc ctggaagtat cacaatcctc 960
caccacactg aaccctcaa ggtagggccca ggtctgatta ctttcaggctc cccagtgtcc 1020

```



335

agcacaaggc tgaggccaaa aaaaggacca ggggatggtt ataaaataaa tcaatgaatt 1080  
 gactgcctaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gaaaaaaaaa 1140  
 aaaaaaaaaa aagt 1154

&lt;210&gt; 324

&lt;211&gt; 258

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 324

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu  
 1 5 10 15  
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val  
 20 25 30  
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser  
 35 40 45  
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly  
 50 55 60  
 Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr  
 65 70 75 80  
 Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile  
 85 90 95  
 Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr  
 100 105 110  
 Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys  
 115 120 125  
 Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met  
 130 135 140  
 Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp  
 145 150 155 160  
 Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn  
 165 170 175  
 Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala  
 180 185 190  
 His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile  
 195 200 205  
 Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly  
 210 215 220  
 Leu Glu Phe Phe Ser Asn Ser Ala Arg Arg Pro Pro Leu Pro Glu Ser  
 225 230 235 240  
 Leu Tyr Ser Thr Pro Ile Arg Arg Asp His Val Phe Leu Gln Pro Ser  
 245 250 255  
 Pro Pro

&lt;210&gt; 325

&lt;211&gt; 1076

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 325

atgcagtgtc tcagcttcat taagaccatg atgacccctc tcaatttgct catctttctg 60  
 tgtggtgcag ccctgttggc agtgggcatc tgggtgtcaa tcgatggggc atcctttctg 120  
 aagatcttcg ggccactgtc gtccagtgtc atgcagtgtg tcaacgtggg ctacttcctc 180  
 atcgagcccg gcgttgtggt ctttgctctt ggtttcctgg gctgctatgg tgctaagact 240  
 gagagcaagt gtgcctcgt gacgttcttc ttcacccctc tcctcatctt cattgctgag 300  
 gttgcagctg ctgtggtcgc cttggtgtac accacaatgg ctgagcactt cctgacgttg 360

336

ctggtagtgc ctgccatcaa gaaagattat ggttcccagg aagacttcac tcaagtgtgg 420  
 aacaccacca tgaaagggct caagtgcgtg ggcttcacca actatacggg ttttgaggac 480  
 tcaccctact tcaaagagaa cagtgccttt cccccattct gttgcaatga caacgtcacc 540  
 aacacagcca atgaaacctg caccgagcaa aaggctcacg accaaaaagt agagggttgc 600  
 ttcaatcagc ttttgtatga catccgaact aatgcagtca ccgtgggtgg tgtggcagct 660  
 ggaattgggg gcctcgagct ggctgccatg attgtgtcca tgtatctgta ctgcaatcta 720  
 caataagtcc acttctgcct ctgccactac tgctgccaca tgggaactgt gaagaggcac 780  
 cctggcaagc agcagtgtat gggggagggg acaggatcta acaatgtcac ttgggccaga 840  
 atggacctgc cctttctgct ccagacttgg ggctagatag ggaccactcc ttttaggcga 900  
 tgctgacttt ccttccattg gtgggtggat ggggtggggg cattccagag cctctaaggt 960  
 agccagttct gttgccatt cccccagctc attaaaccct tgatatgcc cctaggccta 1020  
 gtggtgatcc cagtgtctta ctgggggatg agagaaaggc attttatagc ctgggc 1076

&lt;210&gt; 326

&lt;211&gt; 241

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 326

Met	Gln	Cys	Phe	Ser	Phe	Ile	Lys	Thr	Met	Met	Ile	Leu	Phe	Asn	Leu
1				5					10					15	
Leu	Ile	Phe	Leu	Cys	Gly	Ala	Ala	Leu	Leu	Ala	Val	Gly	Ile	Trp	Val
			20					25					30		
Ser	Ile	Asp	Gly	Ala	Ser	Phe	Leu	Lys	Ile	Phe	Gly	Pro	Leu	Ser	Ser
		35					40					45			
Ser	Ala	Met	Gln	Phe	Val	Asn	Val	Gly	Tyr	Phe	Leu	Ile	Ala	Ala	Gly
	50					55					60				
Val	Val	Val	Phe	Ala	Leu	Gly	Phe	Leu	Gly	Cys	Tyr	Gly	Ala	Lys	Thr
65					70				75					80	
Glu	Ser	Lys	Cys	Ala	Leu	Val	Thr	Phe	Phe	Phe	Ile	Leu	Leu	Leu	Ile
				85				90						95	
Phe	Ile	Ala	Glu	Val	Ala	Ala	Ala	Val	Val	Ala	Leu	Val	Tyr	Thr	Thr
			100					105					110		
Met	Ala	Glu	His	Phe	Leu	Thr	Leu	Leu	Val	Val	Pro	Ala	Ile	Lys	Lys
		115					120					125			
Asp	Tyr	Gly	Ser	Gln	Glu	Asp	Phe	Thr	Gln	Val	Trp	Asn	Thr	Thr	Met
	130					135					140				
Lys	Gly	Leu	Lys	Cys	Cys	Gly	Phe	Thr	Asn	Tyr	Thr	Asp	Phe	Glu	Asp
145				150						155				160	
Ser	Pro	Tyr	Phe	Lys	Glu	Asn	Ser	Ala	Phe	Pro	Pro	Phe	Cys	Cys	Asn
				165				170					175		
Asp	Asn	Val	Thr	Asn	Thr	Ala	Asn	Glu	Thr	Cys	Thr	Glu	Gln	Lys	Ala
		180						185					190		
His	Asp	Gln	Lys	Val	Glu	Gly	Cys	Phe	Asn	Gln	Leu	Leu	Tyr	Asp	Ile
	195						200					205			
Arg	Thr	Asn	Ala	Val	Thr	Val	Gly	Gly	Val	Ala	Ala	Gly	Ile	Gly	Gly
	210					215					220				
Leu	Glu	Leu	Ala	Ala	Met	Ile	Val	Ser	Met	Tyr	Leu	Tyr	Cys	Asn	Leu
225					230					235					240
Gln															

&lt;210&gt; 327

&lt;211&gt; 2244

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

337

&lt;400&gt; 327

```

gggaaggaga tgcctcttcc ttcccttcaa tagtgggtta aaccagctg gcaccctctg 60
gaactacggg aacaatattc ttcaagagaa ggtaactcta ccaaagccag gagcacagta 120
ttctcaggat ctcaacaagg aagagcagac caagggttget tctgattcct tacaaccttc 180
cgtaattcca ggcttgtggc cccaaattca gggccccacc cttccaggaa caaatcatta 240
tagtaataat ttgccttcat cttccatata ccaactaagc atgtttaact acgaacgtcc 300
aaaacacttc atccagtcct aaaacccatg tggctccaga ttgcagcctc ctggaccaga 360
aacctccagc ttctctagcc agaccaaaca gtcttccatt atcatccagc cccgccagtg 420
tacagagcaa agattttctg cctcctcaac actgagctct cacatcacca tgtcctcctc 480
tgctttccct gcttctcccc agcagcatgc tggctccaac ccaggccaaa gggttacaac 540
cagctataac cagtcctccag ccagcttcct cagctccata ttaccatcac agcctgatta 600
caatagcagt aaaatccctt ccgctatgga ttccaactat caacagtcct cagctggcca 660
acctataaat gcaaagccat cccaaactgc aaatgctaag ccataccaa gaactcctga 720
tcatgaaata caaggatcaa aagaagcttt gattcaagat ttggaaagaa agctgaaatg 780
caaggacacc cttcttcata atggaaatca acgtctaaca tatgaagaga agatggctcg 840
cagattgcta ggaccacaga atgcagctgc tgtgtttcaa gctcaggatg acagtggctg 900
acaagactcg cagcaacaca actcagaaca tgcgcgactg caagttccta catcacaagt 960
aagaagtaga tcaacctcaa ggggagatgt gaatgatcag gatgcaatcc aggagaaatt 1020
ttaccaccca cgtttcattc aagtgccaga gaacatgtcg attgatgaag gaagattctg 1080
cagaatggac ttcaaagtga gtggactgcc agctcctgat gtgtcatggt atctaaatgg 1140
aagaacagtt caatcagatg atttgcaaa aatgatagtg tctgagaagg gtcttcattc 1200
actcatcttt gaagtagtca gagcttcaga tgcaggggct tatgcatgtg ttgccaaagaa 1260
tagagcagga gaagccacct tcaactgtgca gctggatgtc cttgcaaaag aacataaaag 1320
agcaccaatg tttatctaca aaccacagag caaaaaagtt ttagagggag attcagtga 1380
actagaatgc cagatctcgg ctatacctcc accaaagctt ttctggaaaa gaaataatga 1440
aatggtacaa ttcaacactg accgaataag cttatatcaa gataacactg gaagagtac 1500
tttactgata aaagatgtaa acaagaaaga tgcctgggtg tatactgtgt cagcagttaa 1560
tgaagctgga gtgactacat gtaacacaag attagacgtt acygcacgtc caaaccaaac 1620
tcttcagct cctaagcagt tacgggttcg accaacattc agcaaattat tagcacttaa 1680
tgggaaagg ttgaatgtaa aacaagcttt taaccagaa ggagaatttc agcgtttggc 1740
agctcaatct ggactctatg aaagtgaaga actttaataa ctttaccac attggaacaa 1800
agccaactac accattagta atatatgtga ttacattttt ttgaaattaa tccatagctg 1860
tattaacaga ttatggtttt aattaggtaa tatagttaat atatatatat aatattattt 1920
atcctttgac tcttgacat tctatgtacc cctccgattt gtgaagccta caggaaatct 1980
gggtatatgg atttgtaact gcagaagact atcttaaaat acaggatttt aacatttaag 2040
tcatgcacat ttaacaatta caggttataa attagtatca acttttttaa cacatctaat 2100
gcttgtaata acgtttactg gtactgcttt cttaaatactg ttttaccctg tttctcttgt 2160
aggaatacta acatggtata gattatctga gtgttcacac gttgtatgtc aaaagaaaat 2220
aaaattcaaa tatttaaaac ggac 2244

```

&lt;210&gt; 328

&lt;211&gt; 498

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 328

```

Met Phe Asn Tyr Glu Arg Pro Lys His Phe Ile Gln Ser Gln Asn Pro
1           5           10           15
Cys Gly Ser Arg Leu Gln Pro Pro Gly Pro Glu Thr Ser Ser Phe Ser
20           25           30
Ser Gln Thr Lys Gln Ser Ser Ile Ile Ile Gln Pro Arg Gln Cys Thr
35           40           45
Glu Gln Arg Phe Ser Ala Ser Ser Thr Leu Ser Ser His Ile Thr Met
50           55           60
Ser Ser Ser Ala Phe Pro Ala Ser Pro Gln Gln His Ala Gly Ser Asn
65           70           75           80
Pro Gly Gln Arg Val Thr Thr Thr Tyr Asn Gln Ser Pro Ala Ser Phe
85           90           95

```

338

Leu Ser Ser Ile Leu Pro Ser Gln Pro Asp Tyr Asn Ser Ser Lys Ile  
 100 105 110  
 Pro Ser Ala Met Asp Ser Asn Tyr Gln Gln Ser Ser Ala Gly Gln Pro  
 115 120 125  
 Ile Asn Ala Lys Pro Ser Gln Thr Ala Asn Ala Lys Pro Ile Pro Arg  
 130 135 140  
 Thr Pro Asp His Glu Ile Gln Gly Ser Lys Glu Ala Leu Ile Gln Asp  
 145 150 155 160  
 Leu Glu Arg Lys Leu Lys Cys Lys Asp Thr Leu Leu His Asn Gly Asn  
 165 170 175  
 Gln Arg Leu Thr Tyr Glu Glu Lys Met Ala Arg Arg Leu Leu Gly Pro  
 180 185 190  
 Gln Asn Ala Ala Ala Val Phe Gln Ala Gln Asp Asp Ser Gly Ala Gln  
 195 200 205  
 Asp Ser Gln Gln His Asn Ser Glu His Ala Arg Leu Gln Val Pro Thr  
 210 215 220  
 Ser Gln Val Arg Ser Arg Ser Thr Ser Arg Gly Asp Val Asn Asp Gln  
 225 230 235 240  
 Asp Ala Ile Gln Glu Lys Phe Tyr Pro Pro Arg Phe Ile Gln Val Pro  
 245 250 255  
 Glu Asn Met Ser Ile Asp Glu Gly Arg Phe Cys Arg Met Asp Phe Lys  
 260 265 270  
 Val Ser Gly Leu Pro Ala Pro Asp Val Ser Trp Tyr Leu Asn Gly Arg  
 275 280 285  
 Thr Val Gln Ser Asp Asp Leu His Lys Met Ile Val Ser Glu Lys Gly  
 290 295 300  
 Leu His Ser Leu Ile Phe Glu Val Val Arg Ala Ser Asp Ala Gly Ala  
 305 310 315 320  
 Tyr Ala Cys Val Ala Lys Asn Arg Ala Gly Glu Ala Thr Phe Thr Val  
 325 330 335  
 Gln Leu Asp Val Leu Ala Lys Glu His Lys Arg Ala Pro Met Phe Ile  
 340 345 350  
 Tyr Lys Pro Gln Ser Lys Lys Val Leu Glu Gly Asp Ser Val Lys Leu  
 355 360 365  
 Glu Cys Gln Ile Ser Ala Ile Pro Pro Pro Lys Leu Phe Trp Lys Arg  
 370 375 380  
 Asn Asn Glu Met Val Gln Phe Asn Thr Asp Arg Ile Ser Leu Tyr Gln  
 385 390 395 400  
 Asp Asn Thr Gly Arg Val Thr Leu Leu Ile Lys Asp Val Asn Lys Lys  
 405 410 415  
 Asp Ala Gly Trp Tyr Thr Val Ser Ala Val Asn Glu Ala Gly Val Thr  
 420 425 430  
 Thr Cys Asn Thr Arg Leu Asp Val Thr Ala Arg Pro Asn Gln Thr Leu  
 435 440 445  
 Pro Ala Pro Lys Gln Leu Arg Val Arg Pro Thr Phe Ser Lys Tyr Leu  
 450 455 460  
 Ala Leu Asn Gly Lys Gly Leu Asn Val Lys Gln Ala Phe Asn Pro Glu  
 465 470 475 480  
 Gly Glu Phe Gln Arg Leu Ala Ala Gln Ser Gly Leu Tyr Glu Ser Glu  
 485 490 495  
 Glu Leu

&lt;210&gt; 329

&lt;211&gt; 3649

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 329

aattttctccg	taattttccac	tgcttgaagg	ctgctcgagg	aacaggagca	gcggcgaaac	60
ccaggtctgt	cggtttacga	gaatgcagtt	tccaagtacg	gctctcagtt	ccaaggcaat	120
tcccagcacg	acgccctgga	attcctgctc	tgggtgctgg	atcgtgtaca	tgaggacctg	180
gagggttcat	cccaggggcc	ggtgtcggag	aagcttccgc	ctgaagccac	taaaacctct	240
gagaactgcc	tgtcaccatc	agctcagctt	cctctaggtc	aaagctttgt	gcaaagccac	300
tttcaagcac	aatatagatc	ttccttgact	tgtccccact	gcctgaaaca	gagcaacacc	360
tttgatcett	tcctgtgtgt	gtccctacct	atccccctgc	gccagacgag	gttcttgagt	420
gtcaccttgg	tcttcccctc	taagagccag	cggttccctg	gggttggcct	ggccgtgccg	480
atcctcagca	cagtggcagc	cctgaggag	atggttgag	aggaaggagg	cgtccctgca	540
gatgaggtga	tcttggttga	actgtatccc	agtggattcc	agcgggtctt	ctttgatgaa	600
gaggacctga	ataccatcgc	agagggagat	aatgtgtatg	cctttcaagt	tcctccctca	660
cccagccagg	ggactctctc	agctcatcca	ctgggtctgt	cgccctcccc	acgcctggca	720
gcccgtagag	gccagcgatt	ctccctctct	ctccacagtg	agagcaaggt	gctaatactc	780
ttctgtaact	tgggtggggtc	agggcagcag	gctagcaggt	ttggggccacc	cttcctgata	840
agggagagca	gagctgtttc	ctgggcccag	ctccagcagt	ctatcctcag	caaggtccgc	900
catcttatga	agagtgaggc	ccctgtacag	aacctggggt	ctctgttctc	catccgtgtt	960
gtgggactct	ctgtggcctg	cagctatctg	tctccgaagg	acagtcggcc	cctctgtcac	1020
tggcgagttg	acagggtttt	gcactcagag	aggccaggag	gccctccaca	tgtcaagctg	1080
gcggtggagt	gggatagctc	tgtcaaggag	cgccgtttcg	ggagcctcca	ggaggagcga	1140
gcgcaggatg	ccgacagtgt	gtggcagcag	cagcaggcgc	atcagcagca	cagctgtacc	1200
ttggatgaat	gttttcagtt	ctacaccaag	gaggagcagc	tggcccagga	tgacgcctgg	1260
aagtgtcctc	actgccaaagt	cctgcagcag	gggatggtga	agctgagttt	gtggacgctg	1320
cctgacatcc	tcatcatcca	cctcaaaagg	ttctgccagg	tgggcgagag	aagaaacaag	1380
ctctccacgc	tgggtgaagtt	tccgctctct	ggactcaaca	tggctcccca	tgtggcccag	1440
agaagcacca	gccctgaggc	aggactgggc	ccctggcctt	cctggaagca	gccggactgc	1500
gtcccacca	gttaccgctc	ggacttccgt	tacgacctgt	atgucgtctg	caaccaccat	1560
ggcaacctgc	aaggtgggca	ttacacagcg	tactgccgga	actctctgga	tggccagtgg	1620
tacagttatg	atgacagcac	ggtggaaccg	cttcgagaag	atgaggtcaa	caccagaggg	1680
gcttatatcc	tgttctatca	gaagcggaac	agcatccctc	cctggtcagc	cagcagctcc	1740
atgagaggct	ctaccagctc	ctccctgtct	gatcactggc	tcttacggct	cgggagccac	1800
gctgycagca	caaggggaag	cctgctgtcc	tggagctctg	ccccctgccc	ctccctgccc	1860
caggttccctg	actctcccat	cttcaccaac	agcctctgca	atcaggaaaa	gggaggggtg	1920
gagcccaggc	gttttggtacg	gggcgtgaaa	ggcagaagca	ttagcatgaa	ggcaccacc	1980
aattcccag	ccaagcaggg	accattcaag	accatgcctc	tgcgggtggc	ctttggatcc	2040
aaggagaaac	caccaggtgc	ctccgtcgag	ttggtggagt	acttggaaatc	cagacgaaga	2100
cctcggtcca	cgagccagtc	cattgtgtcg	ctggtgacgg	gcactgcggg	tgaggatgag	2160
aagt.cagcat	cgccgaggtc	caacgtcgcc	cttcctgcta	acagcgaaga	tgggtggcg	2220
gccattgaaa	gaggtccagc	cggggtgccc	tgtccctcgg	ctcaacccaa	ccactgtctg	2280
gcccttgaa	actcagatgg	tccaaacaca	gcaaggaaac	tcaaggaaaa	tgacgggcag	2340
gacatcaagc	ttcccagaaa	gtttgacctg	cctctcactg	tgatgccttc	agtggagcat	2400
gagaaaccag	ctcgaccgga	gggccagaa	gccatgaact	ggaaggagag	cttcagatg	2460
ggaagcaaaa	gcagcccacc	ctccccctat	atgggattct	ctggaaacag	caaagacagt	2520
cgccgaggca	cctctgagct	agacagacct	ctgcagggga	cactcaccct	tctgaggtcc	2580
gtgtttcgga	agaaggagaa	caggaggaat	gagagggcag	aggtctctcc	acaggtgccc	2640
cccgtctccc	tgggtgagtgg	cgggctgagc	cctgccatgg	acgggcaggc	tccaggctca	2700
cctcctgccc	tcaggatccc	agagggcctg	gccaggggcc	tgggcagccg	gctcgagagg	2760
gatgtctggt	cagccccag	ctctctccgc	ctccctcgta	aagccagcag	ggccccgaga	2820
ggcagtgac	tgggcatgtc	acaaaggact	gttcaggggg	agcaggcttc	ttatggcacc	2880
tttcagagag	tcaaataatca	cactctttct	ttaggtcgaa	agaaaacctt	accggagtcc	2940
agcttttgat	ggagcgtgtc	agtattgtgt	gacgtggca	ttcttgggac	tttgccaagc	3000
aactgtaggc	agctcatgtt	gagaatgggt	ttccaggaaa	cccggtgtct	tgtaatctct	3060
aaaaaaaaat	tttttttttt	ttgtggtggg	gggtctccat	atctagactt	ccaacaccca	3120
aggtccatat	taaaaaaggt	cgaaaacctt	cctgcacatc	tgggtgcttt	gctacagttt	3180
ggccactaga	ggatgctatt	gggtcagtat	taccagtttc	agggcaagaa	ctgatattta	3240
ctaaagagtt	ttggatgtgg	gcaaacaaga	tgaggctggt	ttaataagaa	tcttcaatgt	3300
cgtgtcaaat	actgtcaatg	gcttttccct	tttctttctt	ttttttttta	attgtggact	3360

340

taaagaaaaa tattttattt ttaatgcttt tctgggataa gcattaaaga tgccaaaaag 3420  
 aaaaaaaaac aaaagaatga tagtgatggt aaggcaagat tctagcaaag agagatggga 3480  
 gataaatggc tgagagttca ggtgaatatt taatatatta aaaattgtat taaagttttt 3540  
 caaggtattt taaaaataac tattttgata ctagaaaaaa agtccatttt ttaattttaa 3600  
 tatgagatct atgtacaatt ttaataaaat cctgtccatg aaacacgca 3649

&lt;210&gt; 330

&lt;211&gt; 812

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 330

Met	Val	Ala	Glu	Glu	Gly	Gly	Val	Pro	Ala	Asp	Glu	Val	Ile	Leu	Val
1				5				10						15	
Glu	Leu	Tyr	Pro	Ser	Gly	Phe	Gln	Arg	Ser	Phe	Phe	Asp	Glu	Glu	Asp
			20					25					30		
Leu	Asn	Thr	Ile	Ala	Glu	Gly	Asp	Asn	Val	Tyr	Ala	Phe	Gln	Val	Pro
			35				40					45			
Pro	Ser	Pro	Ser	Gln	Gly	Thr	Leu	Ser	Ala	His	Pro	Leu	Gly	Leu	Ser
			50			55					60				
Ala	Ser	Pro	Arg	Leu	Ala	Ala	Arg	Glu	Gly	Gln	Arg	Phe	Ser	Leu	Ser
65				70				75						80	
Leu	His	Ser	Glu	Ser	Lys	Val	Leu	Ile	Leu	Phe	Cys	Asn	Leu	Val	Gly
			85					90						95	
Ser	Gly	Gln	Gln	Ala	Ser	Arg	Phe	Gly	Pro	Pro	Phe	Leu	Ile	Arg	Glu
			100					105					110		
Asp	Arg	Ala	Val	Ser	Trp	Ala	Gln	Leu	Gln	Gln	Ser	Ile	Leu	Ser	Lys
			115				120					125			
Val	Arg	His	Leu	Met	Lys	Ser	Glu	Ala	Pro	Val	Gln	Asn	Leu	Gly	Ser
			130			135					140				
Leu	Phe	Ser	Ile	Arg	Val	Val	Gly	Leu	Ser	Val	Ala	Cys	Ser	Tyr	Leu
145				150				155						160	
Ser	Pro	Lys	Asp	Ser	Arg	Pro	Leu	Cys	His	Trp	Ala	Val	Asp	Arg	Val
			165					170						175	
Leu	His	Leu	Arg	Arg	Pro	Gly	Gly	Pro	Pro	His	Val	Lys	Leu	Ala	Val
			180					185					190		
Glu	Trp	Asp	Ser	Ser	Val	Lys	Glu	Arg	Leu	Phe	Gly	Ser	Leu	Gln	Glu
			195				200					205			
Glu	Arg	Ala	Gln	Asp	Ala	Asp	Ser	Val	Trp	Gln	Gln	Gln	Gln	Ala	His
			210			215					220				
Gln	Gln	His	Ser	Cys	Thr	Leu	Asp	Glu	Cys	Phe	Gln	Phe	Tyr	Thr	Lys
225				230				235						240	
Glu	Glu	Gln	Leu	Ala	Gln	Asp	Asp	Ala	Trp	Lys	Cys	Pro	His	Cys	Gln
			245					250						255	
Val	Leu	Gln	Gln	Gly	Met	Val	Lys	Leu	Ser	Leu	Trp	Thr	Leu	Pro	Asp
			260					265					270		
Ile	Leu	Ile	Ile	His	Leu	Lys	Arg	Phe	Cys	Gln	Val	Gly	Glu	Arg	Arg
			275				280					285			
Asn	Lys	Leu	Ser	Thr	Leu	Val	Lys	Phe	Pro	Leu	Ser	Gly	Leu	Asn	Met
			290			295					300				
Ala	Pro	His	Val	Ala	Gln	Arg	Ser	Thr	Ser	Pro	Glu	Ala	Gly	Leu	Gly
305				310				315						320	
Pro	Trp	Pro	Ser	Trp	Lys	Gln	Pro	Asp	Cys	Leu	Pro	Thr	Ser	Tyr	Pro
			325					330						335	
Leu	Asp	Phe	Leu	Tyr	Asp	Leu	Tyr	Ala	Val	Cys	Asn	His	His	Gly	Asn
			340					345					350		
Leu	Gln	Gly	Gly	His	Tyr	Thr	Ala	Tyr	Cys	Arg	Asn	Ser	Leu	Asp	Gly
			355				360						365		

341

Gln Trp Tyr Ser Tyr Asp Asp Ser Thr Val Glu Pro Leu Arg Glu Asp  
 370 375 380  
 Glu Val Asn Thr Arg Gly Ala Tyr Ile Leu Phe Tyr Gln Lys Arg Asn  
 385 390 395 400  
 Ser Ile Pro Pro Trp Ser Ala Ser Ser Ser Met Arg Gly Ser Thr Ser  
 405 410 415  
 Ser Ser Leu Ser Asp His Trp Leu Leu Arg Leu Gly Ser His Ala Gly  
 420 425 430  
 Ser Thr Arg Gly Ser Leu Leu Ser Trp Ser Ser Ala Pro Cys Pro Ser  
 435 440 445  
 Leu Pro Gln Val Pro Asp Ser Pro Ile Phe Thr Asn Ser Leu Cys Asn  
 450 455 460  
 Gln Glu Lys Gly Gly Leu Glu Pro Arg Arg Leu Val Arg Gly Val Lys  
 465 470 475 480  
 Gly Arg Ser Ile Ser Met Lys Ala Pro Thr Thr Ser Arg Ala Lys Gln  
 485 490 495  
 Gly Pro Phe Lys Thr Met Pro Leu Arg Trp Ser Phe Gly Ser Lys Glu  
 500 505 510  
 Lys Pro Pro Gly Ala Ser Val Glu Leu Val Glu Tyr Leu Glu Ser Arg  
 515 520 525  
 Arg Arg Pro Arg Ser Thr Ser Gln Ser Ile Val Ser Leu Leu Thr Gly  
 530 535 540  
 Thr Ala Gly Glu Asp Glu Lys Ser Ala Ser Pro Arg Ser Asn Val Ala  
 545 550 555 560  
 Leu Pro Ala Asn Ser Glu Asp Gly Gly Arg Ala Ile Glu Arg Gly Pro  
 565 570 575  
 Ala Gly Val Pro Cys Pro Ser Ala Gln Pro Asn His Cys Leu Ala Pro  
 580 585 590  
 Gly Asn Ser Asp Gly Pro Asn Thr Ala Arg Lys Leu Lys Glu Asn Ala  
 595 600 605  
 Gly Gln Asp Ile Lys Leu Pro Arg Lys Phe Asp Leu Pro Leu Thr Val  
 610 615 620  
 Met Pro Ser Val Glu His Glu Lys Pro Ala Arg Pro Glu Gly Gln Lys  
 625 630 635 640  
 Ala Met Asn Trp Lys Glu Ser Phe Gln Met Gly Ser Lys Ser Ser Pro  
 645 650 655  
 Pro Ser Pro Tyr Met Gly Phe Ser Gly Asn Ser Lys Asp Ser Arg Arg  
 660 665 670  
 Gly Thr Ser Glu Leu Asp Arg Pro Leu Gln Gly Thr Leu Thr Leu Leu  
 675 680 685  
 Arg Ser Val Phe Arg Lys Lys Glu Asn Arg Arg Asn Glu Arg Ala Glu  
 690 695 700  
 Val Ser Pro Gln Val Pro Pro Val Ser Leu Val Ser Gly Gly Leu Ser  
 705 710 715 720  
 Pro Ala Met Asp Gly Gln Ala Pro Gly Ser Pro Pro Ala Leu Arg Ile  
 725 730 735  
 Pro Glu Gly Leu Ala Arg Gly Leu Gly Ser Arg Leu Glu Arg Asp Val  
 740 745 750  
 Trp Ser Ala Pro Ser Ser Leu Arg Leu Pro Arg Lys Ala Ser Arg Ala  
 755 760 765  
 Pro Arg Gly Ser Ala Leu Gly Met Ser Gln Arg Thr Val Pro Gly Glu  
 770 775 780  
 Gln Ala Ser Tyr Gly Thr Phe Gln Arg Val Lys Tyr His Thr Leu Ser  
 785 790 795 800  
 Leu Gly Arg Lys Lys Thr Leu Pro Glu Ser Ser Phe  
 805 810

342

<210> 331  
 <211> 1811  
 <212> DNA  
 <213> Homo sapiens

<400> 331  
 gagtcaccaa ggaaggcagc ggcagctcca ctcagccagt acccagatac gctgggaacc 60  
 ttccccagcc atggcttccc tggggcagat cctcttctgg agcataatta gcatcatcat 120  
 tattctggct ggagcaattg cactcatcat tggctttggt atttcaggga gacactccat 180  
 cacagtcact actgtcgccct cagctgggaa cattggggag gatggaatcc agagctgcac 240  
 ttttgaacct gacatcaaac tttctgatat cgtgatacaa tggctgaagg aaggtgtttt 300  
 aggcttggtc catgagttca aagaaggcaa agatgagctg tcggagcagg atgaaatgtt 360  
 cagaggccgg acagcagtggt ttgctgatca agtgatagtt ggcaatgcct ctttgcggct 420  
 gaaaaacgtg caactcacag atgctggcac ctacaaatgt tatatcatca cttctaaagg 480  
 caaggggaat gctaacccttg agtataaaac tggagccttc agcatgccgg aagtgaatgt 540  
 ggactataat gccagctcag agaccttgcg gtgtgaggct ccccgatggt tccccagcc 600  
 cacagtggtc tgggcatccc aagttgacca gggagccaac ttctcggaa gctccaatac 660  
 cagctttgag ctgaactctg agaatgtgac catgaagggt gtgtctgtgc tctacaatgt 720  
 tacgatcaac aacacatact cctgtatgat tgaaaatgac attgccaaag caacagggga 780  
 tatcaaagtg acagaatcgg agatcaaaag gcggagtcac ctacagctgc taaactcaaa 840  
 ggcttctctg tgtgtctctt ctttctttgc catcagctgg gcacttctgc ctctcagccc 900  
 ttacctgatg ctaaaataat gtgcctcggc cacaaaaaag catgcaaagt cattgttaca 960  
 acagggatct acagaactat ttcaccacca gatatgacct agttttatat ttctggggagg 1020  
 aatgaattc atatatagaa gtctggagtg agcaaacaag agcaagaaac aaaaagaagc 1080  
 caaaagcaga aggtccaat atgaacaaga taaatctatc ttcaaagaca tattagaagt 1140  
 tgggaaaata attcatgtga actagagtca actgtgtcag ggctaagaaa ccctggtttt 1200  
 gagtagaaaa gggcctggaa agaggggagc caacaaatct gtctgcttcc tcacattagt 1260  
 cattggcaaa taagcattct gtctctttgg ctgtctgcctc agcacagaga gccagaactc 1320  
 tatcgggcac caggataaca tctctcagtg aacagagttg acaaggccta tgggaaatgc 1380  
 ctgatgggat tatcttcagc ttgttgagct tctaagtttc tttcccttca ttctaccctg 1440  
 caagccaagt tctgtaagag aaatgcctga gttctagctc aggttttctt actctgaatt 1500  
 tagatctcca gacctgcct ggccacaatt caaatgaag caacaaacat ataccttcca 1560  
 tgaagcacac acagactttt gaaagcaagg acaatgactg cttgaattga ggccttgagg 1620  
 aatgaagctt tgaaggaaaa gaatactttg tttccagccc ccttcccaca ctcttcatgt 1680  
 gttaaccact gccttccttg accttggagc caoggtgact gtattacatg ttgttataga 1740  
 aaactgattt tagagttctg atcgttcaag agaatgatta aatatacatt tcctaaaaaa 1800  
 aaaaaaaaaa a 1811

<210> 332  
 <211> 282  
 <212> PRT  
 <213> Homo sapiens

<400> 332  
 Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile  
 1 5 10 15  
 Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser  
 20 25 30  
 Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly Asn Ile  
 35 40 45  
 Gly Glu Asp Gly Ile Gln Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu  
 50 55 60  
 Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val  
 65 70 75 80  
 His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met  
 85 90 95  
 Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Ile Val Gly Asn  
 100 105 110



343

Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr  
 115 120 125  
 Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu  
 130 135 140  
 Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn  
 145 150 155 160  
 Ala Ser Ser Glu Thr Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln  
 165 170 175  
 Pro Thr Val Val Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser  
 180 185 190  
 Glu Val Ser Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met  
 195 200 205  
 Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser  
 210 215 220  
 Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val  
 225 230 235 240  
 Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser  
 245 250 255  
 Lys Ala Ser Leu Cys Val Ser Ser Phe Phe Ala Ile Ser Trp Ala Leu  
 260 265 270  
 Leu Pro Leu Ser Pro Tyr Leu Met Leu Lys  
 275 280

&lt;210&gt; 333

&lt;211&gt; 1984

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 333

gaagaattag cagcaaaagt gggttcagatg ttttatgtgg ctgagccaaa gcaagtgcc 60  
 catattctct gtagtccttc tatgaagaat attaatcctt taactgccat gagctatcta 120  
 aggaagctgg atacttctgg gttttcatcg atcttagtga cattgaccaa ggcagcagtg 180  
 gctctgaaaa tgggagatct tgacatgcac agaaatgaaa tgaaaagcca ttcagagatg 240  
 aagttggtat gtggcttcat tctggaacct cggctgttga ttcaacagag aaagggacag 300  
 attgttccaa ccgagcttgc acttcacttg aaggaaactc agcctggatt gcttgtggct 360  
 tcagttctgg gcttgcagaa gaacaacaaa attggaattg aagaagcaga ttcctttttt 420  
 aaggtgcttt gtgctaagga tgaagataca attcctcagc tcttggtaga cttttgggaa 480  
 gctcagctag tggcatgtct cccagatgtg gtacttcagg aactcttttt caaactcaca 540  
 tcacagtaca tctggagatt gtctaagagg cagcctcctg acaccacacc attgccaaca 600  
 tcggaggatc tgataaatgc ctgtagtc attggttaa tttatccatg gggtcatgtc 660  
 gtaatatcat ctgattcttt agctgataaa aattatacag aagatctttc aaaattacag 720  
 cttccattat tccgttcttg gagccacttt cagaagacac tattgccggc ctcagtgtcc 780  
 atgttctgtg tcgtacacgc ttgaaagagt atgaacagt catagacata ctgttagaga 840  
 gatgcccgga ggcagtcatt ccatatgcta atcatgaact gaaagaagag aaccggatag 900  
 actctgtggt ggaaaaaact gttgcctgaa ctttgtcaga gaataaaatg tggaggagag 960  
 aagtatcaac tctacctgtc atcattaaaa gcttaatttt cacgggaact gtggaagcta 1020  
 gcagacagta ccactacatt ataaatgagg aacctaggac ttggaagatt aagtgaactt 1080  
 cttaaagcca ctcgaaacat tgtcaattgt tgctgtggaa ctagaactga aggatttcat 1140  
 gaatgttctc ccagaagatg gtactgcaac atttttcttg ccatactctc tctattgcag 1200  
 tcgaaagaaa ccattgactt aaaggatca tttgaaaaat accataatgg catttgagac 1260  
 tgaatttcta aaaattgaat gccaaaagta aagtagagga gttttttatt ttatatatca 1320  
 cacacacaca cacacacaca cacacacaca cacacacaca tatatgatac aaatgctttc 1380  
 aggctgttta ccttaccgtg tagtggtaac tattcacttc ttaatttatg acctcaatca 1440  
 atttaattgt ctagaatgta aaaagtcttt aagacataag aattcctcaa agaagccata 1500  
 ctttttttaa ggtggggatt gacttttatt ccaaggaaca acatcagttc actgtgtgtg 1560  
 gagacatgac aatcattttc atcccaagaa cactttaagg aaacatttta caagtatgct 1620  
 tgaaagaatg tcactaactg gtccagaatt ttatcttctt gattttttcca gatttctcta 1680

344

tgtttttgag aaagatgtta atgttttgcc atggtaaaag atttcaaacc tcattttttt 1740  
 tggttcctttt cttgttactt ttaagaaaac tcatgctctg tttctctgaa tcaaatgaag 1800  
 tagaagttta caaagctaac tttcttcttg tctagctatt aacatgattt gtcaaatgca 1860  
 tgtttttttc agccaaagcc ttgtttccat ttttggtgat gtgtactctt gctcttttag 1920  
 ctagagtgtta tgtgaaaata aagaaataca tcattgtatt cacaaaaaaa aaaaaaaaaa 1980  
 aaaa 1984

&lt;210&gt; 334

&lt;211&gt; 258

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 334

Met	Phe	Tyr	Val	Ala	Glu	Pro	Lys	Gln	Val	Pro	His	Ile	Leu	Cys	Ser	1	5	10	15
Pro	Ser	Met	Lys	Asn	Ile	Asn	Pro	Leu	Thr	Ala	Met	Ser	Tyr	Leu	Arg	20	25	30	
Lys	Leu	Asp	Thr	Ser	Gly	Phe	Ser	Ser	Ile	Leu	Val	Thr	Leu	Thr	Lys	35	40	45	
Ala	Ala	Val	Ala	Leu	Lys	Met	Gly	Asp	Leu	Asp	Met	His	Arg	Asn	Glu	50	55	60	
Met	Lys	Ser	His	Ser	Glu	Met	Lys	Leu	Val	Cys	Gly	Phe	Ile	Leu	Glu	65	70	75	80
Pro	Arg	Leu	Leu	Ile	Gln	Gln	Arg	Lys	Gly	Gln	Ile	Val	Pro	Thr	Glu	85	90	95	
Leu	Ala	Leu	His	Leu	Lys	Glu	Thr	Gln	Pro	Gly	Leu	Leu	Val	Ala	Ser	100	105	110	
Val	Leu	Gly	Leu	Gln	Lys	Asn	Asn	Lys	Ile	Gly	Ile	Glu	Glu	Ala	Asp	115	120	125	
Ser	Phe	Phe	Lys	Val	Leu	Cys	Ala	Lys	Asp	Glu	Asp	Thr	Ile	Pro	Gln	130	135	140	
Leu	Leu	Val	Asp	Phe	Trp	Glu	Ala	Gln	Leu	Val	Ala	Cys	Leu	Pro	Asp	145	150	155	160
Val	Val	Leu	Gln	Glu	Leu	Phe	Phe	Lys	Leu	Thr	Ser	Gln	Tyr	Ile	Trp	165	170	175	
Arg	Leu	Ser	Lys	Arg	Gln	Pro	Pro	Asp	Thr	Thr	Pro	Leu	Arg	Thr	Ser	180	185	190	
Glu	Asp	Leu	Ile	Asn	Ala	Cys	Ser	His	Tyr	Gly	Leu	Ile	Tyr	Pro	Trp	195	200	205	
Val	His	Val	Val	Ile	Ser	Ser	Asp	Ser	Leu	Ala	Asp	Lys	Asn	Tyr	Thr	210	215	220	
Glu	Asp	Leu	Ser	Lys	Leu	Gln	Leu	Pro	Leu	Phe	Arg	Ser	Trp	Ser	His	225	230	235	240
Phe	Gln	Lys	Thr	Leu	Leu	Pro	Ala	Ser	Val	Ser	Met	Phe	Cys	Val	Val	245	250	255	

His Ala

&lt;210&gt; 335

&lt;211&gt; 2180

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(2180)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 335

```

acgcctccgc tcgcagcggc ggccaacatc accgcactg ccacccctcc cagactgtgg 60
acgggaggat ggagtcgat gccgtcgcta ccgacggcgg ggagaggccg ggggtcccag 120
cgggctcagg tctgtcggct tcccagcgtc gggcggagct gcgtcggaga aagctgtctca 180
tgaactcgga acagcgcac aaccggatca tgggctttca caggcccggg agcggcgcg 240
aagaagaaag tcaaacaaaa tcaaagcagc aggacagtga taaactgaac tccctcagcg 300
ttccttccgt ttcaaaagcga gtagtgctgg gtgattcagt cagtacagga acaactgacc 360
agcaggggtg tgtggccgag gtaaagggga cccaactggg agacaaattg gactcgttca 420
ttaaaccacc tgagtgcagt agtgatgtca accttgagct ccggcagcgg aacagagggg 480
acctgcagc ggactcggc cagaggggtt cccgccatgg cctagagcag tacctttcca 540
gattcgaaga agcaatgaag ctaaggaaac agctgattag tgaaaaaccc agtcaagagg 600
atggaaatac aacagaagaa tttgactctt ttcgaatatt tagattggtg ggatgtgtc 660
ttcttgctct tggagtcaga gcttttgtt gcaataactt gtccatattt gctccatttc 720
ttactttaca acttgcgtta catgggatta taaaaatatt ttcccaagag tgaaaagaag 780
ataaagacaa cagtaactaac agctgcactt ctattgtcgg gaattcctgc cgaagtata 840
aatcgatcaa tggataccta tagcaaaatg ggcgaagtct tcacagatct ctgtgtctac 900
tttttcaact ttatctttt tcatgaactg cttgattatt ggggctctga agtaccatga 960
agcctgtaga actgagaagg agaagcttac aaaaaaaaaa aaatcctctt ctatatttga 1020
gtgtctctaa aggaggcaaa ttggtttaca ccttcattga attcttttac tttaggggtt 1080
gtaaagctac tttattagat atagaatggc agattctctg atttaaaagg gctgagtttg 1140
tattattact gatatgaaga atagagtacc aatgtcatta attgattttt cttgttaatc 1200
agaattccta ttctgtacct ttctctaac ttctcagatt tgtaattctt cttttgggag 1260
ctgagctagt gcttttagga gaacagataa atgtggtctc agccagccct agagactgct 1320
tcttggtgtt gtgtcattct gtcctgagaa antgaagtca tctgaaaaat aaaatgacag 1380
aaactgaatt gtctaattgt aactctgcac attgtaactt ttcttggtga gttagtatct 1440
taatttttac tccagcaca gtaatttaac aaagaaaaga ttcatacatg tgaaatttga 1500
aggatattat aaaattttta ttgctgtata ccaaactcag aattggaact ttttacattt 1560
gagtttcaact ttttagaagt atgttttaag caagcaaaaa caaaatggga tgagaagaat 1620
tgaggcatgc aaccaaatag cataaatgtc ctttttcccc ccaaataatg tctagatgag 1680
ttattataaa cattgtttt atttttttga gacagagttt cgctctgtt gccaggcta 1740
gagtgaatg gcgccatct ggctcaccgc aacctccacc ttcttggttc aagggatctc 1800
ctgcctcagc ctccaagta gctgggatta caggcatgca ccaccacgcc cagctaattt 1860
ttatattctt tagtaagac agggtttctc catgttggtc aggtggtct cgaacttctg 1920
acctcaggtg atctgccac ctggcctcc caaagtgtg gattacaggc gtgagcactg 1980
cacctggcct tataaatatc cttttaacta actcagtaac tgccatattt tgttgggttg 2040
tcttcttaaa agaataaag actaaagtgt taatgtcact tgggtgtaca tttccttaca 2100
gatttttgta tagtctaatt tggttaatcc ttgtgacatt aaaaacacat acacttttta 2160
aaaaaaaaa aaaacttttag

```

&lt;210&gt; 336

&lt;211&gt; 234

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 336

```

Met Glu Ser Met Ala Val Ala Thr Asp Gly Gly Glu Arg Pro Gly Val
1           5           10          15
Pro Ala Gly Ser Gly Leu Ser Ala Ser Gln Arg Arg Ala Glu Leu Arg
20          25          30
Arg Arg Lys Leu Leu Met Asn Ser Glu Gln Arg Ile Asn Arg Ile Met
35          40          45
Gly Phe His Arg Pro Gly Ser Gly Ala Glu Glu Glu Ser Gln Thr Lys
50          55          60
Ser Lys Gln Gln Asp Ser Asp Lys Leu Asn Ser Leu Ser Val Pro Ser
65          70          75          80
Val Ser Lys Arg Val Val Leu Gly Asp Ser Val Ser Thr Gly Thr Thr
85          90          95

```

346

Asp Gln Gln Gly Gly Val Ala Glu Val Lys Gly Thr Gln Leu Gly Asp  
 100 105 110  
 Lys Leu Asp Ser Phe Ile Lys Pro Pro Glu Cys Ser Ser Asp Val Asn  
 115 120 125  
 Leu Glu Leu Arg Gln Arg Asn Arg Gly Asp Leu Thr Ala Asp Ser Val  
 130 135 140  
 Gln Arg Gly Ser Arg His Gly Leu Glu Gln Tyr Leu Ser Arg Phe Glu  
 145 150 155 160  
 Glu Ala Met Lys Leu Arg Lys Gln Leu Ile Ser Glu Lys Pro Ser Gln  
 165 170 175  
 Glu Asp Gly Asn Thr Thr Glu Glu Phe Asp Ser Phe Arg Ile Phe Arg  
 180 185 190  
 Leu Val Gly Cys Ala Leu Leu Ala Leu Gly Val Arg Ala Phe Val Cys  
 195 200 205  
 Lys Tyr Leu Ser Ile Phe Ala Pro Phe Leu Thr Leu Gln Leu Ala Leu  
 210 215 220  
 His Gly Ile Ile Gln Ile Phe Ser Gln Glu  
 225 230

<210> 337  
 <211> 3695  
 <212> DNA  
 <213> Homo sapiens

<400> 337  
 tataggagagt cgaccacgcg tccgcgcgtc gcaggggtcg ctggagagga ggcgctccgc 60  
 ccgcccgcgc cgtcctccgc tgcttctccg cgcccggctg gagcccggcg cccgggtcgcc 120  
 ccgtcgcgct cgaccgcgag ggcacgcccgc agccgcaggg gcccgcgctc cccgggtcgg 180  
 cggcgcgggg gaacgtgagc ggatgttcac ttcttctcca caatgaatga gtgtcactat 240  
 gacaagcaca tggacttttt ttataatagg agcaaacactg atactgtcga tgactggaca 300  
 ggaacaaagc ttgtgattgt tttgtgtgtt gggacgtttt tctgcctgtt tttttttttt 360  
 tctaattctc tggatcatcg ggcagtgatc aaaaacagaa aatttcattt ccccttctac 420  
 tacctgttgg ctaatttagc tgctgccgat ttcttcgctg gaattgccta tgtattccctg 480  
 atgtttaaca caggcccagt ttcaaaaact ttgactgtca accgctgggt tctccgtcag 540  
 gggcttcttg acagtacgtt gactgcttcc ctcaccaact tgctggttat cgcctggag 600  
 aggcacatgt caatcatgag gatgcggggt catagcaacc tgacaaaaa gaggggtgaca 660  
 ctgctcattt tgcttgtctg ggccatcgcc atttttatgg gggcggtccc cacactgggc 720  
 tgggaattgcc tctgcaacat ctctgcctgc tcttccctgg ccccatтта cagcaggagt 780  
 taccttgttt tctggacagt gtccaacctc atggccttcc tcatcatggt tgtggtgtac 840  
 ctgcggatct acgtgtacgt caagaggaaa accaacgtct tgtctccgca tacaagtggg 900  
 tccatcagcc gccggaggac acccatgaag ctaatgaaga cggatgatgac tgtcttaggg 960  
 gcgtttgtgg tatgtgggac cccgggectg gtggttctgc tcctcgacgg cctgaactgc 1020  
 aggcagtgtg gcgtgcagca tgtgaaaagg ttggttctgc tgctggcgct gctcaactcc 1080  
 gtcgtgaacc ccatcatcta ctctacaag gacgaggaca tgtatggcac catgaagaag 1140  
 atgatctgct gcttctctca ggagaacca gagaggcgct cctctcgcat cccctccaca 1200  
 gtccctcagca ggagtgcacac aggcagccag tacatagagg atagtattag ccaagggtga 1260  
 gtctgcaata aaagcacttc ctaaaactctg gatgcctctc ggcccaccca ggcctcctct 1320  
 gggaaaagag ctgttaagaa tgattacctg tctctaaca agcccatgta cagtgttatt 1380  
 tgaggctctc attaatcact gctagatttc tttaaaaaat tttttttcat agtttaaaag 1440  
 catgggcagt aaagagagga cctgctgcat ttagagaaa cagagaaacg ggagaggttc 1500  
 ggcgggtccc tgcttgcct atgaactgct cagagctcct gtcagtccag ctgggccttc 1560  
 tgggttcttg caccatttct tagccattct ctttgtattt taaaaggacg ttatgaaagg 1620  
 gcttagacca aaataaatca taatgttact tgagccacct tatatagctg cttggagagt 1680  
 ctatgtagtt ctttctgcat gcattaaaaa tgtttagaaa tgcttcagca atggattttt 1740  
 tttcctcaaa caaacctagg ccagtagcta ggtgttcagt aggaatcaaa gaaaaatcag 1800  
 taagagctcc agattaaacc tgatttttaa ctgaaggaac attctgagga aaaatactta 1860  
 aaagtaaaaa aggtcaatgt gaaaaccctt tttgacctga aaaaggcctt agtatggtcc 1920

```

tccatgcatg tgtgtgtata tgcattgtgtg tgtgtgtgtg tgtgtgtgtc tatatatata 1980
tatatatata tatatatata tttcctgtgt tttactgatt tttattgatt ttgttcaaag 2040
atatctgggg attggattgg ggaatgctta atctgactat tgaaagaaac atggatccct 2100
ggagtatttc agatacgggg ttaccgcccc agactgcctc ccgccagtcc acattagttc 2160
tcattttccc tcatgatggt gaaaaacagt ggagagctag taaagggttt atgcagaaaa 2220
caaggagaag agaattgtgaa gtttgaagtg cctatggaac atccagctga taatcttgcc 2280
tagtaagagc aaaagaagcc aagagaacac caacgtttta ggagcaggta gagaaaaccc 2340
agcaaaagga cagaggaata agaggaccaa agaacaatgt taagaatcaa ggagagaggt 2400
caggcacgct ggctcatgcc tgtaatccca gcactttggg aggttgaggc aggtggatca 2460
cttgaggcca ggagtatgag accagcctgg gcaatgtggt gaaattgcat ctttactaaa 2520
aatacaaaaa ctagccaggc atggtggcac atgcctgtaa taccaggtag ttgggaagct 2580
gaggcataag aatcacttga acccgggagg tggagggtgc agagttagcc aagatcgag 2640
cactgcactc tagtctgggt gacagagcaa gactctgtct caaaaaaaaaa aaaaaaaaaa 2700
aaaaaagact agagaatgtc agggaacaca tgtgtatatt taaacaactt cactttgcat 2760
ttaaaaaact gaaggacagc gaagggtgaaa tcaattcacg ggccacctag actttccagc 2820
ctaggactag agctgtagca atgatctgtt gtgctgtaca agaaaagaga aagaggtggt 2880
catttgagaa cagatgtttt tatacatcag agtaaaagct gtattgaaga gcaggctgaa 2940
tcccttccat atagaatgaa atatgagctt gaccccagtc cttatcttca gttacctcca 3000
taccaactgg tggcatgttg gatthagcat gtagaataat ttcccatctc ttatttttcc 3060
caaggttaat ggcaccttcc ttgtacctgg cttacatgtg aactgaattt tgatctgggt 3120
tctattttga atttttctcc ttcagagacc taagtaggca acatgaaaga caagtagtta 3180
agaaagaaaa aatgatgttt catcacaca ggctaccaac gagagttttc tatgtaaaac 3240
atthagagtg tattctgatt taaaatgaga ataacttcaa ggtagatatt atagtattta 3300
tgtagtttgc aaaagaagtt tacatttttt tgctattgtg atataacatt tatgtgcaag 3360
aactacttgt aataaaagga tttgagatgt catgcttcta aatataatag cctaaaatag 3420
agaatattat gatttgaaag tgtagatttc acaaactctg tatagtatgt ggtctatct 3480
gaagctttta tcgaagctac ctataaaaata aaattttaaa agatctgttc tctcttggtg 3540
aggtgcatta ttgctttgtg tattttctaa gtaaaaatat agtttgtggt aactacagca 3600
taaattttcta ttgcagaaga aaaatcaaat ttgccatgaa gtacatactc tcaatgtttt 3660
atgtaagcat tttgaatcta tagctggcca aaggg 3695

```

&lt;210&gt; 338

&lt;211&gt; 353

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 338

```

Met Asn Glu Cys His Tyr Asp Lys His Met Asp Phe Phe Tyr Asn Arg
 1           5           10           15
Ser Asn Thr Asp Thr Val Asp Asp Trp Thr Gly Thr Lys Leu Val Ile
          20          25          30
Val Leu Cys Val Gly Thr Phe Phe Cys Leu Phe Ile Phe Phe Ser Asn
          35          40          45
Ser Leu Val Ile Ala Ala Val Ile Lys Asn Arg Lys Phe His Phe Pro
          50          55          60
Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala Asp Phe Phe Ala Gly
          65          70          75          80
Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr
          85          90          95
Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Ser Ser
          100         105         110
Leu Thr Ala Ser Leu Thr Asn Leu Leu Val Ile Ala Val Glu Arg His
          115         120         125
Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg
          130         135         140
Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly
          145         150         155         160
Ala Val Pro Thr Leu Gly Trp Asn Cys Leu Cys Asn Ile Ser Ala Cys

```

348

[illegible]

```
<210> 339
<211> 3320
<212> DNA
<213> Homo sapiens
```

<400>	339						
gcgagagccg	cgggggccgc	ggagctggag	ccggagctga	agccggagcc	gggttgga	60	
ctgggcccgg	gccgggccgg	agcgggctcc	agagacatgg	ggtcgaccga	ctccaagctg	120	
aacttccgga	aggcggtgat	ccagctcacc	accaagacgc	agcccgatga	agccaccgat	180	
gatgcctttt	gggaccagtt	ctgggcagac	acagccacct	cggtgcagga	tgtgtttgca	240	
ctggtgcccg	cagcagagat	ccgggcccgtg	cggaagagt	cacctccaa	cttgccacc	300	
ctgtgtaca	aggccgttga	gaagctggtg	cagggagctg	agagtggctg	ccactcggag	360	
aaggagaagc	agatcgtct	gaactgcagc	cggtgctca	cccgcgtgct	gccctacatc	420	
tttgaggacc	ccgactggag	gggttcttc	tggtccacag	tgcgcggggc	agggcgagga	480	
gggcagggag	aagaggatga	tgagcatgcc	aggccctgg	ccgagtcctt	gctcctggcc	540	
attgctgacc	tgctcttctg	cccggacttc	acggttcaga	gccaccggag	gagcactgtg	600	
gactcggcag	aggacgtcca	ctccctggac	agctgtgaat	acatctggga	ggctggtgtg	660	
ggcttcgctc	actccccca	gcctaactac	atccacgata	tgaaccggat	ggagctgctg	720	
aaactgctgc	tgacatgctt	ctccgaggcc	atgtacctgc	cccagctcc	ggaaagtggc	780	
agcaccaacc	catgggttca	gttcttttgt	tccacggaga	acagacatgc	cctgcccttc	840	
ttcacctccc	tctcaacac	cgtgtgtgcc	tatgaccttg	tgggctacgg	gatccctac	900	
aaccacctgc	tcttctctga	ctaccgggaa	ccctgggtg	aggaggctgc	ccagtgctc	960	
attgtcactt	tggaccacga	cagtgccagc	agtgccagcc	ccactgtgga	cggcacacc	1020	
actggcaccg	ccatggatga	tgctgatcct	ccaggccctg	agaacctgtt	tgtgaactac	1080	
ctgtcccgca	tccatcgtga	ggaggacttc	cagttcatcc	tcaagggtat	agcccggtg	1140	
ctgtccaacc	ccctgtcca	gacctacctg	cctaactcca	ccaagaagat	ccagttccac	1200	
caggagctgc	tagttctctt	ctggaagctc	tgcgacttca	acaagaaatt	cctctcttc	1260	
gtctgaaga	gcagcgactg	cctagacatc	cttgatcccc	tctctcttct	cctcaacgat	1320	
gcccgccggc	atcagtcctg	ggtgggctcg	atgcacattg	gtgtcttcat	cttgctgctt	1380	
ctgagcgggg	agcgggaactt	cggggctcgg	ctgaacaaac	cctactcaat	cgcgctggcc	1440	
atggacatcc	cagtcctcac	agggaccac	qccqacctgc	tatttgttgt	gttccacaaq	1500	

```

atcatcacca gcggggcacca gcggttgacg cccctcttcg actgcctgct caccatcgtg 1560
gtcaacgtgt cccctacct caagagcctg tccatgggtga cygccaacaa gttgctgcac 1620
ctgctggagg ccttctccac cacctggttc ctcttctctg cygcccagaa ccaccactg 1680
gtcttcttcc tcttgagggt cttcaacaac atcatccagt accagtttga tggcaactcc 1740
aacctggtct acgccatcat ccgcaagcgc agcatcttcc accagctggc caacctgccc 1800
acggaccgcg ccaccattca caaggccctg cagcggcgcc ggccgacacc tgagcccttg 1860
tctcgaccg gctcccagga gggcacctcc atggagggt cccgcccgcg tgcccctgca 1920
gagccaggca ccctcaagac cagtctggtg gctactccag gcattgacaa gctgaccgag 1980
aagtcccagg tgtcagagga tggcaccttg cggctccctg aacctgagcc ccagcagagc 2040
ttggaggatg gcagcccggc taagggggag cccagccagg catggaggga gcagcggcga 2100
ccgtccacct catcagccag tgggcagtgg agcccaacgc cagagtgggt cctctccttg 2160
aagtcaagc tgcgctgca gacctcatg aggtgctgc aggtgctgt tccgcagggt 2220
gagaagatct gcatcgacaa gggcctgacg gatgagtctg agatcctgcg gttcctgcag 2280
catggcacc tgggtgggct gctgccctg cccacccca tctcatccg caagtaccag 2340
gccaactcgg gcactgccat gtggttccgc acctacatg ggggcgtcat ctatctgagg 2400
aatgtggacc cccctgtctg gtacgacacc gacgtgaagc tgtttgagat acagcgggtg 2460
tgaggatgaa gccgacgagg ggctcagtct aggggaaggc agggccttg tccctgaggc 2520
ttccccatc caccattctg agctttaaat taccacgac agggcctgga acagggcaga 2580
gtggccctg agtgtcatgc cctagagacc cctgtggcca ggacaatgtg aactggctca 2640
gatccccctc aaccctagg ctgactcac aggagccca tctctggggc tatgccccca 2700
ccagagacca ctgccccaa cactcggact cccctttaa gacctggctc agtgctggcc 2760
cctcagtgc caccactcc tgtgctaccc agcccagag gcagaagcca aaatgggtca 2820
ctgtgcccta aggggtttga ccaggaacc acgggctgtc ccttgagggt cctggacagg 2880
gtaaggggt gcttcagcc tctaaccga aagccagctg tccaggtc caggggaaa 2940
aggtgtggcc aggtgtctc tcgaggaggc tgggagctg ccgactgcaa aagccagact 3000
ggggcaccct ccgtatcctt ggggcatggt gtgggtgtg gagggtctcc tgctatatc 3060
tcttgatcc gtggaaatag cctggctccc tcttaccag taatgagggg cagggaaagg 3120
aactggagg cagcgttta gtctccctg cctgcccac tgctggatg ggcgatgcc 3180
acctctatc cttacccaa gctctggcct ctgggtccca ccaccagcc cccgtgtca 3240
gaacaatctt tgctctgtac aatcggcctc tttacaataa aacctcctgc tccccaaaa 3300
aaaaaaaaa aaaaaaaaaa 3320

```

&lt;210&gt; 340

&lt;211&gt; 784

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 340

```

Met Gly Ser Thr Asp Ser Lys Leu Asn Phe Arg Lys Ala Val Ile Gln
  1             5             10             15
Leu Thr Thr Lys Thr Gln Pro Val Glu Ala Thr Asp Asp Ala Phe Trp
             20             25             30
Asp Gln Phe Trp Ala Asp Thr Ala Thr Ser Val Gln Asp Val Phe Ala
             35             40             45
Leu Val Pro Ala Ala Glu Ile Arg Ala Val Arg Glu Glu Ser Pro Ser
             50             55             60
Asn Leu Ala Thr Leu Cys Tyr Lys Ala Val Glu Lys Leu Val Gln Gly
             65             70             75             80
Ala Glu Ser Gly Cys His Ser Glu Lys Glu Lys Gln Ile Val Leu Asn
             85             90             95
Cys Ser Arg Leu Leu Thr Arg Val Leu Pro Tyr Ile Phe Glu Asp Pro
             100            105            110
Asp Trp Arg Gly Phe Phe Trp Ser Thr Val Pro Gly Ala Gly Arg Gly
             115            120            125
Gly Gln Gly Glu Glu Asp Asp Glu His Ala Arg Pro Leu Ala Glu Ser
             130            135            140
Leu Leu Leu Ala Ile Ala Asp Leu Leu Phe Cys Pro Asp Thr Gln Ser
             145            150            155            160

```

350

His Arg Arg Ser Thr Val Asp Ser Ala Glu Asp Val His Ser Leu Asp  
 165 170 175  
 Ser Cys Glu Tyr Ile Trp Glu Ala Gly Val Gly Phe Ala His Ser Pro  
 180 185 190  
 Gln Pro Asn Tyr Ile His Asp Met Asn Arg Met Glu Leu Leu Lys Leu  
 195 200 205  
 Leu Leu Thr Cys Phe Ser Glu Ala Met Tyr Leu Pro Pro Ala Pro Glu  
 210 215 220  
 Ser Gly Ser Thr Asn Pro Trp Val Gln Phe Phe Cys Ser Thr Glu Asn  
 225 230 235 240  
 Arg His Ala Leu Pro Leu Phe Thr Ser Leu Leu Asn Thr Val Cys Ala  
 245 250 255  
 Tyr Asp Pro Val Gly Tyr Gly Ile Pro Tyr Asn His Leu Leu Phe Ser  
 260 265 270  
 Asp Tyr Arg Glu Pro Leu Val Glu Ala Gln Val Leu Ile Val Thr Leu  
 275 280 285  
 Asp His Asp Ser Ala Ser Ser Ala Ser Pro Thr Val Asp Gly Thr Thr  
 290 295 300  
 Thr Gly Thr Ala Met Asp Asp Ala Asp Pro Pro Gly Pro Glu Asn Leu  
 305 310 315 320  
 Phe Val Asn Tyr Leu Ser Arg Ile His Arg Glu Glu Asp Phe Gln Phe  
 325 330 335  
 Ile Leu Lys Gly Ile Ala Arg Leu Leu Ser Asn Pro Leu Leu Gln Thr  
 340 345 350  
 Tyr Leu Pro Asn Ser Thr Lys Lys Ile Gln Phe His Gln Glu Leu Leu  
 355 360 365  
 Val Leu Phe Trp Lys Leu Cys Asp Phe Asn Lys Lys Phe Leu Phe Phe  
 370 375 380  
 Val Leu Lys Ser Ser Asp Val Leu Asp Ile Leu Val Pro Ile Leu Phe  
 385 390 395 400  
 Phe Leu Asn Asp Ala Arg Ala Asp Gln Ser Arg Val Gly Leu Met His  
 405 410 415  
 Ile Gly Val Phe Ile Leu Leu Leu Leu Ser Gly Glu Arg Asn Phe Gly  
 420 425 430  
 Val Arg Leu Asn Lys Pro Tyr Ser Ile Arg Val Pro Met Asp Ile Pro  
 435 440 445  
 Val Phe Thr Gly Thr His Ala Asp Leu Leu Ile Val Val Phe His Lys  
 450 455 460  
 Ile Ile Thr Ser Gly His Gln Arg Leu Gln Pro Leu Phe Asp Cys Leu  
 465 470 475 480  
 Leu Thr Ile Val Val Asn Val Ser Pro Tyr Leu Lys Ser Leu Ser Met  
 485 490 495  
 Val Thr Ala Asn Lys Leu Leu His Leu Leu Glu Ala Phe Ser Thr Thr  
 500 505 510  
 Trp Phe Leu Phe Ser Ala Ala Gln Asn His His Leu Val Phe Phe Leu  
 515 520 525  
 Leu Glu Val Phe Asn Asn Ile Ile Gln Tyr Gln Phe Asp Gly Asn Ser  
 530 535 540  
 Asn Leu Val Tyr Ala Ile Ile Arg Lys Arg Ser Ile Phe His Gln Leu  
 545 550 555 560  
 Ala Asn Leu Pro Thr Asp Pro Pro Thr Ile His Lys Ala Leu Gln Arg  
 565 570 575  
 Arg Arg Arg Thr Pro Glu Pro Leu Ser Arg Thr Gly Ser Gln Glu Gly  
 580 585 590  
 Thr Ser Met Glu Gly Ser Arg Pro Ala Ala Pro Ala Glu Pro Gly Thr  
 595 600 605  
 Leu Lys Thr Ser Leu Val Ala Thr Pro Gly Ile Asp Lys Leu Thr Glu  
 610 615 620



351

Lys Ser Gln Val Ser Glu Asp Gly Thr Leu Arg Ser Leu Glu Pro Glu  
 625 630 635 640  
 Pro Gln Gln Ser Leu Glu Asp Gly Ser Pro Ala Lys Gly Glu Pro Ser  
 645 650 655  
 Gln Ala Trp Arg Glu Gln Arg Arg Pro Ser Thr Ser Ser Ala Ser Gly  
 660 665 670  
 Gln Trp Ser Pro Thr Pro Glu Trp Val Leu Ser Trp Lys Ser Lys Leu  
 675 680 685  
 Pro Leu Gln Thr Ile Met Arg Leu Leu Gln Val Leu Val Pro Gln Val  
 690 695 700  
 Glu Lys Ile Cys Ile Asp Lys Gly Leu Thr Asp Glu Ser Glu Ile Leu  
 705 710 715 720  
 Arg Phe Leu Gln His Gly Thr Leu Val Gly Leu Leu Pro Val Pro His  
 725 730 735  
 Pro Ile Leu Ile Arg Lys Tyr Gln Ala Asn Ser Gly Thr Ala Met Trp  
 740 745 750  
 Phe Arg Thr Tyr Met Trp Gly Val Ile Tyr Leu Arg Asn Val Asp Pro  
 755 760 765  
 Pro Val Trp Tyr Asp Thr Asp Val Lys Leu Phe Glu Ile Gln Arg Val  
 770 775 780

<210> 341  
 <211> 3307  
 <212> DNA  
 <213> Homo sapiens

<400> 341  
 gggccgcgga gctggagccg gagctgaagc cggagccggg ttggagtctg ggcgggggcc 60  
 gggccggagc gggctccaga gacatggggt cgaccgactc caagctgaac ttccggaagg 120  
 cggatgatcca gctcaccacc aagacgcagc ccgtggaagc caccgatgat gccttttggg 180  
 accagttctg ggcagacaca gccacctcgg tgcaggatgt gtttgcactg gtgccggcag 240  
 cagagatccg ggcggtgagg gaagagtcac cctccaactt ggccaccctg tgctacaagg 300  
 ccgttgagaa gctgggtgcag ggagctgaga gtggctgcca ctgggagaag gagaagcaga 360  
 tcgtcctgaa ctgcagccgg ctgctcaacc gcgtgctgcc ctacatcttt gaggaccccg 420  
 actggagggg ctctctcttg tccacagtgc ccggggcagg gcgaggaggg caggggagaag 480  
 aggatgatga gcatccagc cccctggcgg agtccctgct cctggccatt gctgacctgc 540  
 tcttctgccc ggacttcacg gttcagagcc accggaggag cactgtggac tcggcagagg 600  
 acgtccactc cctggacagc tgtgaataca tctgggaggc tgggtgtggc ttcgctcact 660  
 cccccagcc taactacatc cacgatatga accggatgga gctgctgaaa ctgctgctga 720  
 catgcttctc cgaggccatg tacctgcccc cagctccgga aagtggcagc accaaccat 780  
 ggggttcagtt cttttgttcc acggagaaca gacatgccct gccctcttc acctccctcc 840  
 tcaacaccgt gtgtgcctat gaccctgtgg gctacgggat cccctacaac cactgctct 900  
 tctctgacta ccgggaaccc ctggtggagg aggtgcccga ggtgctcatt gtcacttttg 960  
 accacgacag tgccagcagt gccagcccca ctgtggacgg caccaccact ggcaccgcca 1020  
 tggatgatgc cgatccctca ggccctgaga acctgtttgt gaactacctg tcccgcaccc 1080  
 atcgtgagga ggacttccag ttcatcctca aggtatagc ccggtgctg tccaaccccc 1140  
 tgctccagac ctacctgcct aactccacca agaagatcca gttccaccag gagctgctag 1200  
 ttctcttctg gaagctctgc gacttcaaca agaaattcct cttcttctg ctgaagagca 1260  
 gcgacgtcct agacatcctt gtcccatcc tcttcttct caacgatgcc cgggccgac 1320  
 agtctcgggt gggcctgatg cacattgggtg tcttcatctt gctgcttctg agcggggagc 1380  
 ggaacttcgg ggtgaggctg aacaaaccct actcaatccg cgtgcccag gacatcccag 1440  
 tcttcacagg gaccacgccc gacctgctca ttgtggtgtt ccacaagatc atcaccagcg 1500  
 ggcaccagcg gttgcagccc ctcttcgact gcctgctcac catcgtggtc aacgtgtccc 1560  
 cctacctcaa gagcctgtcc atggtgaccg ccaacaagt gctgcacctg ctggaggcct 1620  
 tctccaccac ctgggttctc ttctctgccc ccagaacca ccacctggtc ttcttctcc 1680  
 tggaggtctt caacaacatc atccagtacc agtttgatgg caactccaac ctggtctacg 1740  
 ccatcatccg caagcgcagc atcttccacc agctggccaa cctgcccag gaccgcccc 1800

```

ccattcacaa ggccctgcag cggcgccggc ggacacctga gcccttgtct cgcaccggct 1860
cccaggaggg cactccatg gagggctccc gcccgcgtgc ccctgcagag ccaggcacc 1920
tcaagaccag tctgggtggct actccaggca ttgacaagct gaccgagaag tcccagggtg 1980
cagaggatgg caccttgcg tccctggaac ctgagcccca gcagagcttg gaggatggca 2040
gcccggctaa gggggagccc agccaggcat ggagggagca gcggcgaccg tccacctcat 2100
cagccagtgg gcagtggagc ccaacgccag agtgggtcct ctcttggaag tcgaagctgc 2160
cgctgcagac catcatgagg ctgctgcagg tgctgggtcc gcagggtggag aagatctgca 2220
tcgacaaggg cctgacggat gagtctgaga tcctgcggtt cctgcagcat ggcaccctgg 2280
tggggctgct gcccgtgccc caccatcc tcatccgcaa gtaccaggcc aactcgggca 2340
ctgccatgtg gttccgcacc tacatgtggg gcgtcatcta tctgaggaat gtggaccccc 2400
ctgtctggta cgacaccgac gtgaagctgt ttgagataca gcgggtgtga ggatgaagcc 2460
gacgaggggc tcagcttagg ggaaggcagg gccttggtcc ctgaggcttc cccatccac 2520
cattctgagc tttaaattac cacgatcagg gcctggaaca ggccagagtg gccctggagt 2580
gtcatgccct agagaccct gtggccagga caatgtgaac tggctcagat cccctcaac 2640
ccctaggctg gactcacagg agcccatct ctggggctat gcccaccca gagaccactg 2700
cccccaacac tcggactccc tctttaagac ctggctcagt gctggcccct cagtgccac 2760
ccactcctgt gctaccagc cccagaggca gaagccaaaa tgggtcactg tgccctaagg 2820
ggtttgacca gggaaccacg ggctgtccct tgaggtgcct ggacagggtg agggggtgct 2880
tccagcctcc taacccaaag ccagctgttc caggctccag gggaaaaagg tgtggccagg 2940
ctgtcctcctg aggaggtgg gagctggccg actgcaaaag ccagactggg gcacctccg 3000
tatccttggg gcatgggtg ggtctcctgc tatattctcc tggatccgtg 3060
gaaatagcct ggctccctct taccagtaa tgaggggcag ggaagggaac tgggaggcag 3120
ccgtttagtc ctccctgccc tgcccactgc ctggatgggg cgatgccacc cctcatcctt 3180
caccacagct ctggcctctg ggtcccacca cccagccccc cgtgtcagaa caatctttgc 3240
tctgtacaat cggcctcttt acaataaaac ctctgtctcc ccaaaaaaaaa aaaaaaaaaa 3300
aaaaaaaaa 3307

```

&lt;210&gt; 342

&lt;211&gt; 788

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 342

```

Met Gly Ser Thr Asp Ser Lys Leu Asn Phe Arg Lys Ala Val Ile Gln
1          5          10          15
Leu Thr Thr Lys Thr Gln Pro Val Glu Ala Thr Asp Asp Ala Phe Trp
20          25          30
Asp Gln Phe Trp Ala Asp Thr Ala Thr Ser Val Gln Asp Val Phe Ala
35          40          45
Leu Val Pro Ala Ala Glu Ile Arg Ala Val Arg Glu Glu Ser Pro Ser
50          55          60
Asn Leu Ala Thr Leu Cys Tyr Lys Ala Val Glu Lys Leu Val Gln Gly
65          70          75          80
Ala Glu Ser Gly Cys His Ser Glu Lys Glu Lys Gln Ile Val Leu Asn
85          90          95
Cys Ser Arg Leu Leu Thr Arg Val Leu Pro Tyr Ile Phe Glu Asp Pro
100         105         110
Asp Trp Arg Gly Phe Phe Trp Ser Thr Val Pro Gly Ala Gly Arg Gly
115         120         125
Gly Gln Gly Glu Glu Asp Asp Glu His Ala Arg Pro Leu Ala Glu Ser
130         135         140
Leu Leu Leu Ala Ile Ala Asp Leu Leu Phe Cys Pro Asp Phe Thr Val
145         150         155         160
Gln Ser His Arg Arg Ser Thr Val Asp Ser Ala Glu Asp Val His Ser
165         170         175
Leu Asp Ser Cys Glu Tyr Ile Trp Glu Ala Gly Val Gly Phe Ala His
180         185         190
Ser Pro Gln Pro Asn Tyr Ile His Asp Met Asn Arg Met Glu Leu Leu

```



354

	660		665		670
Ser Ala	Ser Gly Gln Trp Ser	Pro Thr Pro Glu Trp	Val Leu Ser Trp		
	675	680	685		
Lys Ser	Lys Leu Pro Leu Gln Thr	Ile Met Arg Leu Leu	Gln Val Leu		
	690	695	700		
Val Pro	Gln Val Glu Lys Ile Cys Ile	Asp Lys Gly Leu Thr	Asp Glu		
705		710	715		720
Ser Glu	Ile Leu Arg Phe Leu Gln His	Gly Thr Leu Val Gly	Leu Leu		
	725	730	735		
Pro Val	Pro His Pro Ile Leu Ile	Arg Lys Tyr Gln Ala	Asn Ser Gly		
	740	745	750		
Thr Ala	Met Trp Phe Arg Thr Tyr	Met Trp Gly Val Ile	Tyr Leu Arg		
	755	760	765		
Asn Val	Asp Pro Pro Val Trp Tyr	Asp Thr Asp Val Lys	Leu Phe Glu		
	770	775	780		
Ile Gln	Arg Val				
785					

<210> 343  
 <211> 563  
 <212> DNA  
 <213> Homo sapiens

<400> 343  
 aggtacgcgg ggacagctgg cattcagcct ccagagcacc agcactggca ctggcactgg 60  
 cacacgctat ggcaaatgaa gtgcaagacc tgctctcccc tcggaaaggg ggacatcctc 120  
 ctgcagtaaa agctggagga atgagaattt ccaaaaaaca agaaattggc accttgaaa 180  
 gacataccaa aaaaacagga ttcgagaaaa caagtgccat tgcaaatgtt gccaaaatac 240  
 agacactgga tgccctgaat gacgcactgg agaagctcaa ctataaattt ccagcaacag 300  
 tgcacatggc gcatcaaaaa cccacacctg ctctggaaaa ggttggtcca ctgaaaagga 360  
 tctacattat tcagcagcct cgaaaatgtt aagcctggat ttaaaacaca gccgtctggc 420  
 cagctgcctc gaatatctga cagcttagca aaaagggcca aagctttcca taggcgtgct 480  
 gcacttgctt ggtaaatata gcagcttttg tatcttcccc tttgacttta ggtaataaag 540  
 catccaaact tgtaaaaaaa aaa 563

<210> 344  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 344  
 Met Ala Asn Glu Val Gln Asp Leu Leu Ser Pro Arg Lys Gly Gly His  
 1 5 10 15  
 Pro Pro Ala Val Lys Ala Gly Gly Met Arg Ile Ser Lys Lys Gln Glu  
 20 25 30  
 Ile Gly Thr Leu Glu Arg His Thr Lys Lys Thr Gly Phe Glu Lys Thr  
 35 40 45  
 Ser Ala Ile Ala Asn Val Ala Lys Ile Gln Thr Leu Asp Ala Leu Asn  
 50 55 60  
 Asp Ala Leu Glu Lys Leu Asn Tyr Lys Phe Pro Ala Thr Val His Met  
 65 70 75 80  
 Ala His Gln Lys Pro Thr Pro Ala Leu Glu Lys Val Val Pro Leu Lys  
 85 90 95  
 Arg Ile Tyr Ile Ile Gln Gln Pro Arg Lys Cys  
 100 105

<210> 345  
 <211> 3733  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(3733)  
 <223> n = A,T,C or G

<400> 345  
 acgcgtccgg gaaaccaggc actgcctgcc ggctttacat ccgttgatct gacctgactg 60  
 gaagcgcca aagagggacg gctgtcagcc ctgcttgact gagaaccac cagctcatcc 120  
 cagacacctc atagcaacct atttatacaa agggggaaag aaacacctga gcagaatgga 180  
 atcattatct ttttcccaag gagaaaaccg gggtaaaggg aggggaagcaa ttcaatttgg 240  
 agtccctgtg aatgggcttt cagaaggcaa ttaagaaat ccactcagag aggacttggg 300  
 gtgaaacttg ggtcctgttg ttttctgatt gtaagtggaa gcaggtcttg cacacgctgt 360  
 tggcaaatgt caggaccagg ttaagtgact ggcagaaaaa cttccagggtg gaacaagcaa 420  
 cccaggttct gctgcaagct tgaaggagcc tggagcggga gaaagctaac ttgaacatga 480  
 cctgttgcat ttggcaagtt cttagcaacat gctcctaagg aagcgataca ggcacagacc 540  
 atgcagactc cagttcctcc tgctgctcct gatgtcggga tgcgtcctga tgatggtggc 600  
 gatgttgca cctccccacc acaccctgca ccagactgtc acagcccaag ccagcaagca 660  
 cagccctgaa gccaggatcc gcttgactt tggggaatcc caggattggg tactggaagc 720  
 tgaggatgag ggtgaagagt acagccctct ggagggcctg ccacccttta tctcactgct 780  
 ggaggatcag ctgctggtgg ccgtggcctt accccaggcc agaaggaacc agagccaggg 840  
 caggagaggt gggagctacc gcctcatcaa gcagccaagg aggcaggata aggaagcccc 900  
 aaagagggac tggggggctg atgaggacgg ggaggtgtct gaagaagagg agttgacccc 960  
 gttcagcctg gaccacgtg gcctccagga ggcactcagt gcccgcaccc ccctccagag 1020  
 ggctctgccc gaggtgcggc acccactgtg tctgcagcag caccctcagg acagcctgcc 1080  
 cacagccagc gtcacacctc gtttccatga tgagggcctg tccactctcc tgcggactgt 1140  
 acacagcatc ctgcacacag tgcccagggc ctctctgaag gagatcatcc tctgtggacga 1200  
 cctcagccag caaggacaac tcaagtctgc tctcagcgaa tatgtggcca ggctggaggg 1260  
 ggtgaagtta ctgaggagca acaagaggct gggtgccatc agggcccggg tgctgggagc 1320  
 caccagagcc accggggatg tgctcgtctt catggatgcc cactgcgagt gccaccagg 1380  
 ctggctggag cccctcctca gcagaatagc ttgtgacagg agccgagtgg tatctccgg 1440  
 gatagatgtg attgactgga agactttcca gtattacccc tcaaaggacc tgcagcgtgg 1500  
 ggtgttgagc tggaagctgg atttccactg ggaacctttg ccagagcatg tgaggaagc 1560  
 cctccagtc cccataagcc ccactcaggag cctgtggtg cccggagagg ttggtggcct 1620  
 ggacagacat tacttccaaa acactggagc gtatgactct cttatgtcgc tgcgaggtgg 1680  
 tgaaaacctc gaactgtctt tcaaggcctg gctctgtggg ggctctgttg aaatccttcc 1740  
 ctgctctcgg gtaggacaca tctacaaaa tcaggattcc cattcccccc tgcaccagga 1800  
 ggccaccctg aggaacaggg ttgcattgct tgagacctgg ctggggtcat tcaaagaaac 1860  
 cttctacaag catagcccag aggccttctc cttgagcaag gctgagaagc cagactgcat 1920  
 ggaacgcttg cagctgcaaa ggagactggg ttgtcggaca ttccactggg ttctggctaa 1980  
 tgtctaccct gagctgtacc catctgaacc caggcccagt ttctctggaa agctccacaa 2040  
 cactggactt gggctctgtg cagactgcca ggcagaaggg gacatcctgg gctgtcccat 2100  
 ggtgttggt ccttgcaagt acagccggca gcaacagtac ctgcagcaca ccagcaggaa 2160  
 ggagattcac tttggcagcc cacagcacct gtgctttgct gtcaggcagg agcaggtgat 2220  
 tcttcagaac tgcacggagg aaggcctggc catccaccag cagcactggg acttccagga 2280  
 gaatgggatg attgtccaca ttctttctgg gaaatgcat gaagctgtgg tgcaagaaaa 2340  
 caataaagat ttgtacctgc gtccgtgtga tggaaaagcc cgccagcagt ggcgatttga 2400  
 ccagataaat gctgtggtat aacgatgaat gtcaatgtca gaaggaaaag agaattttgg 2460  
 ccatcaaaat ccagctccaa gtgaacttaa agagcttata tatttcatga agctgatcct 2520  
 tttgtgtgtg tgctcctggg gttaggagag aaaaaagctc tatgaaagaa tataggaagt 2580  
 ttctcctttt cacaccttat ttcatctgact gctggctgct ttaaaaaaaa aaaaaaaagg 2640  
 atccattngt accgttngtc ttcatcactg ggaaatgatt attacatagt nacagaagat 2700  
 tctttgtttt tctccactga gcaacttaaca attgncttct tctctggcct ggacattctc 2760  
 tggcagcacc tccaggatac ataaattcaa tggatcaatt tatttgtctt caaatggcct 2820

```

taacttggat tgtctgtttg gccaacccatg aaaattaaag agtctaagca gatgtaattgg 2880
cctgacattc caaaaactct gaattgggtt tattagcaca aatgttgtgt tcatttgttg 2940
agccatatct cagaangaag gaaangggna gctacagaaa nggaggttta ggattgcaga 3000
gaangatgca agnagcactt tggcccaatt ctccnagctn caaccagca gctgaaaagc 3060
ttcaagagat ctaggaaaag acattttcat gttaatgaga atttccacca ttgtagagaa 3120
tttccttctt actgagaatc tacctctatt cccctgccc tagctcttct ctaacttggt 3180
taaccataac cataaccaga ttcccttgca atcgatttct ctttagtctg ttggtgttaga 3240
agtaccagca caatttgagc attcccatta acaaagggtg tcacagttga gaaactctcc 3300
tgccggggcg ggtgggtcat gcctgtaatt ccagcacttt gggaggcaga gttgggagga 3360
ttacctgatg tcagggtgtt gagaccagcc tgggtcaacat tgcaaaacct tgtctctact 3420
aaaaatacaa aaattagctg ggcattggtg cgcataacctg tratcccagc tacttgggag 3480
gctgaggcaa gagaatcgct tgaaccatg angcagaagg tgcaatnagc tganatcatg 3540
ccattgcact tcaacctggg ngacagagt ggactncatc tcaaaaaaaaa aaaaaagagg 3600
gaacctttct gggncctgt tacagggttg cactgctgga gcanaacaca cttttttnaa 3660
aaagcaaacc tttttctggg gaggnaaagc caaaactggg ccaaantttt tgacnggaaa 3720
atttgggggt aag 3733

```

&lt;210&gt; 346

&lt;211&gt; 639

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 346

```

Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln Phe
 1          5          10          15
Leu Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val Ala Met
 20          25          30
Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr Ala Gln Ala
 35          40          45
Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp Phe Gly Glu Ser
 50          55          60
Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly Glu Glu Tyr Ser Pro
 65          70          75          80
Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu Arg Glu Asp Gln Leu Leu
 85          90          95
Val Ala Val Ala Leu Pro Gln Ala Arg Arg Asn Gln Ser Gln Gly Arg
100          105          110
Arg Gly Gly Ser Tyr Arg Leu Ile Lys Gln Pro Arg Arg Gln Asp Lys
115          120          125
Glu Ala Pro Lys Arg Asp Trp Gly Ala Asp Glu Asp Gly Glu Val Ser
130          135          140
Glu Glu Glu Glu Leu Thr Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln
145          150          155          160
Glu Ala Leu Ser Ala Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val
165          170          175
Arg His Pro Leu Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr
180          185          190
Ala Ser Val Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu
195          200          205
Arg Thr Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys
210          215          220
Glu Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser
225          230          235          240
Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu Arg
245          250          255
Ser Asn Lys Arg Leu Gly Ala Ile Arg Ala Arg Met Leu Gly Ala Thr
260          265          270
Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His Cys Glu Cys

```

357

275	280	285
His Pro Gly Trp Leu Glu Pro	Leu Leu Ser Arg Ile Ala Gly Asp Arg	
290	295	300
Ser Arg Val Val Ser Pro Val	Ile Asp Val Ile Asp Trp Lys Thr Phe	
305	310	315
Gln Tyr Tyr Pro Ser Lys Asp	Leu Gln Arg Gly Val Leu Asp Trp Lys	
325	330	335
Leu Asp Phe His Trp Glu Pro	Leu Pro Glu His Val Arg Lys Ala Leu	
340	345	350
Gln Ser Pro Ile Ser Pro Ile	Arg Ser Pro Val Val Pro Gly Glu Val	
355	360	365
Val Ala Met Asp Arg His Tyr	Phe Gln Asn Thr Gly Ala Tyr Asp Ser	
370	375	380
Leu Met Ser Leu Arg Gly Gly	Glu Asn Leu Glu Leu Ser Phe Lys Ala	
385	390	395
Trp Leu Cys Gly Gly Ser Val	Glu Ile Leu Pro Cys Ser Arg Val Gly	
405	410	415
His Ile Tyr Gln Asn Gln Asp	Ser His Ser Pro Leu Asp Gln Glu Ala	
420	425	430
Thr Leu Arg Asn Arg Val Arg	Ile Ala Glu Thr Trp Leu Gly Ser Phe	
435	440	445
Lys Glu Thr Phe Tyr Lys His	Ser Pro Glu Ala Phe Ser Leu Ser Lys	
450	455	460
Ala Glu Lys Pro Asp Cys Met	Glu Arg Leu Gln Leu Gln Arg Arg Leu	
465	470	475
Gly Cys Arg Thr Phe His Trp	Phe Leu Ala Asn Val Tyr Pro Glu Leu	
485	490	495
Tyr Pro Ser Glu Pro Arg Pro	Ser Phe Ser Gly Lys Leu His Asn Thr	
500	505	510
Gly Leu Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp Ile Leu Gly	
515	520	525
Cys Pro Met Val Leu Ala Pro	Cys Ser Asp Ser Arg Gln Gln Gln Tyr	
530	535	540
Leu Gln His Thr Ser Arg Lys	Glu Ile His Phe Gly Ser Pro Gln His	
545	550	555
Leu Cys Phe Ala Val Arg Gln	Glu Gln Val Ile Leu Gln Asn Cys Thr	
565	570	575
Glu Glu Gly Leu Ala Ile His	Gln Gln His Trp Asp Phe Gln Glu Asn	
580	585	590
Gly Met Ile Val His Ile Leu	Ser Gly Lys Cys Met Glu Ala Val Val	
595	600	605
Gln Glu Asn Asn Lys Asp Leu	Tyr Leu Arg Pro Cys Asp Gly Lys Ala	
610	615	620
Arg Gln Gln Trp Arg Phe Asp	Gln Ile Asn Ala Val Asp Glu Arg	
625	630	635

<210> 347  
 <211> 1891  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(1891)  
 <223> n = A,T,C or G

<400> 347

```

gagtcaccaa ggaaggcagc ggcagctcca ctcagccagt acccagatac gctgggaacc 60
ttccccagcc atggcttccc tggggcagat cctcttctgg agcataatta gcatcatcat 120
tattctggct ggagcaattg cactcatcat tggctttggt atttcagga gacactccat 180
cacagtcaact actgtcgcct cagctgggaa cattggggag gatggaatcc tgagctgcac 240
ttttgaacct gacatcaaac tttctgatat cgtgatacaa tggctgaagg aagggtgttt 300
aggcttggtc catgagttca aagaaggcaa agatgagctg tcggagcagg atgaaatgtt 360
cagaggcccg acagcagtggt ttgctgatca agtgatagtt ggcaatgcct ctttgcggct 420
gaaaaacgtg caactcacag atgctggcac ctacaaatgt tataatcatca cttctaaagg 480
caagggaat gctaaccttg agtataaaac tggagccttc agcatgccgg aagtgaatgt 540
ggactataat gccagctcag agaccttgcg gtgtgaggct ccccgatggt tccccagcc 600
cacagtggtc tgggcatccc aagttgacca gggagccaac ttctcggaag tctccaatac 660
cagctttgag ctgaactctg agaatgtgac catgaagggt gtgtctgtgc tctacaatgt 720
tacgatcaac aacacatact cctgtatgat tgaaaatgac attgccaaag caacagggga 780
tatcaaagt acagaatcgg agatcaaaag gcggagtcac ctacagctgc taaactcaaa 840
ggcttctctg tgtgtctctt ctttctttgc catcagctgg gcacttctgc ctctcagccc 900
ttacctgatg ctaaaataat gtgcctcggc cacaaaaaag catgcaaagt cattgttaca 960
acagggatct acagaactat ttcaccacca gatatgacct agttttatat ttctgggagg 1020
aaatgaattc atatctagaa gtctggagtg agcaaacaag agcaagaaac aaaaagaagc 1080
caaaagcaga wrkctscarw atkmccctt agcgtggtcg cssccssagg tacaggacgt 1140
ctccccatta caactacca atccgaagt tcaactgtgt caggactaag aaacctgtgt 1200
tttgagttaga aaaggcctg gaaagagggg agccaacaaa tctgtctgct tctcacatt 1260
agtcattggc aaataagcat tctgtctctt tggctgtgc ctcagcacag agagccagaa 1320
ctctatcggg caccaggata acatctctca gtgaacanga gttgacaagg cctatgggaa 1380
atgcctgatg ggattatctt cagcttgttg agcttctaag tttctttccc ttcattctac 1440
cctgcaagcc aagttctgta agagaaatgc ctgagttcta gctcaggttt tcttactctg 1500
aatttagatc tccagacct tctggccac aattcaaatt aaggcaacaa acatatacct 1560
tccatgaang cacacacaga cttttgaaag caaggacaat gactgcttga attgaggcct 1620
tgaangaatg aangcntttg aaggnaaaag aantactttt gtttccagcc cccnttnc 1680
acactncttc atgtgttaan ccactgcnc tncctggann ccttggngang cccacggntg 1740
nactgntatt nacatngttg tttnatagaa aannontgat tttaganngt tncgtnatcg 1800
nttcnaagna gaatgnattw aaaatatacy attttccbaa aaaaaaaaaa aaaaaaaaaa 1860
maaagtacct cggccgcgac cagcctaagg g 1891

```

&lt;210&gt; 348

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 348

```

Met Ala Ser Leu Gly Gln Ile Leu Phe Trp Ser Ile Ile Ser Ile Ile
  1             5             10             15
Ile Ile Leu Ala Gly Ala Ile Ala Leu Ile Ile Gly Phe Gly Ile Ser
      20             25             30
Gly Arg His Ser Ile Thr Val Thr Val Ala Ser Ala Gly Asn Ile
      35             40             45
Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
      50             55             60
Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val
      65             70             75             80
His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met
      85             90             95
Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Ile Val Gly Asn
      100            105            110
Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
      115            120            125
Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu
      130            135            140
Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn

```



359

145		150		155		160
Ala Ser Ser Glu Thr	Leu Arg Cys Glu Ala	Pro Arg Trp Phe Pro Gln				
	165	170		175		
Pro Thr Val Val Trp	Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser					
	180	185		190		
Glu Val Ser Asn Thr	Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met					
	195	200		205		
Lys Val Val Ser Val	Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser					
	210	215		220		
Cys Met Ile Glu Asn	Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val					
	225	230		235		240
Thr Glu Ser Glu Ile	Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser					
	245	250		255		
Lys Ala Ser Leu Cys	Val Ser Ser Phe Phe Ala Ile Ser Trp Ala Leu					
	260	265		270		
Leu Pro Leu Ser Pro	Tyr Leu Met Leu Lys					
	275	280				

&lt;210&gt; 349

&lt;211&gt; 1517

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1517)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 349

```

ttagggagtc gacccacgcg tccggcccgg acgcggaaga actggcccag cggagggttc 60
cgcttctgaa gcgtgggagg cggaagagac tgcagccccg gccccgtcc ccaagcctcc 120
gcccttagc ccccgcccc agctgccagt cccagcagc tcagtcctgc agtgagagtc 180
ttgggagtc atagctaagc accaggagct gagcactgcc cgctgtgcct gcctgcaagt 240
ctgacatggc tcaggagaaa atggagctgg accttgagcc tgacacatct tatgggggaa 300
ccctgaggag atccagcagc gctcccctaa tccatgggct cagtgcctt tcacagggtt 360
tccaacctta cacacttaga actcggagga atagtacaac aattatgagc cgtcacagcc 420
tggaagaagg cctggatatg gtgaacagag aaactgcaca tgaaagggaa atgcaaacgg 480
caatgcagat aagccaatca tgggatgaga gcttgagcct gagtgcagc gattttgaca 540
agccggagaa attatattct cctaagagaa ttgacttcac tccagtttct ccagcacctt 600
caccaccag gggattcgga aagatgttcg tgagcagcag tggattgcca ccaagtccag 660
ttcccagtc aagacgattt tcaagcagga gaagtcagag tccagtcaag tgcattagac 720
ccagtgttct tggctcctctt aaaagaaaag gtgaaatgga gacagaaagt cagcccaaga 780
gactcttcca aggcactacc aatatgttat ctccagatgc cgcgcaactg tctgatctca 840
gttcatgttc agatattttg gatggcagta gtagcagcag tggcttatcc tcagaccgcg 900
tggctaaagg cagcgctacc gcagagtctc cagtagcatg ctccaattca tgctcttcgt 960
tcatcttgat ggatgatctc tcaccaagt gacttaacca tttctgattc aacgttttaa 1020
ctgctgtttc ctacataaaa tgttttagtg ggaacgcaga gaactttgat ccataatgag 1080
gattaaagtt ttacagattt cacacattct gatgctatta ttactctttg gcattctctc 1140
tctccaaagt tcaattttgt gagcctagtg accttactag tatctggttt tgctgatctc 1200
atcttgatt tagtgattaa atctcaaagt ctgatttttg attgcttaga ggaatctttt 1260
ttcttagtgc ctcaaaaaac acctattttg agtctataca tttaagaaag gcaactgatg 1320
gtattgcctt taatgggtcc ttttcgcgag caagtgatat gacagatttg atcagaaatt 1380
ctcttgcttg agagattttt ttttgcctc tgttgactac atagtttcaa atctctcttt 1440
atctcatgat gatataataa ttgcttttaa ttatatnaaa ttttattttc tggatcagct 1500
tcaagaccat tattttg 1517

```

&lt;210&gt; 350

360

<211> 243  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <221> VARIANT  
 <222> (1)...(243)  
 <223> Xaa = Any Amino Acid

<400> 350  
 Met Ala Gln Glu Lys Met Glu Leu Asp Leu Glu Pro Asp Thr Ser Tyr  
 1 5 10 15  
 Gly Gly Thr Leu Arg Arg Ser Ser Ser Ala Pro Leu Ile His Gly Leu  
 20 25 30  
 Ser Asp Leu Ser Gln Val Phe Gln Pro Tyr Thr Leu Arg Thr Arg Arg  
 35 40 45  
 Asn Ser Thr Thr Ile Met Ser Arg His Ser Leu Glu Glu Gly Leu Asp  
 50 55 60  
 Met Val Asn Arg Glu Thr Ala His Glu Arg Glu Met Gln Thr Ala Met  
 65 70 75 80  
 Gln Ile Ser Gln Ser Trp Asp Glu Ser Leu Ser Leu Ser Asp Ser Asp  
 85 90 95  
 Phe Asp Lys Pro Glu Lys Leu Tyr Ser Pro Lys Arg Ile Asp Phe Thr  
 100 105 110  
 Pro Val Ser Pro Ala Pro Ser Pro Thr Arg Gly Phe Gly Lys Met Phe  
 115 120 125  
 Val Ser Ser Ser Gly Leu Pro Pro Ser Pro Val Pro Ser Pro Arg Arg  
 130 135 140  
 Phe Ser Ser Arg Arg Ser Gln Ser Pro Val Lys Cys Ile Arg Pro Ser  
 145 150 155 160  
 Val Leu Gly Pro Leu Lys Arg Lys Gly Glu Met Glu Thr Glu Ser Gln  
 165 170 175  
 Pro Lys Arg Leu Phe Gln Gly Thr Thr Asn Met Leu Ser Pro Asp Ala  
 180 185 190  
 Ala Gln Leu Ser Asp Leu Ser Ser Cys Ser Asp Ile Leu Asp Gly Ser  
 195 200 205  
 Ser Ser Ser Ser Gly Leu Ser Ser Asp Pro Leu Ala Xaa Xaa Gln Arg  
 210 215 220  
 Tyr Arg Arg Val Ser Ser Ser Met Leu Gln Phe Met Leu Phe Val His  
 225 230 235 240  
 Leu Asp Gly

<210> 351  
 <211> 248  
 <212> PRT  
 <213> Homo sapiens

<400> 351  
 Met Ala Gln Glu Lys Met Glu Leu Asp Leu Glu Pro Asp Thr Ser Tyr  
 1 5 10 15  
 Gly Gly Thr Leu Arg Arg Ser Ser Ser Ala Pro Leu Ile His Gly Leu  
 20 25 30  
 Ser Asp Leu Ser Gln Val Phe Gln Pro Tyr Thr Leu Arg Thr Arg Arg  
 35 40 45  
 Asn Ser Thr Thr Ile Met Ser Arg His Ser Leu Glu Glu Gly Leu Asp  
 50 55 60

361

Met Val Asn Arg Glu Thr Ala His Glu Arg Glu Met Gln Thr Ala Met  
 65 70 75 80  
 Gln Ile Ser Gln Ser Trp Asp Glu Ser Leu Ser Leu Ser Asp Ser Asp  
 85 90 95  
 Phe Asp Lys Pro Glu Lys Leu Tyr Ser Pro Lys Arg Ile Asp Phe Thr  
 100 105 110  
 Pro Val Ser Pro Ala Pro Ser Pro Thr Arg Gly Phe Gly Lys Met Phe  
 115 120 125  
 Val Ser Ser Ser Gly Leu Pro Pro Ser Pro Val Pro Ser Pro Arg Arg  
 130 135 140  
 Phe Ser Ser Arg Arg Ser Gln Ser Pro Val Lys Cys Ile Arg Pro Ser  
 145 150 155 160  
 Val Leu Gly Pro Leu Lys Arg Lys Gly Glu Met Glu Thr Glu Ser Gln  
 165 170 175  
 Pro Lys Arg Leu Phe Gln Gly Thr Thr Asn Met Leu Ser Pro Asp Ala  
 180 185 190  
 Ala Gln Leu Ser Asp Leu Ser Ser Cys Ser Asp Ile Leu Asp Gly Ser  
 195 200 205  
 Ser Ser Ser Ser Gly Leu Ser Ser Asp Pro Leu Ala Lys Gly Ser Ala  
 210 215 220  
 Thr Ala Glu Ser Pro Val Ala Cys Ser Asn Ser Cys Ser Ser Phe Ile  
 225 230 235 240  
 Leu Met Asp Asp Leu Ser Pro Lys  
 245

&lt;210&gt; 352

&lt;211&gt; 1529

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1529)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 352

ttagggagtc gaccacgcg tccggcccg acgcggaaga actggcccag cggagggttc 60  
 cgcttctgaa gcgtgggagg cggaagagac tgcagcccc gccccgctcc ccaagcctcc 120  
 gccccttagc ccccgcccc agctgccagt cccagcagc tcagtcctgc agtgagagtc 180  
 ttgggagtc atagctaagc accaggagct gagcactgcc cgctgtgctt gcctgcaagt 240  
 ctgacatggc tcaggagaaa atggagctgg accttgagcc tgacacatct tatgggggaa 300  
 ccctgaggag atccagcagc gctcccctaa tccatgggct cagtgaacct tcacagggtt 360  
 tccaacctta cacacttaga actcggagga atagtacaac aattatgagc cgtcacagcc 420  
 tggttaagtat agaagaagaa ggccctggata tggatgaacag agaaactgca catgaaaggg 480  
 aaatgcaaac ggcaatgcag ataagccaat catgggatga gagcttgagc ctgagtgaca 540  
 gtgattttga caagccggag aaattatatt ctccaaagag aattgacttc actccagttt 600  
 ctccagcacc ttcacccacc aggggattcg gaaagatgtt cgtgagcagc agtggattgc 660  
 caccaagtcc agttccagc ccaagacgat tttcaagcag gagaagtcag agtccagtca 720  
 agtgcattag acccagtgtt cttggtcttc ttaaaagaaa aggtgaaatg gagacagaaa 780  
 gtcagcccaa gagactcttc caaggcacta ccaatatgtt atctccagat gccgcgcaac 840  
 tgtctgatct cagttcatgt tcagatatat tggatggcag tagtagcagc agtggcttat 900  
 cctcagaccc gctggctaaa ggcagcgcta ccgcagagtc tccagtagca tgctccaatt 960  
 catgctcttc gttcatcttg atggatgac tctcacccaa gtgacttaac catttctgat 1020  
 tcaacgtttt aactgctgtt tctacataa aatgtttagt ggggaacgca gagaactttg 1080  
 atccataatg aggattaaag ttttacagat ttcacacatt ctgatgctat tattactctt 1140  
 tggcatctct cttctccaaa gttcaatttt gtgagcctag tgaccttact agtatctggt 1200  
 tttgctgac tcattttgga tttagtgtt aaatctcaaa tgctgatttt tgattgctta 1260

362

gaggaatctt ttttcttagt gcctcaaaaa acacctatatt tgagtctata catttaagaa 1320  
 aggcactgat gtgtattgcc tttaatgggt ctttttcgcg agcaagtgat atgacagatt 1380  
 tgatcagaaa ttctcttgct tgagagattt ttttttgctc tctgttgact acatagtttc 1440  
 aaatctctct ttatttcacg atgatataa aattgctttt aattatatna aattttattt 1500  
 tctggatcag cttcaagacc attattttg 1529

&lt;210&gt; 353

&lt;211&gt; 252

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 353

Met	Ala	Gln	Glu	Lys	Met	Glu	Leu	Asp	Leu	Glu	Pro	Asp	Thr	Ser	Tyr
1				5					10					15	
Gly	Gly	Thr	Leu	Arg	Arg	Ser	Ser	Ser	Ala	Pro	Leu	Ile	His	Gly	Leu
			20					25					30		
Ser	Asp	Leu	Ser	Gln	Val	Phe	Gln	Pro	Tyr	Thr	Leu	Arg	Thr	Arg	Arg
		35					40					45			
Asn	Ser	Thr	Thr	Ile	Met	Ser	Arg	His	Ser	Leu	Val	Ser	Ile	Glu	Glu
	50					55					60				
Glu	Gly	Leu	Asp	Met	Val	Asn	Arg	Glu	Thr	Ala	His	Glu	Arg	Glu	Met
65					70					75					80
Gln	Thr	Ala	Met	Gln	Ile	Ser	Gln	Ser	Trp	Asp	Glu	Ser	Leu	Ser	Leu
				85					90					95	
Ser	Asp	Ser	Asp	Phe	Asp	Lys	Pro	Glu	Lys	Leu	Tyr	Ser	Pro	Lys	Arg
			100					105					110		
Ile	Asp	Phe	Thr	Pro	Val	Ser	Pro	Ala	Pro	Ser	Pro	Thr	Arg	Gly	Phe
		115					120						125		
Gly	Lys	Met	Phe	Val	Ser	Ser	Ser	Gly	Leu	Pro	Pro	Ser	Pro	Val	Pro
	130						135				140				
Ser	Pro	Arg	Arg	Phe	Ser	Ser	Arg	Arg	Ser	Gln	Ser	Pro	Val	Lys	Cys
145					150					155					160
Ile	Arg	Pro	Ser	Val	Leu	Gly	Pro	Leu	Lys	Arg	Lys	Gly	Glu	Met	Glu
				165					170					175	
Thr	Glu	Ser	Gln	Pro	Lys	Arg	Leu	Phe	Gln	Gly	Thr	Thr	Asn	Met	Leu
			180					185					190		
Ser	Pro	Asp	Ala	Ala	Gln	Leu	Ser	Asp	Leu	Ser	Ser	Cys	Ser	Asp	Ile
		195					200					205			
Leu	Asp	Gly	Ser	Ser	Ser	Ser	Ser	Gly	Leu	Ser	Ser	Asp	Pro	Leu	Ala
	210					215					220				
Lys	Gly	Ser	Ala	Thr	Ala	Glu	Ser	Pro	Val	Ala	Cys	Ser	Asn	Ser	Cys
225					230					235					240
Ser	Ser	Phe	Ile	Leu	Met	Asp	Asp	Leu	Ser	Pro	Lys				
				245					250						

&lt;210&gt; 354

&lt;211&gt; 1574

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(1574)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 354

ttagggagtc gaccacacgcg tccggcccg acgcggaaga actggcccag cggaggttcc 60

363

```

cgcttctgaa gcgtgggagg cggaagagac tgcagccccc gcccccgccc ccaagcctcc 120
gcccccttagc ccccgccccc agctgccagt cccagcagc tcagtcctgc agtgagagtc 180
ttgggagtc atagctaagc accaggagct gagcactgcc cgctgtgcoct gcctgcaagt 240
ctgacatggc tcaggagaaa atggagctgg accttgagcc tgacacatct tatgggggaa 300
ccctgaggag atccagcagc gctcccctaa tccatgggct cagtgcctt tcacagggtt 360
tccaacctta cacacttaga actcggagga atagtacaac aattatgagc cgtcacagcc 420
tggttgctgtc atcctcacct aatcgtattc ctagtagcag actgcatcag atcaaaaggg 480
aagaaggcct ggatatgggtg aacagagaaa ctgcacatga aagggaaatg caaacggcaa 540
tgcagataag ccaatcatgg gatgagagct tgagcctgag tgacagtgat tttgacaagc 600
cggagaaatt atattctcct aagagaattg acttcactcc agtttctcca gcaccttcac 660
ccaccagggg attcggaaag atgttcgtga gcagcagtg attgccacca agtccagttc 720
ccagtccaag acgattttca agcaggagaa gtcagagtcc agtcaagtgc attagacca 780
gtgttcttgg tcctcttaaa agaaaagggtg aaatggagac agaaagtcag cccaagagac 840
tcttccaagg cactaccaat atgttatctc cagatgccgc gcaactgtct gatctcagtt 900
catgttcaga tattttggat ggcagtagta gcagcagtg cttatcctca gaccgctgg 960
ctaaaggcag cgctaccgca gagtctccag tagcatgctc caattcatgc tcttcgttca 1020
tcttgatgga tgatctctca cccaagtgc ttaaccattt ctgattcaac gttttaactg 1080
ctgtttccta cataaaatgt ttagtgggga acgcagagaa ctttgatcca taatgaggat 1140
taaagtttta cagatttcac acattctgat gctattatta ctctttggca tctctcttct 1200
ccaaagttca atttgtgag cctagtggacc ttactagtat ctggttttgc tgatctcatt 1260
ttggatttag tgattaaatc tcaaatgctg atttttgatt gcttagagga atcttttttc 1320
ttagtgctc aaaaaacacc tattttgagt ctatacattt aagaaaggca ctgatgtgta 1380
ttgcctttaa tgggtccttt tccgcagcaa gtgatatgac agatttgatc agaaattctc 1440
ttgcttgaga gatttttttt tgtcctctgt tgactacata gtttcaaatc tctctttatt 1500
tcatgatgat atataaattg cttttaatta tatnaaattt tattttctgg atcagcttca 1560
agaccattat tttg 1574

```

&lt;210&gt; 355

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 355

```

Met Ala Gln Glu Lys Met Glu Leu Asp Leu Glu Pro Asp Thr Ser Tyr
1      5      10      15
Gly Gly Thr Leu Arg Arg Ser Ser Ser Ala Pro Leu Ile His Gly Leu
20      25      30
Ser Asp Leu Ser Gln Val Phe Gln Pro Tyr Thr Leu Arg Thr Arg Arg
35      40      45
Asn Ser Thr Thr Ile Met Ser Arg His Ser Leu Leu Leu Ser Ser Ser
50      55      60
Pro Asn Arg Ile Pro Ser Ser Arg Leu His Gln Ile Lys Arg Glu Glu
65      70      75      80
Gly Leu Asp Met Val Asn Arg Glu Thr Ala His Glu Arg Glu Met Gln
85      90      95
Thr Ala Met Gln Ile Ser Gln Ser Trp Asp Glu Ser Leu Ser Leu Ser
100     105     110
Asp Ser Asp Phe Asp Lys Pro Glu Lys Leu Tyr Ser Pro Lys Arg Ile
115     120     125
Asp Phe Thr Pro Val Ser Pro Ala Pro Ser Pro Thr Arg Gly Phe Gly
130     135     140
Lys Met Phe Val Ser Ser Ser Gly Leu Pro Pro Ser Pro Val Pro Ser
145     150     155     160
Pro Arg Arg Phe Ser Ser Arg Arg Ser Gln Ser Pro Val Lys Cys Ile
165     170     175
Arg Pro Ser Val Leu Gly Pro Leu Lys Arg Lys Gly Glu Met Glu Thr
180     185     190
Glu Ser Gln Pro Lys Arg Leu Phe Gln Gly Thr Thr Asn Met Leu Ser

```

364

195	200	205
Pro Asp Ala Ala Gln Leu Ser	Asp Leu Ser Ser	Cys Ser Asp Ile Leu
210	215	220
Asp Gly Ser Ser Ser Ser	Gly Leu Ser Ser	Asp Pro Leu Ala Lys
225	230	235
Gly Ser Ala Thr Ala Glu Ser	Pro Val Ala Cys	Ser Asn Ser Cys Ser
245	250	255
Ser Phe Ile Leu Met Asp Asp	Leu Ser Pro Lys	
260	265	

<210> 356  
 <211> 4458  
 <212> DNA  
 <213> Homo sapiens

<400> 356

gtcgacccac	gcgtccggcg	atgcctcgct	ggctttctgct	ttcattgacc	tttgccgggtc	60
tgttcccgc	gcggcgccgg	cagctgcttg	gtagtgtgcg	ggggcgtag	ggcggtggcc	120
cagaccaacc	ggctggcagc	ccagctccgc	tccgcccgc	cctgcctcgg	accctgcgcc	180
tgaggaagta	tcgaggcaac	cctctgccac	ccgaagtctg	tgggtcgctc	ccagaggcg	240
cgccctggag	ccgagcgccc	ttgggcggcc	atctggaggc	caggtgcggg	ccgcaaccc	300
gcgaggagcg	cgcgccgggc	gcggcgccga	cggcaggagg	aggggcggg	agcccggg	360
ccgccgaagg	acgccccgtc	ctccacatgc	tgccacttgg	ctgagccggg	cgccggcgag	420
aaggcgggcg	cgctgcccctg	gcagctggac	tgcactttgc	ccccgccgg	cctcagctgc	480
cgcccgccca	gacgccagca	agccccctc	ccacgacagg	gctgctccgg	gagcttcgga	540
gaccgcgccc	gggcctgagc	gcaggctgcc	tccgggaccc	cacggctgtc	cggacgtgcc	600
atgggcgcgc	agctgcccgg	caacgtgttg	tgtaagtga	catctgggag	gtaaacacta	660
cacgtgaaga	gtggtgaaag	ggaacattga	ttactgaagt	gcctggaga	gggaaagcac	720
tggtcaacat	gcataggaca	aatttcattg	ttttctaaag	atggcctgga	agtagtcttt	780
gccactgctt	cctccacaaa	cagctcttca	taacatgggc	tgcatgaaat	caaagcaaac	840
tttcccat	cctaccatat	atgaagtgga	gaagcagcat	gagagtgaag	aaccctttat	900
gccagaagag	agatgtctac	ctaggatggc	ttctccagtt	aatgtcaaag	aggaagtga	960
ggaacctcca	gggaccaata	ttgtgatctt	ggaatatgca	caccgcctgt	ctcaggatat	1020
cttgtgtgat	gccttgacgc	aatgggcatg	caataacatc	aagtaccatg	acattccata	1080
cattgagagt	gaggggcctt	gaggctgtag	gatgacaaca	ctttgactgt	ggaggtgcta	1140
gtttgaataa	atgtgacaaa	agcaaaaact	ggtgtgaaaa	agtacaaata	actatctgga	1200
tttaaaaatg	tgtctacgat	aatgtcacta	ttataagaac	aactaggatg	aaatgcattt	1260
taagtacttc	tatgttaaca	gcaatttctg	tttagtctta	gatttttagtc	atctgaagg	1320
ctgaacagag	gtcctgtgac	acccaataat	cagctgaatg	tcacagcact	tcttcctaag	1380
taatggcatc	accaaagaaa	atgctaagga	ataaaaactg	cccaaattc	caatggttga	1440
agtttatcct	ttaaaataac	aatttttggt	tatacccaaa	aaaagtccag	atatgaaaag	1500
ggcttttcta	aaatttcttg	gcgagggaat	ggcactcaaa	tcatagtgat	taacagtaag	1560
tcttgtttgt	ttgtcaagga	tctctacttc	ttgacacaaa	tgaaccctgt	ctttaataag	1620
ataagatatt	tatttttgta	gatgagaagt	gtaactacca	ccttggacct	cagggcccta	1680
actaattaca	gctgttactg	gacgactcag	actttgtgcc	taaagccatc	ttagagataa	1740
cagtttatag	aagccatgac	attagtgttt	attgcattga	attaagccca	gtgatataac	1800
tatacaagaa	aacaagtatg	ggtacctttt	acaaagagca	atccaataaa	tcttaaaaaat	1860
aacagaaact	tagtctgcaa	ggtagaaagt	ttcagtttta	attctgtatt	aagctttact	1920
atctcagagg	tacagagggc	tggaatatgg	gcatttattt	ccagtttttt	cttgactagt	1980
aaggcggtca	ccattaaaat	agaccagatg	ataatgcatg	aagatttaca	gttgatttgc	2040
aaaacggaaa	agataaaaact	gtccttttgag	gagagtactc	gttttctggg	tttttggtat	2100
tttttagtgg	taacacaagc	ctatagggca	tttatagcca	cctattatac	tgtttccata	2160
agcctggcta	ccttttaggg	aagctatttt	ttctctttca	tttttactgt	cacagcacat	2220
acacacacac	ctttttgttt	taaaggatta	agtactgttt	gaagatcagt	ggtaacagaa	2280
aatttgggag	ggagaagaag	aaattaagac	atgacttggt	agaaaattaa	gacttcagtt	2340
tctagaatta	tcttttcac	aagatttggt	agacattgag	tttaaatgga	aaggaaatta	2400
tttaagcctg	tgtatgttag	atccacaata	caccattggt	attgaaatat	aaagggttaa	2460

```

aaaaaggctt atgacctctt taatgagata aatatgtatt tgtcttgtaa gcaggcagaa 2520
aatctacctc taattttaac actaatactt tgaaacccac aatcaaatag agtgaattct 2580
ccaagttaca taagcaagga aaacattatt tgaatatatgc catgttttcg ttgccttttg 2640
acacctcatc attcaactct aattttaccg agtcccgga tttgtactgt cccattgtac 2700
ttgcaatcta caatttatat aatagaaaaa caaccaaac cattcataca aggatctgaa 2760
gttataaggt taagggcaga aagtttccca taagtataaa acatttccag gtcataga 2820
gtagtttagg ttgagtgaaca aaagcctagg tgtggttggt tttcattcat tttgcatctc 2880
acaccaagac atttttgctg caaggtcatc tgctgcttaa aatgtacaat taggtatata 2940
aaataagtac aatggtgaaa acacaaagcc aggtaaagca gcatgccccca cttaaattttt 3000
cagtatacat agggacagac aagtgaagtt tggttgatc taaatatttt aatttcaggt 3060
tccttctgtg ccctgggcca ctatttccca ggggtgtgac agagatgcct gccagatcca 3120
tatcaactag aagtctgatt tctgttgctg cccttctca gcaactatgg cagtatactt 3180
ttatcaccaa gcaccactcc cttgtccctg aatcacattt taatagagta caatatcttc 3240
tgtacaatat ttctgaaaca cttatgtctg aaatatatgc tgtattgtat gtttaacccat 3300
gacatatatg aactacaagg cttgcataat cagtgaagta gtggataaat caagacagga 3360
gcaaatggga gaaagatgaa taaacaaatg aaaaaagatg aataaatgaa taagagagat 3420
gaataaacia atttacatta catgtgatag ttatcatggt atggccttca tgacaagatg 3480
gatgagaata tcaactgatag gatattagcc ttctttcata tctttatatt gaaatatggg 3540
ctttacttta atttgaaggt ctttcatgaa caataaaaga gagtagaagg actgtctgag 3600
aaggcaggag acatataaaa cagatgactg aaagactgac tagctcctgg aaagggaac 3660
atttggaaca tccagagtaa ggcaaatggg cttctaccag cacaacaaag agcctccagg 3720
tggaacatg gaagcaggtt atcagagaaa ataatgtgc aaattcctta tttacaatga 3780
ctcacttaac cccacaaaca tgtttactg ctgccttccc cagttgtcgc ttatgtactg 3840
ttgttacctt tcagttacat gcctttgatc ctaaaattct ctacttttgt tgccttatca 3900
gttctttgca atctgcctgt gggtatcagc acttaaagca caattttgaa ggggaaaaaa 3960
atgataatca ccttagtccc aaagaaataa tttgtcaaac tgccttatta gtattaaaaa 4020
cagacacact gaatgaagta gcatgatagc catatatcct actcagtatc attggccttt 4080
tatcaaatgg ggaactata cttttgtatt acatagtttt agaaatcgaa agttagagac 4140
tctttataag taatgtcaag gaacagtaat ttaaaaacaa agttctaaca aatatattgt 4200
ttgtttaatc acaatgcct caacttgtat ttgaataact aaataggaca tgtcttcctt 4260
ggagctgtgg gcattagtgc agaagcacta cctgcatctt aattttcaaa acttaagttt 4320
tattagcaaa tcctcttctc tgtaagactt agctatgaag tggatatatt tttccaaata 4380
tttttctgaa aacatttggt gttgtaactg cacaataaaa gtccagttgc aattaaaaaa 4440
aaaaaaaaa aaaaaaaa 4458

```

&lt;210&gt; 357

&lt;211&gt; 127

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 357

```

Met Pro Arg Trp Leu Leu Ser Leu Thr Phe Ala Gly Leu Phe Pro
 1           5           10          15
Leu Arg Arg Arg Gln Leu Leu Gly Ser Cys Gly Gly Arg Glu Gly Gly
 20          25          30
Gly Pro Asp Gln Pro Ala Gly Ser Pro Ala Pro Leu Arg Pro Pro Leu
 35          40          45
Pro Arg Thr Leu Arg Leu Arg Lys Tyr Arg Gly Asn Pro Leu Pro Pro
 50          55          60
Glu Val Arg Gly Ser Leu Pro Glu Gly Ala Pro Trp Ser Arg Ala Pro
 65          70          75          80
Leu Gly Gly His Leu Glu Ala Arg Cys Gly Pro Arg Thr Arg Glu Glu
 85          90          95
Arg Ala Ala Gly Ala Ala Ala Thr Ala Gly Gly Gly Ala Gly Ser Pro
100         105         110
Gly Ala Ala Glu Gly Arg Pro Val Leu His Met Leu Pro Leu Gly
115         120         125

```

<210> 358  
 <211> 1168  
 <212> DNA  
 <213> Homo sapiens

<400> 358  
 gtcgacccac gcgtccggcg atgcctcgct ggcttctgct ttcattgacc tttgcgggtc 60  
 tgttcccgcg gcggcgccgg cagctgcttg gtagttgcgg ggggcgtgag ggcggtggcc 120  
 cagaccaacc ggctggcagc ccagctccgc tccgcccgcg cctgcctcgg accctgcgcc 180  
 tgaggaagta tcgaggcaac cctctgccac ccgaagtctg tgggtcgctc ccagaggcg 240  
 cgccctggag ccgagcgccc ttgggcggcc atctggaggc caggtgcggg ccgcgaaccc 300  
 gcgaggagcg gcggcggggc gcggcggcga cggcaggagg aggggcccgg agcccgggcg 360  
 ccgccgaagg acgcccgcgc ctccacatgc tgcacttggt ctgagccggg cgccggcgag 420  
 aaggcgggcg cgctgccctg gcagctggac tgcactttgc ccccgcccgg cctcagctgc 480  
 cgcccgccca gacgccagca agccccctc ccacgacagg gctgctccgg gagcttcgga 540  
 gacccgcccc gggcctgagc gcaggctgcc tccgggaccc cacggctgtc cggacgtgcc 600  
 atgggcgcgc agctgccggg caacgtgttg tgtaagtga catctgggag gtaaacacta 660  
 cagctgaaga gtggtgaaag ggaacattga ttactgaagt gccctggaga gggaaagcac 720  
 tgggtcaacat cacatggaca aatttcattg ttttctaaag atggcctgga agtagtcttt 780  
 gccactgctt cctccacaaa cagctcttca taacatgggc tgcataaaat caaagcaaac 840  
 tttcccattt cctaccatat atgaaggatga gaagcagcat gagagtgaag aaccctttat 900  
 gccagaagag agatgtctac ctaggatggc ttctccagtt aatgtcaaag aggaagtga 960  
 ggaacctcca gggaccaata ttgtgatctt ggaatatgca caccgcctgt ctcaggatat 1020  
 cttgtgtgat gccttgacgc aatgggcatg caataacatc aagtaccatg acattccata 1080  
 cattgagagt gaggggcctt gaggtgtag gatgacaaca ctttgactgt ggaggtgcta 1140  
 gtttgaataa atgtgacaaa agcaaaaa 1168

<210> 359  
 <211> 4458  
 <212> DNA  
 <213> Homo sapiens

<400> 359  
 gtcgacccac gcgtccggcg atgcctcgct ggcttctgct ttcattgacc tttgcgggtc 60  
 tgttcccgcg gcggcgccgg cagctgcttg gtagttgcgg ggggcgtgag ggcggtggcc 120  
 cagaccaacc ggctggcagc ccagctccgc tccgcccgcg cctgcctcgg accctgcgcc 180  
 tgaggaagta tcgaggcaac cctctgccac ccgaagtctg tgggtcgctc ccagaggcg 240  
 cgccctggag ccgagcgccc ttgggcggcc atctggaggc caggtgcggg ccgcgaaccc 300  
 gcgaggagcg gcggcggggc gcggcggcga cggcaggagg aggggcccgg agcccgggcg 360  
 ccgccgaagg acgcccgcgc ctccacatgc tgcacttggt ctgagccggg cgccggcgag 420  
 aaggcgggcg cgctgccctg gcagctggac tgcactttgc ccccgcccgg cctcagctgc 480  
 cgcccgccca gacgccagca agccccctc ccacgacagg gctgctccgg gagcttcgga 540  
 gacccgcccc gggcctgagc gcaggctgcc tccgggaccc cacggctgtc cggacgtgcc 600  
 atgggcgcgc agctgccggg caacgtgttg tgtaagtga catctgggag gtaaacacta 660  
 cacgtgaaga gtggtgaaag ggaacattga ttactgaagt gccctggaga gggaaagcac 720  
 tgggtcaacat cacatggaca aatttcattg ttttctaaag atggcctgga agtagtcttt 780  
 gccactgctt cctccacaaa cagctcttca taacatgggc tgcataaaat caaagcaaac 840  
 tttcccattt cctaccatat atgaaggatga gaagcagcat gagagtgaag aaccctttat 900  
 gccagaagag agatgtctac ctaggatggc ttctccagtt aatgtcaaag aggaagtga 960  
 ggaacctcca gggaccaata ttgtgatctt ggaatatgca caccgcctgt ctcaggatat 1020  
 cttgtgtgat gccttgacgc aatgggcatg caataacatc aagtaccatg acattccata 1080  
 cattgagagt gaggggcctt gaggtgtag gatgacaaca ctttgactgt ggaggtgcta 1140  
 gtttgaataa atgtgacaaa agcaaaaa ggtgtgaaaa agtacaata actatctgga 1200  
 tttaaaaatg tgtctacgat aatgtcacta ttataagaac aactaggatg aaatgcattt 1260  
 taagtacttc tatgttaaca gcaatttctg tttagtctta gattttagtc atctgaaggg 1320  
 ctgaacagag gtccgtgtgac acccaataat cagctgaatg tcacagcact tcttccaaag 1380  
 taatggcatc accaaagaaa atgctaagga ataaaaactg ccccaaattc caatggttga 1440



```

agttttatcct ttaaaataaac aatTTTTgtt tatacccaaa aaaagtccag atatgaaaag 1500
ggctttttcta aaatttcttg gcgaggggaat ggcactcaaa tcatagtgat taacagtaag 1560
tcttggttgt ttgtcaagga tctctacttc ttgacacaaa tgaaccctgt ctttaataag 1620
ataagatat ttttttgt gatgagaagt gtaactacca ccttggaact cagggcccta 1680
actaattaca gctgttactg gacgactcag actttgtgcc taaagccatc ttagagataa 1740
cagtttatag aagccatgac attagtgttt attgcattga attaagccca gtgatataac 1800
tatacaagaa aacaagtatg ggtacctttt acaaagagca atccaataaa tcttaaaaaat 1860
aacagaaact tagtctgcaa ggtagaaagt ttcagtttta attctgtatt aagctttact 1920
atctcagagg tacagagggc tggaatatgg gcatttattt ccagtttttt cttgactagt 1980
aaggcggtca ccattaaaat agaccagatg ataatgcatg aagatttaca gttgtattgc 2040
aaaacggaaa agataaaaat gtcctttgag gagagtactc gttttctggg tttttgttat 2100
tttttagtgg taacacaaagc ctatagggca tttatagcca cctattatac tgtttccata 2160
agcctggcta ctttttaggg aagctatttt ttctctttca tttttactgt cacagcacat 2220
acacacacac ctttttgttt taaaggatta agtactgttt gaagatcagt ggtaacagaa 2280
aatttgggag ggagaagaag aaattaagac atgacttgtt agaaaattaa gacttcagtt 2340
tctagaatta tcttttcatc aagatttggt agacattgag tttaaatgga aaggaaatta 2400
tttaagcctg tgtatgttag atccacaata caccattggg attgaaatat aaaggttaaa 2460
aaaaaggctt atgacctctt taatgagata aatatgtatt tgtcttgtaa gcaggcagaa 2520
aatctacctc taattttaac actaatactt tgaaacccac aatcaaatag agtgaattct 2580
ccaagtatac taagcaagga aaacattatt tgaaatatgc catgttttcg ttgccttttg 2640
acacctcatc attcaactct aattttaccg agtcccgga tttgtactgt cccattgtac 2700
ttgcaatcta caatttatat aatagaaaaa caaccaaacc cattcataca aggatctgaa 2760
gttataaggt taagggcaga aagtttccca taagtataaa acatttccag gtcataga 2820
gtagtttagg ttgagtgaac aaagcctagg tgtggttgtt tttcattcat tttgcatctc 2880
acaccaagac atttttgctg caaggtcatc tgctgcttaa aatgtacaat taggtatata 2940
aaataagtac aatggtgaaa acacaaagcc aggtaaagca gcatgcccc aataattttt 3000
cagtatacat agggacagac aagttagttt tggttgtatc taaatatttt aatttcaggt 3060
tcttctgtg cctggggcca ctatttccca ggggtgtgac agagatgcct gccagatcca 3120
tatcaactag aagtcgtatt tctgttgctg ccttctctca gcaactatgy cagtatactt 3180
ttatcaccaa gcaccactcc cttgtccctg aatcacattt taatagagta caatatcttc 3240
tgtacaatat ttctgaaaca cttatgtctg aaatatatgc tgtattgtat gtttaacccat 3300
gacatatatg aactacaagg cttgcataat cagttagcta gtggataaat caagacagga 3360
gcaaatyggg gaaagatgaa taaacaaatg aaaaaagatg aataaatgaa taagagagat 3420
gaataaacia atttacatta catgtgatag ttatcatggg atggccttca tgacaagatg 3480
gatgagaata tcactgatag gatattagcc ttctttcata tctttatatt gaaatatggg 3540
ctttacttca atttgaaggt ctttcatgaa caataaaaaga gagtagaagg actgtctgag 3600
aaggcaggag acatataaaa cagatgactg aaagactgac tagctcctgg aaagggaac 3660
atttggaaaca tccagagtaa ggcaaaggg cttctaccag cacaacaaag agcctccagg 3720
tggaacatg gaagcagggt atcagagaaa ataaatgtgc aaattcctta tttacaatga 3780
ctcacttaac ccacaaaca tgtttcactg ctgccttccc cagttgtcgc ttatgtactg 3840
ttgttacctt tcagttacat gcctttgatc ctaaaattct ctacttttgt tgccttatca 3900
gttctttgca atctgcctgt ggttatcagc acttaaagca caattttgaa ggggaaaaaa 3960
atgataatca ccttagtccc aaagaaataa tttgtcaaac tgccttatta gtattaaaaa 4020
cagacacact gaatgaagta gcatgatacg catatatcct actcagtatc attggccttt 4080
tatcaaagtg ggaaactata cttttgtatt acatagtttt agaaatcgaa agttagagac 4140
tctttataag taatgtcaag gaacagtaat ttaaaaaaca agttctaaca aatatattgt 4200
ttgcttaate acaatgccct caacttgat ttgaataact aaataggaca tgtcttcctt 4260
ggagctgtgg gcattagtgc agaagcacta cctgcatctt aattttcaaa acttaagttt 4320
tattagcaaa tctcttctc tgtaagactt agctatgaag tggatatatt tttccaaata 4380
tttttctgaa aacatttggt gttgtaactg cacaataaaa gtccagttgc aattaaaaaa 4440
aaaaaaaaa aaaaaaaa
4458

```

&lt;210&gt; 360

&lt;211&gt; 583

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 360

368

```

cccctgcacc ccgcccggca tagcaccatg cctgcttgtc gcctaggccc gctagccgcc 60
gccctcctcc tcagcctgct gctgttcggc ttcaccctag tctcaggcac aggagcagag 120
aagactggcg tgtgccccga gctccagggt gaccagaact gcacgcaaga gtgctgtctcg 180
gacagcgaat gcgcgcgaca cctcaagtgc tgcagcgcg gctgtgccac cttctgcctt 240
ctctgccccca atgataagga gggttcctgc ccccaggtga acattaactt tccccagctc 300
ggcctctgtc gggaccagtg ccaggtggac acgcagtgtc ctggccagat gaaatgctgc 360
cgcaatggct gtgggaaggt gtcctgtgtc actcccaatt tctgaggtcc agccaccacc 420
aggctgagca gtgaggagag aaagtctctg cctggccctg catctgggtc cagcccacct 480
gccctcccct ttttcgggac tctgtattcc ctcttggggg gaccacagct tctccctttc 540
ccaaccaata aagtaaccac tttcagcaaa aaaaaaaaaa aaa 583

```

&lt;210&gt; 361

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 361

```

Met Pro Ala Cys Arg Leu Gly Pro Leu Ala Ala Ala Leu Leu Leu Ser
1          5          10          15
Leu Leu Leu Phe Gly Phe Thr Leu Val Ser Gly Thr Gly Ala Glu Lys
20          25          30
Thr Gly Val Cys Pro Glu Leu Gln Ala Asp Gln Asn Cys Thr Gln Glu
35          40          45
Cys Val Ser Asp Ser Glu Cys Ala Asp Asn Leu Lys Cys Cys Ser Ala
50          55          60
Gly Cys Ala Thr Phe Cys Leu Leu Cys Pro Asn Asp Lys Glu Gly Ser
65          70          75          80
Cys Pro Gln Val Asn Ile Asn Phe Pro Gln Leu Gly Leu Cys Arg Asp
85          90          95
Gln Cys Gln Val Asp Thr Gln Cys Pro Gly Gln Met Lys Cys Cys Arg
100         105         110
Asn Gly Cys Gly Lys Val Ser Cys Val Thr Pro Asn Phe
115         120         125

```

&lt;210&gt; 362

&lt;211&gt; 3310

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 362

```

ggcgggcgac caaagcgcct gaggaccggc aacatgggtc ggtcggggaa taaggcagct 60
gttggtgctgt gtatggacgt gggctttacc atgagtaact ccattcctgg tatagaatcc 120
ccatttgaac aagcaaagaa ggtgataacc atgtttgtac agcgacaggt gtttgctgag 180
aacaaggatg agattgcttt agtcctgttt ggtacagatg gcactgacaa tcccccttct 240
ggtggggatc agtatcagaa catcacagtg cacagacatc tgatgctacc agattttgat 300
ttgctggagg acattgaaag caaaatccaa ccagggtctc aacaggctga cttcctggat 360
gcactaatcg tgagcatgga tgtgattcaa catgaaacaa taggaaagaa gtttgagaag 420
aggcatattg aaatatccac tgacctcagc agccgattca gcaaaagtca gctggatatt 480
ataattcata gcttgaagaa atgtgacatc tccctgcaat tcttcttgcc tttctcactt 540
ggcaaggaag atggaagtgg ggacagagga gatggcccct ttcgcttagg tggccatggg 600
ccttcctttc cactaaaagg aattaccgaa cagcaaaaag aaggtcttga gatagtgaag 660
atggtgatga tatctttaga aggtgaagat gggttggatg aaatttattc attcagtga 720
agtctgagaa aactgtgcgt cttcaagaaa attgagaggc attccattca ctggccctgc 780
cgactgacca ttggctccaa tttgtctata aggattgcag cctataaatc gattctacag 840
gagagagtta aaaagacttg gacagttgtg gatgcaaaaa cctaataaaa agaagatata 900
caaaaagaaa cagttttattg cttaaattgat gatgatgaaa ctgaagtgtt aaaagaggat 960
attattcaag ggttcgcta tggaagtgat atagttcctt tctctaaggt ggatgaggaa 1020

```

369

```

caaatgaaat ataaatcgga ggggaagtgc ttctctgttt tgggattttg taaatcttct 1080
caggttcaga gaagatttctt catgggaaat caagttctaa aggtctttgc agcaagagat 1140
gatgaggcag ctgcagttgc actttctctc ctgattctatg ctttgatga cttagacatg 1200
gtggccatag ttcatatgc ttatgacaaa agagctaatac ctcaagtcgg cgtggctttt 1260
cctcatatca agcataaacta tgagtgttta gtgtatgtgc agctgccttt catggaagac 1320
ttgcggcaat acatgttttc atccttgaaa aacagtaaga aatatgctcc caccgaggca 1380
cagttgaatg ctgttgatgc tttgattgac tccatgagct tggcaaagaa agatgagaag 1440
acagacaccc ttgaagactt gttccaacc accaaaatcc caaatcctcg atttcagaga 1500
ttatttcagt gtctgctgca cagagcttta catccccggg agcctctacc cccaattcag 1560
cagcatattt ggaatatgct gaatcctccc gctgaggtga caacaaaaag tcagattcct 1620
ctctctaaaa taaagaccct ttttctctg attgaagcca agaaaaagga tcaagtgact 1680
gctcaggaaa ttttccaaga caaccatgaa gatggaccta cagctaaaaa attaaagact 1740
gagcaagggg gagcccactt cagcgtctcc agtctggctg aaggcagtg cactctgtt 1800
ggaaagtgtga atcctgctga aaacttcogt gttctagtga aacagaagaa ggccagcttt 1860
gaggaagcga gtaaccagct cataaatcac atcgaacagt ttttggtac taatgaaaca 1920
ccgtatttta tgaagagcat agactgcac cgagccttcc gggaagaagc cattaagttt 1980
tcagaagagc agcgttttaa caacttctg aaagccctc aagagaaagt ggaaattaaa 2040
caattaaatc atttctggga aattgttgtc caggatggaa ttactctgat caccaaagag 2100
gaagcctctg gaagtctctg cacagctgag gaagccaaaa agtttctggc ccccaaagac 2160
aaaccaagtg gagacacagc agctgtattt gaagaaggtg gtgatgtgga cgatttattg 2220
gacatgatal aggtcgtgga tgtatgggga atctaagaga gctgccatcg ctgtgatgct 2280
gggagttcta acaaaacaag ttggatgagg ccattcaagg ggagccaaaa tctcaagaaa 2340
ttcccagcag gttacctgga ggcgatcat ctaattctct gtggaatgaa tacacacata 2400
tatattacaa gggataattt agaccccata caagtttata aagagtcatt gttattttct 2460
ggttggtgta ttattttttc tgtgttctta ctgactcttg tatattacat acatgctttg 2520
aagtttctgg aaagtagatc ttttcttgac ctagtatatc agtgacagtt gcagcccttg 2580
tgatgtgatt agtgtctcat gtggaacctt ggcaggttta ttgatgagtt tcttaaccct 2640
ttccagagtc ctcttttgcc tgatcctcca acagctgtca caacttgtgt tgagcaagca 2700
gtagcatttg ctctctccca acaagcagct ggggttaggaa aacctgggt aaggacggag 2760
tcacttctct ttttagttga ggcttctag ttaccacatt actctgcctc tgtatatagg 2820
tggttttctt taagtgggtt gggaagggga gcacaatttc ccttcatact ccttttaagc 2880
agtgagttat ggtggtggtc tcatgaagaa aagacctttt ggcccaatct ctgccatata 2940
agtgaaacct tagaaactca aaaactgaga aatttacttc agtagttaga attatatcac 3000
ttcactgttc tctacttgca agcctcaaag agagaaagt tctgttatatt aaaacactta 3060
ggtaactttt cgggtctttcc catttctacc taagtcagct ttcactcttg tggtgggtgt 3120
ctcctttact aaataagaaa ataacaaagc ccttattctc tttttttctt gtcctcatte 3180
ttgccttgag ttccagttcc tctttggtgt acagacttct tggtaaccag tcacctctgt 3240
cttcagcacc ctcataagtc gtcactaata cacagttttg tacatgtaac attaaaggca 3300
taaatgactc                                     3310

```

&lt;210&gt; 363

&lt;211&gt; 732

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 363

```

Met Val Arg Ser Gly Asn Lys Ala Ala Val Val Leu Cys Met Asp Val
1      5      10      15
Gly Phe Thr Met Ser Asn Ser Ile Pro Gly Ile Glu Ser Pro Phe Glu
20      25      30
Gln Ala Lys Lys Val Ile Thr Met Phe Val Gln Arg Gln Val Phe Ala
35      40      45
Glu Asn Lys Asp Glu Ile Ala Leu Val Leu Phe Gly Thr Asp Gly Thr
50      55      60
Asp Asn Pro Leu Ser Gly Gly Asp Gln Tyr Gln Asn Ile Thr Val His
65      70      75      80
Arg His Leu Met Leu Pro Asp Phe Asp Leu Leu Glu Asp Ile Glu Ser
85      90      95

```

370

Lys Ile Gln Pro Gly Ser Gln Gln Ala Asp Phe Leu Asp Ala Leu Ile  
 100 105 110  
 Val Ser Met Asp Val Ile Gln His Glu Thr Ile Gly Lys Lys Phe Glu  
 115 120 125  
 Lys Arg His Ile Glu Ile Phe Thr Asp Leu Ser Ser Arg Phe Ser Lys  
 130 135 140  
 Ser Gln Leu Asp Ile Ile Ile His Ser Leu Lys Lys Cys Asp Ile Ser  
 145 150 155 160  
 Leu Gln Phe Phe Leu Pro Phe Ser Leu Gly Lys Glu Asp Gly Ser Gly  
 165 170 175  
 Asp Arg Gly Asp Gly Pro Phe Arg Leu Gly Gly His Gly Pro Ser Phe  
 180 185 190  
 Pro Leu Lys Gly Ile Thr Glu Gln Gln Lys Glu Gly Leu Glu Ile Val  
 195 200 205  
 Lys Met Val Met Ile Ser Leu Glu Gly Glu Asp Gly Leu Asp Glu Ile  
 210 215 220  
 Tyr Ser Phe Ser Glu Ser Leu Arg Lys Leu Cys Val Phe Lys Lys Ile  
 225 230 235 240  
 Glu Arg His Ser Ile His Trp Pro Cys Arg Leu Thr Ile Gly Ser Asn  
 245 250 255  
 Leu Ser Ile Arg Ile Ala Ala Tyr Lys Ser Ile Leu Gln Glu Arg Val  
 260 265 270  
 Lys Lys Thr Trp Thr Val Val Asp Ala Lys Thr Leu Lys Lys Glu Asp  
 275 280 285  
 Ile Gln Lys Glu Thr Val Tyr Cys Leu Asn Asp Asp Asp Glu Thr Glu  
 290 295 300  
 Val Leu Lys Glu Asp Ile Ile Gln Gly Phe Arg Tyr Gly Ser Asp Ile  
 305 310 315 320  
 Val Pro Phe Ser Lys Val Asp Glu Glu Gln Met Lys Tyr Lys Ser Glu  
 325 330 335  
 Gly Lys Cys Phe Ser Val Leu Gly Phe Cys Lys Ser Ser Gln Val Gln  
 340 345 350  
 Arg Arg Phe Phe Met Gly Asn Gln Val Leu Lys Val Phe Ala Ala Arg  
 355 360 365  
 Asp Asp Glu Ala Ala Ala Val Ala Leu Ser Ser Leu Ile His Ala Leu  
 370 375 380  
 Asp Asp Leu Asp Met Val Ala Ile Val Arg Tyr Ala Tyr Asp Lys Arg  
 385 390 395 400  
 Ala Asn Pro Gln Val Gly Val Ala Phe Pro His Ile Lys His Asn Tyr  
 405 410 415  
 Glu Cys Leu Val Tyr Val Gln Leu Pro Phe Met Glu Asp Leu Arg Gln  
 420 425 430  
 Tyr Met Phe Ser Ser Leu Lys Asn Ser Lys Lys Tyr Ala Pro Thr Glu  
 435 440 445  
 Ala Gln Leu Asn Ala Val Asp Ala Leu Ile Asp Ser Met Ser Leu Ala  
 450 455 460  
 Lys Lys Asp Glu Lys Thr Asp Thr Leu Glu Asp Leu Phe Pro Thr Thr  
 465 470 475 480  
 Lys Ile Pro Asn Pro Arg Phe Gln Arg Leu Phe Gln Cys Leu Leu His  
 485 490 495  
 Arg Ala Leu His Pro Arg Glu Pro Leu Pro Pro Ile Gln Gln His Ile  
 500 505 510  
 Trp Asn Met Leu Asn Pro Pro Ala Glu Val Thr Thr Lys Ser Gln Ile  
 515 520 525  
 Pro Leu Ser Lys Ile Lys Thr Leu Phe Pro Leu Ile Glu Ala Lys Lys  
 530 535 540  
 Lys Asp Gln Val Thr Ala Gln Glu Ile Phe Gln Asp Asn His Glu Asp  
 545 550 555 560

371

Gly	Pro	Thr	Ala	Lys	Lys	Leu	Lys	Thr	Glu	Gln	Gly	Gly	Ala	His	Phe
				565					570					575	
Ser	Val	Ser	Ser	Leu	Ala	Glu	Gly	Ser	Val	Thr	Ser	Val	Gly	Ser	Val
			580					585					590		
Asn	Pro	Ala	Glu	Asn	Phe	Arg	Val	Leu	Val	Lys	Gln	Lys	Lys	Ala	Ser
		595					600					605			
Phe	Glu	Glu	Ala	Ser	Asn	Gln	Leu	Ile	Asn	His	Ile	Glu	Gln	Phe	Leu
	610					615					620				
Asp	Thr	Asn	Glu	Thr	Pro	Tyr	Phe	Met	Lys	Ser	Ile	Asp	Cys	Ile	Arg
625					630					635				640	
Ala	Phe	Arg	Glu	Glu	Ala	Ile	Lys	Phe	Ser	Glu	Glu	Gln	Arg	Phe	Asn
			645						650					655	
Asn	Phe	Leu	Lys	Ala	Leu	Gln	Glu	Lys	Val	Glu	Ile	Lys	Gln	Leu	Asn
			660					665					670		
His	Phe	Trp	Glu	Ile	Val	Val	Gln	Asp	Gly	Ile	Thr	Leu	Ile	Thr	Lys
		675					680					685			
Glu	Glu	Ala	Ser	Gly	Ser	Ser	Val	Thr	Ala	Glu	Glu	Ala	Lys	Lys	Phe
	690					695					700				
Leu	Ala	Pro	Lys	Asp	Lys	Pro	Ser	Gly	Asp	Thr	Ala	Ala	Val	Phe	Glu
705					710					715					720
Glu	Gly	Gly	Asp	Val	Asp	Asp	Leu	Leu	Asp	Met	Ile				
				725					730						

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
19 September 2002 (19.09.2002)

PCT

(10) International Publication Number  
**WO 02/071928 A3**

(51) International Patent Classification<sup>7</sup>: **C07H 21/04**,  
21/02

(21) International Application Number: **PCT/US02/07826**

(22) International Filing Date: **14 March 2002 (14.03.2002)**

(25) Filing Language: **English**

(26) Publication Language: **English**

(30) Priority Data:

60/276,025	14 March 2001 (14.03.2001)	US
60/276,026	14 March 2001 (14.03.2001)	US
60/311,732	10 August 2001 (10.08.2001)	US
60/323,580	19 September 2001 (19.09.2001)	US
60/325,149	26 September 2001 (26.09.2001)	US
60/324,967	26 September 2001 (26.09.2001)	US
60/325,102	26 September 2001 (26.09.2001)	US

(71) Applicant (for all designated States except US): **MILLENNIUM PHARMACEUTICALS, INC.** [US/US]; 75 Sidney Street, Cambridge, MA 02139 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **MONAHAN, John**, E. [US/US]; 942 West Street, Walpole, MA 02081 (US). **GANNAVARAPU, Manjula** [IN/US]; 10 Windemere Drive, Acton, MA 01720 (US). **HOERSCH, Sebastian** [US/US]; 127 Brattle Street, Arlington, MA 02474 (US). **KAMATKAR, Shubhangi** [US/US]; 655 Saw Mill Brook Parkway, Apt. 1, Newton, MA 02459 (US). **KOVATIS, Steven, G.** [US/US]; 94 Aldrich Road, Wilmington, MA 01887 (US). **MEYERS, Rachel, E.** [US/US]; 115 Devonshire Road, Newton, MA 02468 (US). **MORRISSEY, Michael, P.** [US/US]; 140 Kenrick Street, Apt. 32, Brighton, MA 02135 (US). **OLANDT, Peter, J.** [US/US]; 29 Florence Street, Newton, MA 02459 (US). **SEN, Ami** [US/US]; 66 Dinsmore Avenue, Apt. 507, Framingham,

MA 01702 (US). **VEIBY, Petter, Ole** [US/US]; 16 Nipmuck Drive, Westborough, MA 01581 (US). **MILLS, Gordon, B.** [CA/US]; 4124 Amherst Street, Houston, TX 77005 (US). **BAST, Robert, C., Jr.** [US/US]; 14 Memorial Point Lane, Houston, TX 77024 (US). **LU, Karen** [US/US]; 4127 Amherst Street, Houston, TX 77005 (US). **SCHMANDT, Rosemarie, E.** [CA/US]; 7300 Brompton Road, Apt. 5512, Houston, TX 77025 (US). **ZHAO, Xumei** [US/US]; 6 Wildwood Lane, Burlington, MA 01803 (US). **GLATT, Karen** [US/US]; 17 Beacon Street, Natick, MA 01760 (US).

(74) Agents: **SMITH, DeAnn, F.** et al.; Lahive & Cockfield, LLP, 28 State Street, Boston, MA 02109 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— with international search report

(88) Date of publication of the international search report:  
13 March 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: **NUCLEIC ACID MOLECULES AND PROTEINS FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF OVARIAN CANCER**

(57) Abstract: The invention relates to newly discovered nucleic acid molecules and proteins associated with ovarian cancer. Compositions, kits, and methods for detecting, characterizing, preventing, and treating human ovarian cancers are provided.



WO 02/071928 A3

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/07826

**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(7) :C07H 21/04, 21/02

US CL :536/23.1, 24.31, 24.33

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1, 24.31, 24.33

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

WEST, DIALOG ONESEARCH ovary, ovarian, tumor, cancer, expression, level, marker, RNA, DNA, polynucleotide, oligonucleotide,

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 5,976,799 A (O'BRIEN et al) 02 November 1999, column 2, lines 27-47.	1
Y	US 5,709,999 A (SHATTUCK-EIDENS et al.) 20 January 1998, column 8, lines 38-67; column 15, lines 52-56; column 69, lines 26-30.	1
Y	US 6,087,125 A (BANDMAN et al) 11 July 2000, column 3, lines 15-25.	1
Y	WO 96/05308 A1 (MYRIAD GENTICS, INC) 22 February 1996, page 3, lines 9-17; page 12, lines 2-11; page 21, lines 24-25	1

☐ Further documents are listed in the continuation of Box C.
 ☐ See patent family annex.

* Special categories of cited documents:	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E" earlier document published on or after the international filing date	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Z" document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means	
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

11 JULY 2002

Date of mailing of the international search report

16 SEP 2002

 Name and mailing address of the ISA/US  
 Commissioner of Patents and Trademarks  
 Box PCT  
 Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

STEPHANIE ZITOMER

Telephone No. (703) 308-0196

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/07826

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
1, SEQ ID NO:1

### Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.  
☐ No protest accompanied the payment of additional search fees.



**BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING**

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Groups 1-198, claim(s)1-198, each drawn to a different method of detecting ovarian cancer.

The inventions listed as Groups 1-198 do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Claim 1 comprises 198 different methods each defined by a different nucleotide sequence each of which constitutes a different special technical feature and therefore a different invention. Thus, there is no single special technical feature in claim 1 nor a single inventive group. PCT Rule 13 permits a product, process of making the product and process of using the product in an inventive group but does not permit multiple methods of the same type in an inventive group